Technical Report: Review of Quantitative Risk Assessment of foodborne norovirus transmission

Assessment and authorship information

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Authors	Iulia Gherman; Darren Holland; Robin Clifford; Nazmina Mahmoudzadeh; Frederique Uy; Amie Adkin; Bobby Kainth; Paul Cook; Andrew Day; Anthony Wilson
NoVAS risk assessment	Original author: Paul Hunter developed as part of the FSA-funded Norovirus Attribution Survey (NoVAS) project (reference FS101040)
Expert contributors	

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Reviewer type	Name of reviewer/ SAC	Risk assessment version & date distributed	Date comments addressed
Internal			
Internal expert peer reviewer	**Darren Holland**	**v0.9, 2019-09-20**	**2019-09-22 (v1.0)**
Internal expert peer reviewer	**Amie Adkin**	**v1.0, 2019-10-04**	**2019-10-11 (v1.1)**
Science Lead	**Anthony Wilson**		
Policy Lead	**Ian Woods**		
External			
NoVAS modelling lead	**Paul Hunter**	**v1.1, 2019-10-16**	**2019-10-29 (v1.2)**
Scientific Advisory Committee	**Gary Barker**	**V1.2, 2020-01-05**	**2020-01-20 (V1.3)**

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1. Executive Summary

A Quantitative Microbiological Risk Assessment (QMRA) was developed by Paul Hunter as part of the FSA-funded "Norovirus Attribution Study" (NoVAS) to investigate the relative contribution of five pathways (oysters, lettuce, raspberries, meals eaten out and takeaways) to the total number of symptomatic foodborne norovirus infections in the UK. The work was parameterised by new UK data collected within the project and that available in the literature. The risk assessment estimated a significant burden of norovirus disease transmitted via those food pathways based on a prevalence survey of viable virus found at retail. The work which was developed over five years was externally peer reviewed and accepted by FSA in September 2019.

To better understand the impact of risk assessment assumptions and to review the impact of using alternative assumptions and other data sources available in the literature an internal FSA review has been completed. Additional refinement of the way immunity was incorporated into the risk assessment was recommended and it was determined whether commissioning further research in this area would be justified. The key questions to be addressed by the internal FSA review were as follows:

- Are the parameters and assumptions used in the risk assessment up to date, appropriate and adequately referenced?
- Is the risk assessment approach taken appropriate to use the outputs for further analysis or decision-making?
- Can any control measures be varied in the assessment and, if so, what is the impact of varying the control measured on the final output?

As a result of the review, additional data held by the FSA and from the literature was used to revise and update the norovirus food pathway risk assessment for the UK. This technical report details the review of the work completed within the NoVAS project and the revised risk assessment.

Key results

The revised assessment estimates a mean rate of 7.21 symptomatic infections per 1000 person-years in intrinsically susceptible individuals, although with significant uncertainty (5^{th} and 95^{th} percentile values of 0.212 and 27.0 respectively). The mean value would translate to an estimated 383,000 cases in the population as a whole per year, based on 2018 population data.

Most of the reduction relative to the estimate in the original project report is attributable to our modifications to the immunity component. The revisions to other parameter estimates make relatively little difference to the estimated total number of symptomatic infections, although do increase the estimated proportion of cases due to lettuce.

Key Assumptions

The assessment assumes that all norovirus genotypes and strains are the same. This is consistent with EFSA recommendations given the number of data gaps relating to specific genotypes and strains, but some variability is believed to exist.

Similarly, we assume that so-called nonsecretor individuals are resistant to both symptomatic and asymptomatic norovirus infection. This is true for most genotypes and

strains, including the dominant GII.4 genotype, but such individuals may be susceptible to some strains (such as GII.2 SMV).

The assessment assumes that asymptomatic infections are one possible outcome when an infectious exposure is resisted as a result of acquired immunity. This was considered appropriate given currently available knowledge of determinants of the clinical outcome of infection.

Seasonality was not considered. Data gaps exist for seasonal variation in multiple parameters so it is not possible to incorporate this at present.

Due to a lack of available data, processes that might result in cross-contamination when preparing food for catered and takeaway consumption were represented in a simplified manner.

Key uncertainties and data gaps

Sensitivity analysis suggested that estimated risk remained relatively sensitive to several parameters estimated directly from data collected during the NoVAS study, including the load of virus on the hand of individuals involved in food preparation and the level of contamination of lettuce and raspberries, although more accurate estimation of these values than was achieved via NoVAS seems unlikely to be cost-effective (with the possible exception of estimation of contamination of prewashed lettuce and other leafy greens, since the NoVAS estimate surveyed loose whole-head lettuce only). The estimated risk was also relatively sensitive to several parameters estimated from other FSA datasets and the scientific literature, including the frequency of oyster consumption, the number of times takeaway food is touched during preparation, and the probability that takeaway food is heated after touching. In the view of the authors these are all likely to represent relatively achievable and cost-effective targets for future research.

Scenario analysis suggests that significant new evidence regarding the duration of acquired immunity, the infectivity of norovirus particles, the frequency of produce washing in domestic environments or the rate of asymptomatic carriage in the population would all have the potential to substantially alter the mean disease burden estimates generated by the assessment. Similarly, changes to the likelihood of domestic produce-washing would also substantially change the mean disease burden estimate, suggesting that this could be a useful target for future social science projects or information campaigns, and of these four areas a study to improve estimates of domestic produce-washing frequency is felt to be the most likely to represent a relatively achievable and cost-effective target for future research.

Although more difficult to address in a formal sensitivity analysis, we note that the outcomes may also be sensitive to wider uncertainty around the structure chosen for the modelling approach.

2. Introduction

2.1 Summary of the original NoVAS risk assessment framework

The original NoVAS risk assessment used data generated during the NoVAS project, as well as information from the literature and public surveys, to construct a risk assessment

to estimate the number of symptomatic norovirus infections for a random individual via a number of food pathways. The risk assessment was implemented as two spreadsheet models (exposure module and risk module) which included uncertain and variable parameters where quantified, which were simulated using the software package @Risk (C Palisade) Version 7.0, an add-on package within Microsoft Excel (C Microsoft). The risk assessment framework is provided in Appendix 1.

The number of symptomatic foodborne infections was modelled on an individual level and considered the probability of the individual chosen at random being intrinsically susceptible to infection, as well as the probability of acquired immunity due to previous infections. Foodborne infections in the risk assessment were attributed to the consumption of oysters, lettuce, raspberries, catered meals and takeaway meals. These pathways were originally chosen on the basis of an analysis of 2,922 US norovirus outbreaks by Hall et al. (2012), which identified infected food handlers, leafy vegetables, fruits/nuts and molluscs as the most important contributors.

The potential norovirus dose was calculated for a single portion of each of these five foods. As not all norovirus particles detected are capable of causing infection, viability was considered. The proportion of viable particles for norovirus transferred onto catered/takeaway food due to faecal contamination of hands was assumed to be 100%; for all other cases, the proportion of viable particles was sampled from a truncated log-normal distribution fitted to the data available in 2017 from a study led by Cefas as part of the NoVAS project; the final dataset was described in Lowther et al. (2019). The number of oyster/lettuce/raspberry/takeaway/catered meals eaten and the portion size were taken from the NDNS survey available in 2017 (years 1-6 of the study).

The risk assessment first calculated the dose of viable norovirus particles per meal for each of the five exposure pathways in the exposure module. Data were available for the amount of norovirus per unit weight in oyster glands, and for lettuce and raspberries from surveys implemented during the project. These data were fitted to a log-normal distribution for oysters and a log-linear model for lettuce and raspberries. A Bernoulli distribution, based on data of norovirus prevalence in oysters at retail, was used to determine whether simulated individual oysters were contaminated. However, in the case of lettuce and raspberries, there was no initial check to determine whether the produce is contaminated or not, with the potential for norovirus gene copies per gram to be less than 1.

The oyster pathway included the concentration of norovirus particles present in the oyster digestive gland. The proportion of the whole oyster that is the digestive gland was drawn from a shifted gamma distribution, fitted to the data generated by Cefas as part of the NoVAS project. The final dose per oyster meal was a multiplication of the norovirus concentration in the gland with the proportion of the oyster comprised of the digestive gland, the amount eaten in one sitting in grams (drawn from a truncated normal distribution), and the proportion of norovirus particles that were considered viable.

In the case of raspberry and lettuce, there is a probability that such foods will be washed before eating, based on data of prevalence of produce-washing behaviours across Melbourne, Australia (Barker et al. 2013). If the product was washed, the

proportion of norovirus removed was sampled from a pert distribution fitted to data from the Barker et al. (2013) study; whereas if the product was not washed, the initial norovirus concentration was unchanged. The final dose per raspberry or lettuce meal was estimated from a multiplication of the norovirus concentration with the amount eaten in grams (modelled for each as a truncated normal distribution) and the percentage of viable particles.

When simulating takeaway/catered meals the number of times food was touched was also taken into account. It was assumed that each time the food was handled, there was a probability that norovirus was transferred from the food handler to the food. Data for norovirus counts on food handlers' hands were taken from a survey carried out as part of the NoVAS project and fitted to a log-linear distribution. The number of times a given meal was touched during its preparation was sampled from a Poisson distribution with a mean based on observations of sandwich preparers in a kitchen reported by Stals et al (2015), with the amount of virus transferred during each touch based on the same study. The number of times a meal was touched was capped at 20 because the array used to store the samples values needed to have a finite size. The amount of viable norovirus transferred during all handling events was then summed to give a total dose per takeaway/catered meal.

The norovirus dose for a single serving of each of these five foods was simulated 10,000 times in the exposure module. National Dietary and Nutrition Survey (NDNS) data was then used in the risk module to estimate the number of oyster/ lettuce/ raspberry/ catered/ takeaway meals eaten in a year. Each of these 10,000 iterations were then sampled to estimate the norovirus dose ingested each time one of these foods was consumed. The dose-response was calculated on a daily basis using an Approximate Beta Poisson model described by van Abel et al. (2017). The daily probability of infection, after accounting for loss of immunity and the probability of being infected by a novel norovirus strain, was then summed to calculate the annual number of infections with foodborne norovirus. Immunity and intrinsic susceptibility of the UK population were then factored in to derive the final figures for the number of symptomatic foodborne norovirus infections per 1000 person years, assuming that each year represented the same probability of illness.

2.2 Scope of the Internal FSA review

The specific questions to be addressed by the internal FSA review were:

- Is the risk assessment approach taken appropriate to use the outputs for further analysis or decision-making? Are the food pathways that have been modelled appropriate for the UK and what is the impact of assumptions made, for example, in the immunity component and handling component of the model.
- Are the parameters used in the risk assessment up to date, appropriate and adequately referenced?
- Can any control measures be varied in the assessment and, if so, what is the impact of varying the control measured on the final output?

A significant percentage of food consumed in the UK is prepared in advance of retail or available in catered establishments. Therefore, the QMRA included both domestic kitchen food pathways, catering establishments and take away foods.

The UK is a net importer of certain food products and the percentage of imported versus domestically produced varies between seasons and between food product types. The prevalence of norovirus and level of contamination in both imported and domestically produced goods is poorly understood. As a key data gap, the NoVAS project was funded to experimentally test the prevalence of norovirus and level of contamination found at UK retail. Currently, there are insufficient data to stratify between domestically produced and imported products, or to assess the seasonal consumption of food products.

3. Review of NoVAS Risk Assessment pathways and immunity

3.1 Review of food transmission pathways

The purpose of the risk assessment was to compare the relative importance of multiple food-borne pathways in addition to improving the UK estimate of total norovirus from food burden. The assessment is therefore more complex than other quantitative microbiological risk assessment which may focus on a single pathogen-pathway combination. To ensure that the limited resources available were allocated efficiently, the first step of the project was to identify which risk pathways were likely to be sufficiently important to model quantitatively. The contractors therefore performed a systematic literature review of outbreaks attributed to norovirus between January 2003 and July 2017; this constituted work package 1 (WP1) of the NoVAS project.

At the start of the FSA internal review of the assessment approach, this step was revisited and the following criteria were considered when deciding on whether a norovirus-food pathway should be included or excluded from the risk assessment:

- The number of norovirus outbreaks associated with the food both within the UK and Europe. Few or no outbreak data or data linked to infected food handlers would suggest the food pathway should not be included.
- UK consumption data for specific foods which have been reported to be associated with norovirus infection.
- For products of animal origin, whether the animal host is considered a reservoir for norovirus.
- If there is UK data on norovirus contamination (prevalence and levels) within these foods.
- Whether the production methods used would represent a risk factor for the food becoming contaminated with norovirus.
- Foods that are likely to undergo further processing and cooking which would reduce or eliminate norovirus were excluded.
- Composite or mixed foods were excluded as it would prove too difficult to pinpoint which food ingredient(s) were contaminated with norovirus.

The following sections detail the pathways that were included in the original NoVAS QMRA and rationale for their retention in the revised norovirus risk assessment.

3.1.1 Oysters

Bivalve molluscs are a well-documented food vehicle for norovirus as they are able to accumulate and concentrate the virus within their digestive tract during filter-feeding in

water contaminated with human sewage. Once the virus has attached to the digestive tract, it is difficult to remove and depuration[1] is only partially effective as a decontamination step. The risk of foodborne norovirus infection is also higher for oysters specifically as they are routinely consumed raw.

UK outbreak data from 1992-2016, which can be found in Appendix 2, attributed 54 outbreaks of norovirus to oysters. RASFF data between 1979 and 2017 and also details 51 alerts being issued for norovirus being detected in oysters. Surveillance of UK oysters sampled at harvesting sites (pre-depuration) and at retail, collected as part of the NoVAS project, indicates that these oysters frequently contain high levels of norovirus RNA. EFSA have published a scientific report on analysis of the European baseline survey of norovirus in oysters which estimated the prevalence of norovirus RNA in oysters from production areas and dispatch centres to be 34.5% (CI: 30.1-39.1%) and 10.8% (CI: 8.2-14.4%) respectively. The mean norovirus levels from batches of oysters from production areas was 337 genome copies/g and 168 copies/g from dispatch centres. The consumption of oysters in the UK is rare compared to many food products; Table 1.6 of the Wave 5 Food and You report states that only 1.4% of respondents consume raw oysters at least once a month.

Other types of bivalve molluscs, including mussels, cockles, clams and scallops, are also consumed in the UK. Most of these will tend to be cooked before consumption. Although thorough cooking should eliminate the risk of norovirus, methods such as steaming can result in incomplete inactivation. RASFF data from 1979 to 2017 (shown in Appendix 3) contains 10 alerts for other bivalve molluscs and UK outbreak data between 1992 and 2016 details two outbreaks, one in clams and the other in mussels and cockles. Therefore, although they are less frequent than oysters, outbreaks resulting from the consumption of other bivalve molluscs do occur.

Recommendation:

- Risk assessment continues to include the oyster pathway as defined in the original model.
- Future work could include the collection of improved data on the inactivation of norovirus during cooking methods used for non-oyster bivalve mollusc (clams, mussels, cockles), and/or on contamination of these food types at source, and if these data are available a separate pathway could be added to the model to explore the relative importance of these food types.

3.1.2 Lettuce and other uncooked leafy greens

Lettuce have been included as they can become contaminated with norovirus during agriculture production and post-harvest. The 2014 EFSA scientific opinion on norovirus and leafy greens covered a range of leaves, stems and shoots and identified the main risk factors for the contamination of these products with norovirus as (i) environmental factors, in particular climatic conditions (e.g. heavy rainfall or floods) that increase the transfer of norovirus from sewage or sewage effluents to irrigation water sources or

[1] Depuration of seafood is the process by which marine or freshwater animals are placed into a clean water environment for a period of time to allow purging of biological contaminants (such as *E. coli*) and physical impurities (such as sand and silt).

fields of leafy greens; (ii) use of water for irrigation or pesticide treatment which has been contaminated by sewage; (iii) contamination by food handlers or equipment at harvest or on farm post-harvest. The leafy greens of major concern are those that are minimally processed salads, eaten raw. They are identified as risky foods as they are not subjected to physical interventions or other processing steps. Whilst washing is used for some types of lettuce, this is not true for all, and washing is only able to reduce norovirus contamination of the surface of the lettuce, it will not remove virus internalised within the plant tissue.

There is a lack of data on allowing outbreaks to be attributed to specific leafy green products. Looking at UK outbreak data from 1992-2016 (Appendix 2), eight were attributed to salads, but the specific vehicle for infection is not readily apparent. RASFF data from 1979-2017 (Appendix 3) showed that, of 41 RASFF alert and border rejections raised for fruit and vegetables, the only vegetable named (on two occasions) was lettuce. The VITAL study (FP7-KBBE project 213178) found norovirus in 2.5% butterhead lettuce (3/122) but found none in romaine lettuce (0/27) in at-retail samples from Greece, Poland and Serbia.

Consumption data for uncooked leafy greens shows that lettuce makes up about two-thirds of the total. Some leafy greens such as cabbage are chiefly consumed cooked. Leafy greens are also recorded as being consumed in composite foods such as mixed salads and salad served with burgers and kebabs.

Table 1: Summary of UK consumption data for uncooked leafy green

Type of uncooked leafy green	Population mean for adults (19+) (g/d)
Lettuce	4.9
Celery	0.8
Spinach	0.7
Cabbage	0.4
Rocket	0.3
Watercress & mustard cress	0.2
Chicory/endive/radicchio	0.0

Source: National Diet and Nutrition Survey (NDNS) Years 1 to 8 (not including cooked leafy greens or leafy greens in composite foods)

Data on non-lettuce leafy greens consumed uncooked is available to FSA as a result of combining the NDNS and Food and You surveys, meaning that portion size estimates and consumption frequencies could theoretically be estimated from the entire “leafy greens consumed uncooked” category. However, the decision was explicitly taken within the NoVAS study to only sample from the category of lettuce assumed to present a particularly high risk, as stated in section 6.3.2:

> “Only samples of open leafed lettuce (e.g. not Iceberg or any lettuce with a similar closed leaf appearance and not ready-to-eat bagged lettuce) were collected. Lettuces of this type were considered most likely, due to the loose nature of their leafy heads, to retain viruses that may have contaminated them at primary production.”

Estimating portion size and frequency of consumption based on all uncooked leafy greens would represent the implicit assumption that all leafy greens were as high-risk as open-leafed loose (non-bagged) lettuces. A significant proportion of UK retail lettuce is sold bagged and, frequently, pre-cut and washed, which is likely to reduce contamination loads, meaning that even using consumption frequency data on lettuce alone may overestimate the risk from this category, but the proportion of retail lettuce washed or otherwise treated in a way likely to reduce contamination before sale at retail cannot be inferred from the available FSA survey data at the current time.

It is also likely that as the market for leafy greens has changed to include a greater proportion of pre-washed product, the frequency with which consumers wash these products at home is likely to have declined. This means that combining recent estimates of domestic washing with contamination estimates taken from a subset of the leafy green range that is likely to represent a high probability of contamination would be inappropriate. In light of this risk and the current availability of data, we believe the best compromise is to use lettuce-only data for portion size and consumption frequency, using domestic washing estimates likely to reflect washing preferences for open-leafed non-bagged lettuce, and give consideration to collecting better data on bagged and prewashed products in this sector in future.

Recommendation:

- Risk assessment continues to include only the lettuce pathway as defined in Appendix 5 to limit overestimating the risk associated with leafy greens.
- Future work could include collection of improved data on the proportion of retail and catered lettuce, and potentially other leafy greens, in the UK that has been washed or otherwise treated before or after sale in a way likely to reduce its contamination with norovirus.

3.1.3 Raspberries (fresh and frozen)

Raspberries, like some other berry products, can be contaminated with norovirus during their agricultural production and post-harvest. The main risk factors for the contamination of raspberries (and other berries) with norovirus are (i) environmental factors, in particular climatic conditions (e.g. heavy rainfall) that increase the transfer of norovirus from sewage or sewage effluents to irrigation water sources or fields of berries; (ii) use of sewage-contaminated agricultural water either for irrigation or for application of agricultural chemicals such as fungicides (iii) contamination and cross-contamination by harvester, food handlers and equipment at harvest or post-harvest.

Consumption data from years 1-8 of the National Diet and Nutrition Survey indicated that, in the UK, strawberries are the most consumed uncooked berry fruit, followed by blueberries/bilberries. The quantity of strawberries consumed is over three times that of raspberries. The only other berry group consumed in significant quantities is blackberries, which are consumed in approximately one third of the quantity of raspberries, with the consumption of all other berries being considerably lower. These consumption figures are shown in

Table 2 below (berries recorded as cooked and berries in composite foods such as puddings, drinks and other foods are not included).

Table 2: Summary of UK consumption data for uncooked berry fruit

Type of uncooked berry fruit	Population mean for adults (19+) (g/d)
Strawberries	4.3
Blueberries & Bilberries	1.7
Raspberries	1.3
Blackberries	0.4
Cranberries	0.1
Blackcurrants & Redcurrants	0.0
Other berries	0.0

Source: NDNS Years 1 to 8

However, raspberries are historically more often associated with norovirus outbreaks. The 2013 EFSA scientific opinion on the risk posed by pathogens in food of non-animal origin ranked the combination of *Salmonella* and norovirus with raspberries as the hazard fourth most often linked to foodborne human cases originating from food of non-animal origin in the EU. Frozen raspberries have also previously been implicated in European and international outbreaks of norovirus. A 2014 EFSA scientific opinion on norovirus and berries found that between 2007 and 2011, there were 27 norovirus outbreaks associated with raspberries. RASFF data from 1979-2017 (Appendix 3) showed that, of the 63 alerts and border rejections raised for norovirus in fruit and vegetables, 32 were for raspberries.

Various reasons have been suggested to explain this pattern. Raspberries are less likely to be washed (which may help to remove norovirus surface contamination) than strawberries and blueberries, due to their more fragile structure. In addition, norovirus is more likely to become internalised within the raspberry fruit structure itself, although this is recognised as an area where further research is warranted.

There has been no routine/regular monitoring of berry fruits for the presence of norovirus in most of the EU Member States and there is very limited prevalence data on the rates of contamination of berries (not involved in foodborne outbreaks) by norovirus in the peer-reviewed literature. There is some UK data on the prevalence and levels of norovirus contamination found on both fresh and frozen raspberries at retail (collected as part of NoVAS). Maunula et al. (2013) did not detect norovirus in the retail samples of fresh (0/60) and 39 frozen raspberries (039) from 3 Eastern European countries (Czech Republic, Poland and Serbia).

It remains possible that some infections do occur via exposure to other berry groups but these have not been associated with norovirus as strongly as raspberries. Between September and October 2012, an extremely large outbreak of norovirus occurred in Germany that was associated with a single lot of frozen strawberries imported from China (Bernard et al. 2014).

Recommendations:

- No change to the current decision to include raspberries in the risk assessment and to exclude other berry fruits.

3.1.4 Pathways excluded from the risk assessment

A number of other foodborne pathways were considered including food of animal origin, fish, eggs, milk and other dairy products for example. Each was considered according to the inclusion criteria and were excluded. Appendix 4 gives a more detailed explanation of the rationales for exclusion.

Where UK consumption is described as low, this indicates that fewer than 50 out of 4,788 adults have reported consuming the food in the National Diet and Nutrition Survey years 1-8, and that the mean consumption by the adult population is estimated to be less than less than 0.5 g per person per day.

3.2 Immunity component

In order to model the immunity aspect of norovirus infection a model component was developed formed of the following steps:

- Estimation of the cumulative dose of norovirus from different foods
- Assessment of the immunity status of the individual
- Estimation of the loss of immunity
- Generating new infections
- Probability of previous infection with similar strains
- Adjusted probability of symptomatic infection from food

3.2.1 Estimation of the cumulative dose of norovirus from different foods

The risk assessment estimated the total exposure to norovirus from food pathways for an intrinsically susceptible individual. This is calculated by aggregating the individual exposures from each of the pathways that were estimated previously (oysters, lettuce, raspberries, catered food and takeaways). The model simulated 365 days (one year) taking random exposures from each pathway a day.

Once the daily exposure was calculated the number of infections on that day was estimated by applying the dose response model. At this stage no account of immunity was made.

Implications of assumptions and limitations for usage: While meals for individual pathways were limited to three a day, exposures via each pathway were estimated independently, so it would be possible (although very unlikely) to be exposed to all 5 food types 3 times on any day. This was not considered to be a significant limitation of the study.

Recommended changes: none.

3.2.2 Assessment of the immunity status of the individual

The risk assessment then estimated whether the individual was likely to be immune on each day as follows:

3.2.2.1 Probability of an infection occurring to an individual while immune

The probability of infection of a random individual is based on the strain similarity of the strains that individual is immune to on each day of the year. A Poisson distribution was sampled with a rate parameter representing the number of symptomatic and asymptomatic infections that a person has in a year multiplied by the duration of immunity. The step is separately simulated on a daily timestep over 365 days, increasing in response to new infection events in preceding days and decreasing in response to immunity loss events.

Implications of assumptions and limitations for usage: The original risk assessment assumed that each of the infections that a random person had the previous year were from different norovirus strains. It may be possible to represent this process in a more realistic fashion, particularly if data were incorporated on relative strain diversity or changing strain diversity through time, but at the expense of significantly greater complexity of the risk assessment. It is also possible that such an approach would still oversimplify other factors such as differing levels of cross immunity between different strains.

Recommended changes: In the NoVAS risk assessment, the number of previous (symptomatic and asymptomatic) infections that a person has on average each year was calculated from the detection rate in the whole population. We chose to rescale this calculation to reflect that a proportion of the population are not intrinsically susceptible and so would not have any infections, meaning the average number of infections for those who are susceptible increases. This is addressed in the revised risk assessment by changing the way the parameters “Estimated incidence of symptomatic” and “Symptomatic incidence” are calculated. Specifically, the Phillips paper states, based on the results of the IID survey, that the proportion of the population with asymptomatic infection at any one time (A_i) is 12.6%. Assuming a mean duration of carriage (D_c) of 12.4 days, the estimated number of asymptomatic infections per person per year will be:

$$365 * \frac{A_i}{D_c} = 2.804$$

However, because only proportion Is of the population are intrinsically susceptible, assumed to be 80% in this analysis, the number of infections for those that are susceptible increase (because as 20% will never be asymptomatic):

$$365 * \frac{A_i}{I_s D_c} = 3.505$$

Similarly, from the IID2 study the number of symptomatic infections a year (S_i) a person has is 0.047; correcting for intrinsic susceptibility increases this value to 0.05875.

3.2.2.2 Estimation of the loss of immunity

The risk assessment modelled the loss of immunity on a given day using a Bernoulli distribution, with the probability of losing immunity on a given day the reciprocal of the duration of immunity in days. For example, if immunity lasts an average of 6 months (182.5 days), then the chance of losing immunity on any given day was 1/182.5, or 0.0548. A person lost immunity if they had immunity to a least one strain on that day.

In the original report the duration of immunity for the most likely scenario is sampled from a PERT distribution with min and mod = 6 months and max = 24 months while for the extreme scenarios the average duration is fixed at 6 or 24 months.

Implications of assumptions and limitations for usage: The approach used results in an exponentially distribution duration of immunity, which is unlikely to be realistic. In addition, within each simulation the rate of loss of immunity is the same for all infections even where this parameter is drawn from a PERT distribution rather than taking a fixed value. It would be possible to resample the average duration of immunity per infection or depending on strain.

Recommended changes: none.

3.2.2.3 Generating new infections

The model used a Bernoulli distribution. The probability of a new infection on any day was the number of symptomatic infections from food as described previously plus the average number of non-foodborne symptomatic and all (food and non-food) asymptomatic infections per day.

Implications of assumptions and limitations for usage: To estimate non-foodborne symptomatic cases, the model was set up without pre-existing immunity to provide a baseline estimate of daily foodborne symptomatic infection, and then subtracted this from total symptomatic cases, as estimated during the FSA's Second study of infectious intestinal disease in the community (IID2) study. The daily number of infections from food was then added back in.

Recommended changes: The revised risk assessment uses total symptomatic and asymptomatic infections (food and non-food) per day in the generation of new infections with between individual variability described by the Bernoulli distribution.

3.2.2.4 Probability of previous infection with similar strains

The probability *P* of a person becoming immune to infection from a particular strain each day was calculated using the following equation:

$$P = 1 - D^n$$

Where D is the Hunter-Gaston index and *n* is the number of prior infections in the immune period, as described in section 3.2.1.

3.2.3 Adjusted probability of symptomatic infection from food

The probability of symptomatic infection for each individual for each day was calculated by multiplying the probability of infection from food (section 3.2.1) by 1 minus the probability of previous infection with similar strains. This was then summed over each day in the year to get an overall probability of symptomatic infection for the year. A final adjustment was then made for the proportion of the population who were intrinsically not susceptible.

Implications of assumptions and limitations for usage: The risk assessment does not represent seasonality, and norovirus is highly seasonal. The assessment also assumes that infectious exposures that are resisted as a result of acquired immunity result either in asymptomatic infection or no infection, while unresisted infections result in symptomatic infection.

Recommended changes: The risk assessment should be modified to use the adjusted probability of infection from food to simulate the variable daily infection outcome using a Bernoulli distribution. This could also include probability of intrinsic susceptibility. This is unlikely to make a large difference to the risk assessment results but is a more intuitive approach. Ideally, seasonality should be added to any future development of the risk assessment, but this would require access to data on seasonal variation in model inputs such as food consumption which are not currently available.

The representation of symptomatic and asymptomatic infections was considered appropriate given current knowledge of determinants of the clinical outcome of infection but could be updated if new data become available.

3.3. Handling component approach

The transmission of norovirus within the catered and takeaway food sectors in this component is based on the pathway from infected food handler to food. Whilst calculated separately, the catered and takeaway pathways share several parameters describing the process of handling and potentially contaminating food. They each model, per touch, the transfer by staff hands of viable norovirus to a food that undergoes no further heat processing using the following equation:

Count on hand * proportion transferred * proportion infectious * (1-probability of subsequent heating)

The parameter values for the proportion transferred, probability of heating and the number of touches are derived from a study looking at the preparation of delicatessen sandwiches (Stals et al. 2015). The count on the hand and proportion infectious values are derived from the NoVAS report and are the result of experiments carried out during the project.

Implications of assumptions and limitations for usage: The current assessment only represents the transfer of virus from hand to food; other similar QMRAs for norovirus have modelled six-way transfer between hand, food and preparation surfaces. However, hand-food transfer is likely to contain a higher proportion of virus derived from faecal contamination and therefore, if the assumption about infectivity of virus derived from faecal contamination is correct, this is likely to be the most important of these transfer processes.

Secondly, the method used in the current assessment is based on data obtained for sandwich preparation environments. Both the modelling approach and the parameter values are likely to vary for different food preparation environments. For example, currently the count on the hand is sampled independently for each contact, as though the touches were all performed by separate individuals. Other norovirus QMRAs model the count on the hand dynamically, assuming the same individual each time. Either method may be more appropriate depending on the kitchen environment to be represented; the latter is likely to be a better reflection of small kitchens with a small number of individuals involved in food preparation, while the current approach is likely to represent medium-large kitchens better. As more catered and takeaway meals consumed by the public are likely to be prepared in such environments (assessor's opinion) we consider the chosen option to be preferable, but users should be aware that this assumption may be less appropriate when modelling small business preparation environments. We also recommend that data on a wider variety of preparation environments is collected.

Recommended changes: None.

4. Parameterisation of the risk assessment

In this section we review all the parameters and distributions in the risk assessment and discuss the information provided on the selection of the values and choice of distribution (where relevant). The available literature was reviewed and any additional sources of information and, where necessary, updated estimates values have been proposed for the baseline results, sensitivity analysis and any alternative scenarios recommended for the revised risk assessment.

4.1. Dietary parameters

Oyster Meal Size (g)

Original NoVAS parameter: The original NoVAS report estimated this value using a truncated Normal distribution (μ=37.22, σ=14.67, truncated to values between 20 and 60) fitted to data on serving size provided by the FSA which was extracted from the National Diet and Nutrition Survey (NDNS). Data were from adults and included data from years one to six of the surveys.

Updated value: Since the NDNS data were provided for the NoVAS consortium, years seven and eight of the NDNS were completed. However, no additional oyster meals were recorded in those years, so the meal size dataset remains unchanged. The estimated mu and sigma remained unchanged with values truncated to between 0.1 and 100g, as there was no clear rationale for the narrower previous truncation range.

Implications of assumptions and limitations for usage: As oysters are consumed relatively infrequently, the estimation of a 'typical' meal size using the NDNS data is associated with increased uncertainty.

Proportion of the oyster meal that is formed of the digestive gland

Original NoVAS parameter: The source of this value is derived from the periodic surveillance of the weight of total oyster and weight of the digestive gland conducted by Cefas as part of the NoVAS project.

Updated value: The combined weight of 10 oysters was recorded in a sample for the species *C. gigas* and *O. edulis* (James Lowther, pers. comm. 2019). There were 125 samples for each species. The minimum proportion of digestive gland for 10 oysters was 0.017, whilst the maximum proportion was 0.158. The mean proportion over all samples was 0.061.

As the risk assessment does not stratify to the number of oysters consumed or type of oyster, the sample data for all 10 oysters was used to represent variability by meal in a pert distribution fitted to the minimum and maximum with a most likely value of 0.048 to have the same mean value as the sample data.

New values: PERT distribution; min = 0.017, max = 0.158, most likely value = 0.047.

Leafy Greens Meal Size (g)

Original NoVAS parameter: The original NoVAS report estimates lettuce meal size using a truncated Normal distribution (μ=24.50, σ=16.13, truncated to values between 1.5 and 135) fitted to data on serving size provided by the FSA extracted from the National Diet and Nutrition Survey. Data were from adults and included data from years one to six of the surveys.

Updated value: A distribution was fitted to include years seven and eight of the NDNS in the dataset, which have become available since the NoVAS consortium analysis was conducted, and to include these categories in composite foods, as detailed further in Appendix 3. For the reasons described in the pathway review in section 3.2.2 previously, other leafy green categories were not included.

The estimated portion size using combined lettuce and lettuce recipe data, using a log-normal distribution for portion size (μ=2.97 and σ=0.69 on the natural log scale). To avoid the lognormal distribution occasionally giving unrealistically extreme values, we truncated the distribution at the 99.9th percentile.

Number of Oyster meals consumed per year (meals per person per year)

Original NoVAS parameter: In order to estimate the number of meals consumed per day which contain oysters, the original study used National Diet and Nutrition Survey adult data from study years 1 to 6 provided by the Food Standards Agency. In this data 0.15% of the study population reported having a single meal of oysters during the four-day follow-up. This is then multiplied by 365/4 to give an annual figure of 0.137.

Updated value: Since these data were originally requested, years 7 and 8 of the NDNS survey have been completed. Updating these figures to include years 7 and 8 gives 0.10% consuming a single meal in the four-day follow-up and a rate of 0.0981 oyster meals per person-year.

For the purpose of sensitivity analysis, values from 0.03 to 0.2 oyster meals per person-year are used to reflect the uncertainty in the point estimate from sampling, based on a 95% credible interval without weighting (assessor's opinion).

Number of leafy greens meals consumed per year (meals per person per year)

Original NoVAS parameter: In the original report, the food consumption calculation for lettuce and raspberries was derived from the meal/portion size and the average amount consumed over the four-day period. For lettuce 44% of people reported eating lettuce in the four-day period, the mean weight consumed per day in those eating lettuce was 10.99 g and (as stated above in the relevant section) the mean portion size was 24.5g. The mean number of meals consumed per day in those eating lettuce was 0.449 (obtained as 10.99/24.5) and in the population as a whole 0.198. This latter figure was then multiplied by 365 to give an annual number of meals consumed of 72.1 as shown in table 35, p166 of the original report. The actual number of meals consumed was assumed to vary according to a Poisson distribution.

Updated value: since these data were originally requested, years 7 and 8 of the NDNS survey have been completed. In addition, data on the number of meals consumed containing a given ingredient are available directly from the NDNS results. The value was updated to directly represent the measured number of meals of the product. Using years 1 to 8 to calculate the frequency of consumption of lettuce as composite foods as well as non-composite foods produced a rate of 88.9 meals per person-year.

The frequency of lettuce meals is then assumed to vary between people described by a Poisson distribution with this value as a rate parameter.

Number of raspberry meals consumed (meals per person per year)

Original NoVAS parameter: In the original study, the mean number of raspberry meals per year was assumed to vary between people following a Poisson distribution (table 35, p166). This was then used to determine the actual number of meals in a given period. The rate used in the original risk assessment was 7.99 meals per year, based on raspberries (not including recipes) consumed by all adults in NDNS Years 1 to 6. Using recipes to include composite foods and updating to include Years 1 to 8 would increases the value to 10.7 meals per person year.

Updated value: Data on the number of meals consumed containing a given ingredient are available directly from the NDNS results. This value has been updated to directly represent the measured number of meals of the product.

Raspberry Meal Size (g)

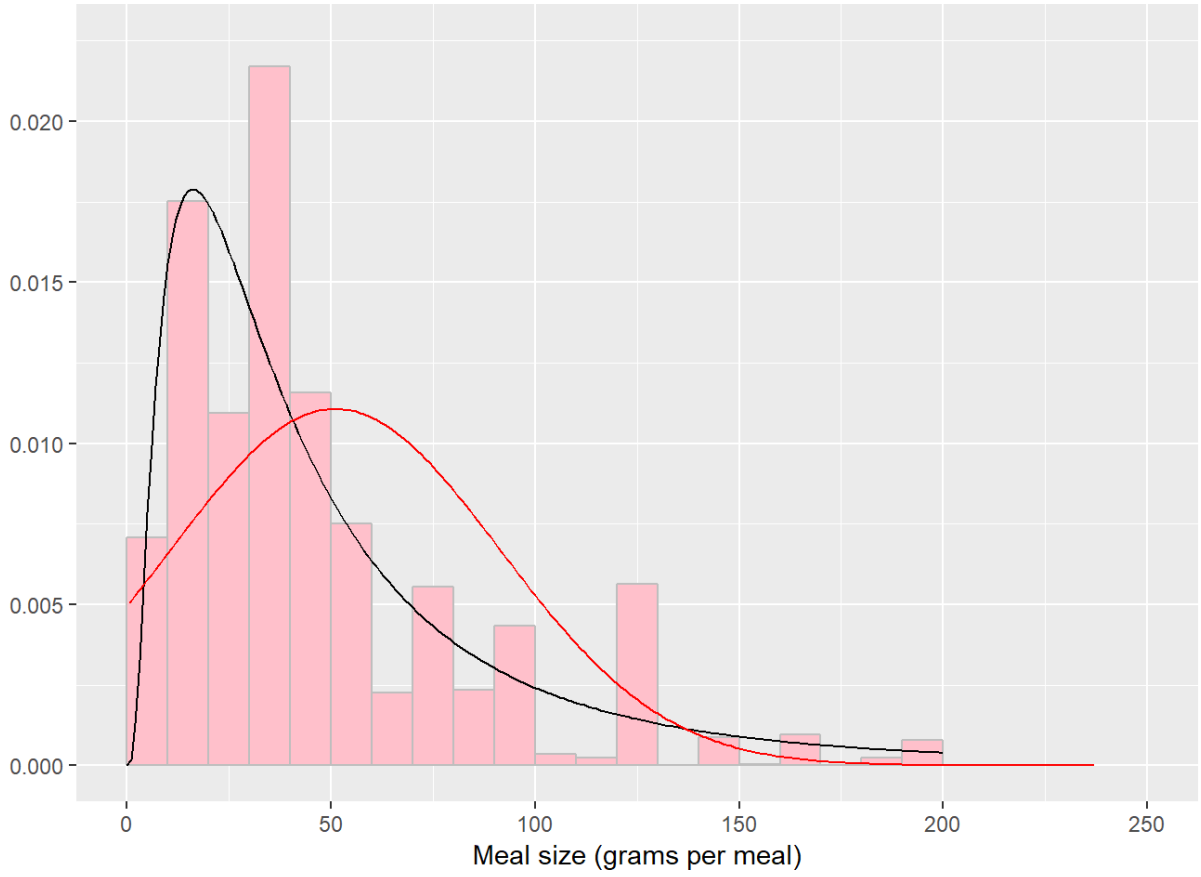
Original NoVAS parameter: The model was based on the same approach for lettuce as for raspberries. The portion size was estimated using a truncated Normal distribution (μ=51.0, σ=40.3, truncated to values between 0.6 and 237) fitted to data on serving size provided by the FSA extracted from the National Diet and Nutrition Survey. The mean amount eaten each day was 23.3g. Data were from adults and included data from years one to six of the surveys.

Updated value: The dataset was increased and used to fit this distribution to include years seven and eight of the NDNS, which have become available since the NoVAS consortium analysis was conducted, and reviewed NDNS food codes to ensure all

consumption of non-processed raspberries was captured. This identified 8 relevant food codes (6 non-composite codes plus 2 composite codes) shown in Annexe 4. The recipe data was used to estimate the quantity of raspberries in composite foods and include it to the total consumption to provide a conservative estimate.

The lognormal distribution (black line) fitted the data better than the Normal distribution (red line) (see Figure 1), as assessed by comparing several empirical percentiles with those estimated from the fitted distributions. Therefore, these data were fitted to a lognormal distribution (with a mu of 3.42 and a sigma of 1.01, on the natural log scale).

Figure 1: Quantity consumed on each occasion (in grams) of raspberries (excluding recipes)



Number of catered meals, eaten out or take away, consumed per year

Original NoVAS parameter: The number of meals out and take-aways were derived from Adams *et al*. (2015) which in turn was based on the NDNS data available at the time. This resulted in the proportion of people who reported eating out (27.1%) or buying a take-away to eat at home at least one per week (21.1%). Therefore, 72.9% of adults are assumed not eat a meal out, and 78.9% assumed not to buy a takeaway meal in a one-week period.

Data on consumption of catered food in the NoVAS report was taken from Adams et al. (2015), which used NDNS data from 2008-2012, and in particular the results from these two questions to analyse the number of meals eaten out and takeaway meals:

“On average, how often do you/does child eat meals out in a restaurant or cafe?”;

“On average, how often do you/does child eat take-away meals at home?”.

In both questions it is specified that “‘meals’ referred to more than a beverage or bag of chips” and participants were asked to “include pizza, fish and chips, Indian, Chinese, burgers, kebab etc.”

Updated value: Since data from Years 1 to 8 of the NDNS are now available, these data were used to derived updated consumption frequencies based on the whole of this period. The proportion of respondents consuming less than one meal out a week was estimated at 72.1%, and the proportion of respondents consuming less than one takeaway meal a week was estimated at 79.2%.

4.2 Pathogen parameters

Probability of an oyster at retail in the UK testing positive for norovirus

Original NoVAS parameter: A one-year survey of oysters collected from the point-of-sale to the consumer was carried out from March 2015 – March 2016. A total of 630 samples, originating from five different European Union Member States, were collected from 21 regions across the UK. 433 (68.7%) were positive for norovirus RNA.

Updated value: The uncertainty associated with the true prevalence of contamination was described in the risk assessment using a Beta distribution:

$$Beta \sim (S + 1, N - S + 1)$$

This represents the posterior belief for a binomial process where the number of successes (S) = 433 and the number of trials (N) = 630.

Implications of assumptions and limitations for usage: The effect of seasonality on norovirus RNA prevalence was statistically significant, with 79.7% positive samples in October to March and 57.0% positive samples in April to September. The risk assessment is currently unable to represent seasonality despite the high seasonal variation in several of the risk assessment’s parameters. As mentioned earlier in this report, ideally seasonality should be added to any future development of the risk assessment, but this would also require access to data on seasonal variation in model inputs such as food consumption which are not currently available.

Concentration of norovirus genome copies in oyster digestive gland (copies/g)

Original NoVAS parameter: norovirus gene copy counts in oyster digestive glands were measured via qPCR as part of NoVAS Work Package 3. The geometric mean of norovirus RNA detected in the NoVAS survey dataset was 76 copies/g, and 9.7% of samples had levels of norovirus exceeding 100 copies/g.

The log10-transformed concentration of norovirus genome copies in oyster digestive gland was modelled using a Normal distribution with a mean of 1.27 and a standard deviation of 0.762.

The effect of seasonality on norovirus RNA levels was statistically significant.

Updated value: no change.

Other data on oysters at retail in the UK is not currently available. While it is possible to use data on gene copy number in production areas (Lowther et al., 2012 and EFSA 2019), this would not correspond to the level at retail due to risk reduction measures taken by FBOs such as depuration and other factors touched on in the NoVAS report. Similarly, data from other countries for oysters at retail would potentially be very different from UK-specific data due to local environmental differences.

Implications of assumptions and limitations for usage: The NoVAS risk assessment did not differentiate between norovirus GI and GII, or the different strains within genotypes, which reportedly have different bioaccumulation efficiencies and seasonal effects (Maalouf et al., 2011). This reflected a decision at the time by FSA, based in turn on the 2012 EFSA scientific opinion on norovirus in oysters, which concluded that the lack of strain-specific data made it more appropriate to model strains in combination. However, if additional strain-specific data becomes available this assumption could be revisited. Also, as noted above, the quantity of norovirus RNA varied significantly by season which the risk assessment is currently unable to represent and would add considerable complexity if strains were further stratified in the assessment.

Concentration of norovirus genome copies in lettuce and raspberries (gene copies/g)

Original NoVAS parameter: The norovirus gene copy counts in lettuce were measured via qPCR as part of NoVAS Work Package 4. In the NoVAS study, the number of lettuce samples where replicate norovirus RT-PCR signals were detected was 30/568 (5.3%). The prevalence used in the risk assessment was 79/568 (13.9%), which included samples where detection could not be replicated. Unlike the oyster data, insufficient positive values were obtained to be able to obtain a reasonable fit to any distribution, so to obtain sampled values the observed log10-transformed counts were sorted into ascending order and fitted to a linear model (lettuce: Log_{10}Intercept -23.2, Log_{10}Slope 24.2; raspberries: Log_{10}Intercept -28.1, Log_{10}Slope 28.9).

The final dose per meal for both lettuce and raspberries is assumed to be the product of the concentration of RNA per gram of retail product, the proportion remaining after washing, the proportion that represents infectious virus and the size of the meal.

In the original NoVAS project, 37/310 (11.9%) samples of fresh raspberries gave norovirus RT-PCR signals; 7 samples (2.3%) gave replicate RT-PCR results. Most (6/7) of the positively-testing fresh raspberry samples in the NoVAS survey were imported, but no predominance of a genogroup, or any seasonality, was observed. Thirty four of the 274 (~12.6%) samples of frozen raspberries gave norovirus positive results; 10 samples (3.6%) gave replicate RT-PCR results.

Updated value: no change.

Other surveys have generated data relevant to both lettuce and raspberries, although these are unlikely to be as relevant to the UK as the NoVAS-funded survey. Mattison *et al*. (2010) sampled 641 samples of lettuce sold in supermarkets in Canada and found 181 positive for norovirus (28.2%). The level of norovirus contamination of lettuce in this Canadian study appears to be much higher than the levels found in NoVAS (range 1.4 copies to 9×10^6 copies with a median of 500). The data for this study is not available

therefore parameter estimation is not possible. Kokkinos *et al*. (2012), analysed lettuce samples at point of sale in three European countries, and found 2/149 (1.3%) samples to be norovirus GI positive and 1/126 (0.8%) to be norovirus GII positive. The same issue arose with accessing data in this study as with Mattison *et al*. (2010).

In Baert et al., 2011, soft red fruits (raspberries and strawberries) were tested for norovirus using real-time RT-PCR. 34.5% (10) of the 29 Belgian samples and 6.7% (10) of the 150 French samples were found positive. However, only a range of Ct values were provided, and not gene copy counts, therefore these results could not be used. In a study by Stals *et al*. (2011), 4/10 fresh raspberry samples obtained from a processing company in Belgium tested positive for norovirus. However, when Maunula *et al*. (2013) analysed 60 samples of fresh raspberries at point of sale in 4 European countries, no norovirus positive samples were identified. Most (6/7) of the positively-testing fresh raspberry samples in the NoVAS survey were imported from identified countries, and no predominance of a genogroup, or any seasonality, was observed.

If the underlying data were available then these results could be combined with the original NoVAS data to derive updated European parameters

Proportion of gene copies representing infectious virus

Original NoVAS parameter: The $\log_{10}$-transformed proportion was fitted to a Normal distribution with a mean of -1.52 and a standard deviation of 0.678, truncated at 0 and -3.16. The truncation at 0 indicates that the proportion of gene copies representing infectious virus cannot exceed 1; the lower boundary is not explicitly justified.

This is a highly uncertain parameter due to the limitations of current infectivity assays for norovirus. It is also likely to be a highly variable parameter as the proportion is determined by the effects of environmental conditions on capsid integrity and RNA inactivation, and different environmental conditions will affect these processes differently. For retail samples, the estimated infectivity proportion ranged from 0.02 to 100%. For outbreak-related samples, calculated proportions ranged from 0.02 to 13.4%.

However, although the total number of symptomatic norovirus infections may be highly sensitive to this value, unless it varies consistently between the food pathways considered in this risk assessment it should make far less difference to our estimation of the relative importance of pathways, as the same variation will apply across all products.

Although a capsid integrity assay was developed in another work package specifically to obtain better estimates of this value, subsequent research (e.g. Walker et al. 2019) using both murine norovirus and human virus in enteroids has suggested that capsid integrity assays may substantially over-estimate norovirus infectivity. As a result, the submitted NoVAS report used a Normal distribution fitted to the log10-transformed infectivity estimates obtained using an F-specific RNA bacteriophage as a proxy for norovirus due to the difficulties of culturing the latter in the laboratory.

The dataset used for the report was later expanded; the Lowther et al. manuscript uses the final, full dataset. There are two further differences between the analysis described in the earlier report and the later Lowther et al. analysis: firstly, that test results where no viable phage was detected the inferred values were censored differently (the report

assumes that viable phage was present at the limit of detection, i.e. 1.5 cfu/g, while the manuscript assumes half the limit of detection, 0.75 cfu/g). Although there is no clear a priori reason to prefer either approach, the method used in the report is more conservative and results in a better fit to the lognormal distribution. The final difference between the analyses is that the F-RNA negative samples were reselected from the full dataset for the analysis in the manuscript.

The estimates given in Stals *et al.* (2015) are lower than these (lognormal with mean -3.65, SD 0.98, truncated at -2, -5.4), and the NoVAS authors raise concerns that the methodology used will underestimate infectivity (essentially that the studies upon which the estimate is based on artificially inoculated samples and then assume further RNA inactivation does not occur, which is not likely to be a realistic assumption).

Updated value: The new data used to parameterise this distribution was obtained (James Lowther, Cefas, pers. Comm.) and a Normal distribution fitted with a mean of -1.58 and a standard deviation of 0.705, truncated at 0 and with no lower boundary.

For the sensitivity analysis means between -1.0 (since few samples were identified where the proportion of infectious virus was estimated to be higher than 10%) and -3.5 (representing the mean of the Stals *et al.* estimate) were considered.

Norovirus dose response

Original NoVAS parameter: The published report assumes that the dose-response relationship follows an approximate beta-Poisson distribution:

$$P_{infection} \approx 1 - \left(1 + \frac{dose}{\beta}\right)^{-\alpha}$$

Where α = 0.349 and β = 357, obtained by van Abel et al. (2017) via maximum likelihood from the dataset described in Atmar et al. (2014).

van Abel et al. (2017) discuss the assumptions that relate to the selection of an appropriate model for norovirus dose-response, particularly those made about the number of viral particles represented by a given PCR result, and whether the virus is aggregated or not. Evidence obtained elsewhere in the NoVAS project from the quantification of viral RNA in the oyster samples (section 8.4.2) is consistent with the presence of aggregates – essentially, that the distribution of copies observed appears to be a zero-inflated lognormal rather than a single distribution, although similar evidence was not available for the other products considered. However, the authors note that the results obtained from the computationally more efficient approximate beta-Poisson model yield similar results to those from the (technically more correct) ${}_2F_1$ hypergeometric model.

Implications of assumptions and limitations for usage: Firstly, the assumption that virus in all the products considered in this model are aggregated is, as the authors note, not strongly supported by the evidence available, and the review in van Abel et al suggests that in this situation both possibilities should be considered. The discrepancy between aggregated and disaggregated models is highest at low doses; as an extreme example, at very low doses (<1 genomic-equivalent copy), almost all models considered by van Abel et al. predict a probability of infection close to 0.001 but the “1F1x_TGIa+b” model fitted by Teunis et al. (a ${}_1F_1$ hypergeometric model assuming disaggregation with

a = 0.04, b = 0.055), the most commonly used dose-response model in norovirus QMRA, predicts a probability of 0.22.

Finally, genetic change in the dominant strain is relatively common for norovirus, and as a result this parameter might be variable over time and between strain as well as uncertain.

Updated value: no change. The van Abel et al. review indicates that the approximate beta-Poisson model is the model best supported by the available evidence and our understanding of the processes involved.

However, there are significant knowledge gaps around the infectivity of very low doses and about the aggregation of virus particles and whether this might vary between different products, although given the review of conditions resulting in virus aggregation in Gerba & Betancourt (2017) it seems likely that most virus existing under the conditions represented in this model would indeed be aggregated. While there are significant criticisms of the Teunis et al. fit (refer to Schmidt et al. 2015), currently available data do not exclude the possibility that the probability of infection at very low doses is significantly higher than that predicted by the model used in the NoVAS risk assessment. Given that aggregation has important implications for environmental survival and the effectiveness of disinfectants and filtration, this assumption should be reviewed if further evidence becomes available.

4.3 Immunity component parameters

4.3.1 Probability of person being "intrinsically sensitive" for NoV

Original NoVAS parameter: The baseline probability of a person being intrinsically sensitive to norovirus used by the NoVAS contractors was 0.75. This was derived from a number of genotyping studies (mostly from Nordgren group (2010, 2016, 2019), who estimate that positive secretors constitute approximately 80% of the population, and King *et al*. (2018). No UK specific data were located, so the report authors assumed the Swedish population to be representative of the UK/European population.

Updated value: On reviewing the data it is proposed that the baseline value should be 0.8, which is the actual figure in the Nordgren group studies cited by the original report. The sensitivity of the risk assessment to this value is estimated by considering a lower value of 0.7 and a higher estimate of 0.9, largely reflecting uncertainty in the reported estimate as well as the different proportion of people with susceptible genotypes in some ethnic groups in the UK compared to Sweden).

4.3.2 Carriage rate of norovirus in asymptomatic individuals

This parameter is used in two places. Firstly, the incidence per person per year is used to estimate the total incidence of norovirus in the population and therefore the population immunity. Secondly, the incidence is used to estimate the proportion of food handlers with an asymptomatic infection i.e. that are excreting norovirus, on the assumption that those with a symptomatic infection are mostly not at work.

Original NoVAS parameter: The baseline value used in the NoVAS report was 16% adapted from Amar *et al.* (2007). This was based on retesting of both cases and case-

control samples taken as part of the Infectious Intestinal Disease study[2] (IID1). The tests used polymerase chain reaction (PCR) assays. The 16% is based on detection in 358 out 2,205 samples. No quantification of viral load was given, although the manuscript states that preliminary analysis found higher norovirus loads in cases as compared to controls. The case definition for a control in the IID1 study was "persons who have been free of loose stools or significant vomiting for three weeks prior to the onset of illness in the case, matched to case by age and sex […] cohort members who had already been a case were subsequently eligible to be controls as long as they fulfilled the criteria of no loose stools or significant vomiting in the previous three weeks".

Another paper by Phillips *et al* (2010) provides an age-adjusted figure of 12% (95% confidence interval 11 -14). This is also based on retesting IID1 case controls using PCR. The authors reference Amar *et al.* (2007) and Amar is mentioned in their acknowledgements, but it not clear how the two pieces of work are related. As Phillips *et al* (2010) is the later study there is an argument for using this later value and it is possible that the difference is simply the age adjustment, but it is not clear from the manuscript whether a different Ct cut-off value is also used.

The original IID1 used less sensitive EM/ELISA tests and found rates of 0.3% in the case controls. A study in the Netherlands (Wit et al. (2001)) which also used PCR and found a rate of 5.2% in controls. Amar *et al* suggest this difference may be due to the use of the more sensitive broader spectrum real-time PCR in their study. It is acknowledged in the paper that test specificity is low.

There is no suggestion in the NoVAS report that asymptomatic cases could previously have been symptomatic. However, Simmons *et al* (2013) suggest this can be the case which could mean that the asymptomatic cases may be an overestimate. Phillips *et al* (2010) mention that they do not know how many were truly asymptomatic rather than post-symptomatic shedding and that "post symptomatic shedding after experimental inoculation has been demonstrated lasting up to 8 weeks". They also consider the possibility that some asymptomatic norovirus infections could be due to pre-symptomatic shedding, although numbers will be low due to the short incubation period (24-48 hours).

Updated value: The IID1 data do not represent all age groups equally. As mentioned above, Philips *et al* (2010) present a method for estimating age-adjusted figures. We applied the same method to the IID1 case control data while adjusting for the fraction of the population assumed to not be intrinsically susceptible, to estimate both a whole-population carriage rate (used to calculate the frequency of infection and therefore infer the proportion of the population immune at any one time) and a working-age (18-65) estimate (used to infer the proportion of food handler contacts that have the potential to contaminate food during preparation in catering and takeaway kitchens).

This approach yields estimates of 12.6% and 8.7% for the entire and adult populations respectively.

[2] A report of the Study of Infectious Intestinal Disease in England

In view of the different rate measured in the Netherlands and the lack of consensus in the literature over whether some asymptomatic cases may in fact have been post-symptomatic cases during recovery, a scenario using a lower rate could be explored in future but was not considered a priority for this review.

4.3.3 Duration of acquired immunity post-infection

Original NoVAS parameter: The NoVAS report provides results for three different scenarios for duration of immunity. These three scenarios were used to produce the minimum, most likely and maximum estimates of norovirus immunity duration. The most likely scenario used a PERT distribution with 6 months for minimum value and 6 for most likely value with a maximum value of 24 months. For the other two scenarios fixed durations of immunity of 6 months and 24 months were trialled.

The justification for these values are Lane (2014), Robilotti *et al* (2015) and Simmons *et a*l (2013) (the former also refers to the latter). In the former study, the author discusses the uncertainty for immunity and suggests "the only way to test whether such uncertainties matter is to try creating and running different models, models which explore alternative formulations and parameter values", so it is unclear why so much weight is put on the 6 month value. Lawrence *et al* (2004) appears to be the source of the 6 month figure for Lane, although here the authors also run their risk assessment with scenarios of duration of acquired immunity at 9 and 12 months. Simmons *et a*l (2013) mention studies giving lengths of immunity from 6 months to 2 years and use a modelling approach to come up with length of immunity from 4.1 to 8.7 years, although this approach was criticised by the NoVAS contractors as being too simplistic to generate credible estimates, essentially fitting a simple SIR-type model with a sinusoidal function to represent seasonality to some observed data.

Implications of assumptions and limitations for usage: The NoVAS technical report acknowledges that the largest impact on prevalence of foodborne illness in the risk assessment is the duration of immunity, and that the duration of immunity is a major area of uncertainty. While the duration of 6 to 24 months largely fits with the published literature, a mathematical model produced by Simmons et al (2013) led to an estimated duration of immunity of 4.1 years to 8.7 years. It may be worthwhile exploring a scenario using significantly longer durations of immunity than those used in the original risk assessment to assess the potential impact of such claims. The NoVAS report also recommends further research to understand norovirus immunity.

Updated value: The use of the original baseline is supported; in view of the uncertainty around length of immunity using ranges based on 6 and 24 months. A scenario was used to explore the impact of using a PERT distribution with a most likely value of the distribution of 9 months.

4.3.4 Duration of excretion of norovirus post-infection in days

Original NoVAS parameter: The baseline in the original report is 16.4 days, derived from Milbrath *et al.*, (2013). Milbrath quotes a range of 2-54 days. These values were based on data extraction from a literature search; 18 papers were identified with individual human norovirus molecular-shedding data and 2 which did not include original data.

The value of 16.4 assumes that the individual is classed as an operational regular shedder (is >1-year-old and immunocompetent). Milbrath et al. also provide a value for operational long shedders (<1-year-old or immunocompromised) of 105.6 days (range 2-298).

An alternative functional division is given by Milbrath et al. where regular shedders shed for ⩽34 days and long shedders for > 34 days. On this definition, the average duration is 14.5 days (range 2-34) for functional regular shedder individuals (where shedding takes ⩽ 34 days) and 136 days (range 35-898) for functional regular shedders (Table.4 in article reference). This second division is given in recognition that the operational definition does not split exactly into regular and long shedders. Note that as the IID1 study use a definition that a case control "persons who have been free of loose stools or significant vomiting for three weeks prior to the onset of illness in the case" if any of the asymptomatic found in the work by Amar *et al.* (2007) were symptomatic hosts that became asymptomatic then the duration date would have to be at least 21 days.

A separate paper by Teunis et al (2014) found that length of norovirus shedding for symptomatic and asymptomatic were similar with a range of 8 to 60 days. This was based on four volunteer studies of outbreaks in hospitals and nursing homes. Both staff and patients were included in the study. While actual durations were not given in detail looking at the graphs the median symptomatic duration for staff was around 19 days while asymptomatic duration for staff was slightly higher at around 25 days

Atmar et al 2014 in a randomised, double-blind, placebo-controlled evaluation of different dosages of norovirus found that the median duration of shedding for persons who fulfilled the definition of gastroenteritis was 29 days compared to 19 days for those without gastroenteritis.

Implications of assumptions and limitations for usage: The value used was based on symptomatic carriage, while the value was part of the calculation for asymptomatic carriage in the risk assessment. The data in Atmar et al. suggests that these values may be different. Should the FSA fund a third Infectious Intestinal Disease study, and a control element is included, then this parameter value could be an area to investigate.

Updated value: It is recommended that the original value is retained, but a scenario is completed in which the duration is doubled to 32.8 days in view of the uncertainty around the multiple studies available in this area.

4.3.5 Diversity of norovirus in England and Wales

Original NoVAS parameter: The Hunter-Gaston index of 0.5639 is calculated utilising data from Gallimore *et al*., (2007), referring to table 3 and the formula from Hunter and Gaston, 1988, which appears as equation 10 in the NoVAS final report (pp. 169):

$$D = 1 - \frac{1}{N(N-1)} \sum_{j=1}^{S} n_j(n_j - 1),$$

where N = 615 GII-4 strains; s = 5 types; n_1 = 54; n_2 = 371; n_3 = 155; n_4 = 11; n_5 = 24.

$$D = 1 - (\frac{164{,}664}{377{,}610})$$

$$\boldsymbol{D = 0.5639}$$

Noroviruses of the genocluster genogroup II-genotype 4 (GII.4) were the most frequently detected in England and Wales during 2018 and 2019, accounting for 74.4% and 50.0% of characterised samples, respectively (PHE, with data to week 22 of 2019).

Updated value: The original value is retained.

Implications of assumptions and limitations for usage: The diversity of norovirus strains by region varies over time. For instance, replacement events result in the dominant GII.4 strain being replaced every few years, with GII.4/Sydney/2012 being the current major strain. Further studies of variation in norovirus diversity are recommended.

4.3.6 Symptomatic incidence in UK

Original NoVAS parameter: This symptomatic incidence estimates the number of symptomatic infections of norovirus from all sources, not just food. The estimate is derived from the Second Study of Infectious Intestinal Disease in the Community (IID2 Study), which gave an estimate of 47 cases per 1000 person years. This was a cohort study using PCR assays. The study gave rise to estimated 95% confidence intervals of 39.1 to 56.5.

The previous cohort study “A Report of the Study of Infectious Intestinal Disease in England” (IID1 study) estimated a rate of 12.5 cases per 1000 person years. This used EM/ELISA tests. Retesting of the samples by Phillips *et al* (2010) by using PCR produced revised estimates of 45 per 1000 person years (95% credibility interval 38 to 52).

Updated value: No change.

4.4 UK food handling parameters

4.4.1 Probability of lettuce/raspberries being washed before consumption

The original NoVAS report uses a baseline value of 0.8704, derived from a survey of Australian households in 2004 with 524 respondents on their handling of lettuce. A distribution was modelled from the responses using quantitative interpretations of the qualitative categories, as shown in Table 2 (Mitakakis et al., 2004). Data for the proportion of the population who washed their vegetables came from a survey in Melbourne in 1998, and was modelled in the Mitakakis study as a mixture model rather than a binomial. Creating uniform distributions of the quantitative categories, weighting the output by the percentage of respondents and summing the results gave a distribution with a mean of 0.8704. This was then subsequently used as the percentage value in a binomial distribution and extrapolated to raspberries.

The recently released Food and You Wave Five data for England, Wales and Northern Ireland asked 2241 respondents about washing of fruits and vegetables intended to be consumed raw and cooked separately. Following the same method as described above, the estimated mean is 0.60. However, this value was the average for all fruit and vegetables and there is likely to be considerable variability in the domestic washing of foods between different fruit and vegetable types and between differently packaged foods, e.g. between open whole lettuce and pre-washed prepared bagged lettuce.

The original baseline value used is likely to reflect washing frequency for lettuce of the type sampled in the NoVAS study (loose whole head lettuce) but it is possible that the washing frequency for raspberries is better represented by the newer value.

Updated value: No change to the baseline value used.

Implications of assumptions and limitations for usage: Given the variability between different fruit and vegetables and in the different ways food are sold (pre-prepared versus loose at retail) it is recommended that further data are collected to investigate further. A scenario has been conducted using the value of 0.6.

4.4.2 Number of times preparer touches food - meals eaten out/ take away meals

The original NoVAS report assumed a mean value for this parameter of 7.8 times. This input is derived from Stals et al 2015 and is based on observations of sandwich preparers in a kitchen. Sandwiches are thought likely to be touched more times than the average meal, and therefore this may produce a conservative estimate when applied to other food types that are commonly consumed from restaurants and supplied as takeaways, although in restaurants other contacts with e.g. waiters may mitigate this difference.

Updated value: in the absence of further available data this parameter was not revised, but further studies in this area are likely to be cost-effective and logistically feasible.

4.4.3 Proportion of norovirus contamination of lettuce and raspberries removed by washing

Original NoVAS parameter: The proportion of virus removed by washing is described as the product of two values: whether or not the food product is washed post-retail and, if so, the proportion of virus removed by washing. The probability of lettuce being washed before consumption is modelled, as described previously, as a Bernoulli distribution (p=0.8704). The $\log_{10}$ proportion of virus removed by washing was modelled as a PERT distribution (minimum: 0.1, most common: 1, maximum: 2) based on values reported in the QMRA by Barker et al. 2013, based on review of a number of primary studies (Baert et al., 2008, 2009; Butot et al., 2008; Croci et al., 2002; Gulati et al., 2001; Predmore and Li, 2011) which reported reductions ranging 0.1 to 2 $\log_{10}$units, of which nine were reported as 1±0.2 (mean±sd).

Following Barker *et al*. 2013, the same values are used for both lettuce and raspberries.

Some other studies of this parameter have been published. Bae et al. (2011) report a reduction of 0.77 log when iceberg lettuce was washed in running water for 30 seconds. This value is consistent with the PERT distribution used in NoVAS. Tian et al., 2011 reported that 75% of hNoV was removed from surface-inoculated romaine lettuce, and >95% of hNoV was removed from surface-inoculated raspberries, by rinsing in tap water. The original data to support this statement are however not included in the publication.

Updated value: in the absence of further available data this parameter was not revised.

4.4.4 Number of NoV counts on hands, meals eaten out/take away meals

Original NoVAS parameter: log10-linear distributions ($\log_{10}$Intercept -88.38, $\log_{10}$Slope 91.06).

Data were obtained from the NoVAS survey of the prevalence of norovirus genome in the catering environment in outbreak and non-outbreak premises (WP5 of NoVAS) described in Chapter 7 of the final report. Hand swabs were taken from catering premises, defined as a commercial or voluntary organisation that prepares and serves food to the final consumer. This included restaurants, public houses, cafes, takeaways, hotels, guesthouses, and caterers, but excluded passenger carrying ships that travel outside the UK, private houses, mobile retailers, manufacturers and suppliers. Premises were selected at random to represent the food hygiene rating scores and premise types that are represented in their areas. 502 hand swabs were taken in total, with only 15 positive for norovirus.

This chapter contains details of a ‘prevalence survey of norovirus in the catering environment’ but contains no data on enumeration.

Other reports calculate the amount of norovirus particles on food handlers’ hands in different ways. Stals et al., 2015 have made an estimation by multiplying the mass of faecal contamination on the hands of a norovirus shedder by the norovirus contamination per gram of faeces. Duret et al., 2017 calculate this parameter by multiplying the mass of contamination on hands from faeces and vomit with the

norovirus concentration in faeces and vomit. However, the NoVAS data is more specific to the UK and more recent than the data used in the other studies.

Table 3: Data extracted from Figure 37 of the NoVAS report showing the inverse cumulative density function of the count of norovirus particles on the hand.

Inverse cumulative density (Probability that the number of log10-transformed gene copies is below the value in the second column)	Log_{10} gene copies	Equation
0.970	0	Intercept -88.4 Slope 91.1
0.972	0.301	
0.974	0.477	
0.976	0.477	
0.978	0.602	
0.980	0.778	
0.982	1	
0.984	1.04	
0.986	1.26	
0.988	1.54	
0.990	1.57	
0.992	1.85	
0.994	1.91	
0.996	2.69	
0.998	2.80	

Updated value: in the absence of further available data this parameter was not revised.

4.4.5 Proportion of NoV counts transferred from hands to food, meals eaten out/take away meals

Original NoVAS parameter: alpha 0.76, beta 1.04, min 0.026, max 0.46

The risk assessment used a distribution defined in Stals *et al.* 2015, which was derived from observations of surrogate viruses feline calicivirus, hepatitis A virus, human adenovirus and murine norovirus 1. More complicated interactions for norovirus transfer between, ungloved hands, gloved hands, surfaces and food (meat or non-meat) can be found in Duret et al., 2017.

Updated value: in the absence of further available data this parameter was not revised.

4.4.6 Proportion of transferred virus derived from direct faecal contamination

Original NoVAS parameter: Minimum 0, Most likely 0.2, Maximum 1

In the original study this parameter was described by a PERT (0, 0.2, 1) distribution. The most likely value was assumed to be 0.2 because 20% was the next highest decile from the proportion of asymptomatic people excreting norovirus (Amar et al. 2007). The

same proportion was used for gene copies that represent infectious virus when not direct from human faeces as for the other food pathways.

Updated value: Using data presented in Philips *et al* (2010) this parameter has been re-estimated for the adult population giving an updated value for food handlers of 8.7% for the most likely estimate.

4.4.7 Proportion of food not cooked, post handling

The original NoVAS study uses a mean value of 0.667, derived from the following data sources: *'We were unable to find any data on the proportion of touches that would be before or after cooking in catering establishments. Duret and colleagues (2017) assumed that "The food serving includes three ingredients, one of the ingredients is cooked". In the absence of other data, we consequently assumed that on average 1/3 of all touches precede a final cooking step or 2/3 of touches of food ready to eat without further heat treatment.'*

Updated value: Defra data reports that sandwiches, on which Duret *et al.* based their figures, account for less than 2% of takeaways consumed by weight and that the majority of takeaways contain food likely to be cooked (https://www.gov.uk/government/statistical-data-sets/family-food-datasets). This may therefore be an overly conservative estimate. However, no further information was found to provide a quantitative estimate for the wider catered and takeaway food sector. The value has been revised with a mean of 0.5 and used a broader range (min 0.3, max 0.7) to represent the substantial uncertainty in this value (assessor's opinion).

Implications of assumptions and limitations for usage: Further studies in this area are likely to be feasible and cost-effective.

5. Sensitivity analysis and scenario analysis

5.1 Sensitivity analysis

The sensitivity of the assessment to the input value distributions was measured in two ways.

Built-in @Risk Sensitivity analysis functionality

Firstly, we ran both the Exposure and Risk components to convergence and applied @Risk's built-in regression analysis functionality to the results, considering dose per meal for each of the five food pathways, the risk per meal for each of the five food pathways and the total yearly risk as the key outputs. The regression coefficient for each input variable measures the sensitivity of the output to that particular input distribution.

Combined regression analysis in R

Because the risk assessment consist of two separate @Risk models – an exposure model and a risk model – the built-in function could not analyse sensitivity jointly across these two components. We therefore also conducted a combined sensitivity analysis by running the Exposure component for 10,000 iterations, saving sampled input values, and then using each Exposure output in turn for a single run of the Risk component,

then fitting a linear regression model using the inputs and outputs (function `lm`; R version 3.6.1 (2019-07-05), RStudio Version 1.0.153, packages tidyverse 1.2.1, readxl 1.3.1 and kabelExtra 1.1.1).

Iterations where the sampled “intrinsically susceptible” value is zero return an estimated risk of zero, as do iterations where no contaminated exposures occur (although this would be considerably rarer). Including these iterations in the analysis allows the sensitivity of the analysis to the “intrinsic susceptibility” distribution to be estimated, but means the residuals are less normally distributed.

This approach used has the limitation that each Risk component iteration would normally use multiple, independent Exposure iteration results, rather than repeatedly using the same result.

To improve the normality of the residuals and reduce the influence of extreme we fitted both the complete dataset and a dataset filtered to remove iterations where “intrinsically susceptible” took a value of zero, which removes the vast majority of the zero-valued outputs. We also tried fitting the regression to two transformations of the data – rank-transformed and $\log_{10}$-transformed – as well as to the untransformed data. For log transformation, zero values were replaced with a value of 1 in 10 billion.

We used the Standardised Regression Coefficients (SRC) to interpret the importance of each input. These measure the contribution of each input to the overall variance of the output variable. For the rank-transformed data we used Standardised Rank Regression Coefficients (SRRC).

5.2 Scenario analysis

In addition to this sensitivity analysis, the impact of unquantified uncertainty associated with specific key parameters on the number of symptomatic norovirus infections as estimated by the risk assessment was investigated. Alternative scenarios for the values of parameters describing the **duration of immunity**, **proportion of virus that is infectious**, **proportion of consumers washing their retail fruit and vegetables,** and **duration of excretion of virus post-infection** were simulated.

5.2.1 Duration of immunity

The duration of immunity was originally modelled as a PERT distribution with minimum, most likely, and maximum values of 6, 6 and 24 months, respectively. In order to explore the effects of a longer duration of immunity, as predicted in other studies (see section 4.3), the most likely value within the PERT distribution was changed to 9 months.

5.2.2 Proportion of infectious particles

The proportion of norovirus gene copies that are infectious is still a matter of debate and is difficult to measure as wild-type virus cannot be cultured in cells. A scenario was modelled where the proportion of infectious particles assumed in the original NoVAS risk assessment was replaced by the estimates given in Stals *et al.*, 2015.

5.2.3 Frequency of washing

The baseline value of the frequency with which consumers wash purchased fresh produce (0.8704) was derived from a study by Mitakakis et al., 2004. Although the

recently released Food and You Wave Five data for England, Wales and Northern Ireland gave a lower estimate for this value (0.60), the original baseline value used is likely to better reflect washing frequency for lettuce of the type sampled in the NoVAS study (loose whole head lettuce). However, it is credible that the washing frequency for raspberries is better represented by the newer value. We therefore model a scenario using the estimate from Food and You Wave Five.

5.2.4 Duration of excretion of norovirus post-infection

The baseline value used in the NoVAS report was 16.4 days, based on Milbrath et al., 2013. Given other studies which found shedding to be of longer duration (see section 4.3), a scenario was modelled with the mean duration of excretion being double the original value, or 32.8 days.

6. Results of the 2019 revised risk assessment

The following results are presented within each section:

- the arithmetic mean and the 5th and 95th percentile values for the probability of infection per meal via each of the five pathways considered in the model (oysters, leafy greens, raspberries, catered food and takeaway) in an individual who is intrinsically susceptible but has no acquired immunity, for comparability to the original report;
- the average number of exposures per infection (i.e. the reciprocal of the arithmetic mean value above) as this is simpler to interpret;
- the percentage of infection risk (in an individual who is intrinsically susceptible but has no acquired immunity) represented by each of the five pathways considered in the model;

The results below are also reported within each section but are also collected in section 6.6 to allow comparison between all risk assessment model versions, parameter sets and scenarios:

- the arithmetic mean of the total expected number of symptomatic infections per 1000 person-years in an individual who is intrinsically susceptible and including acquired immunity;
- the arithmetic mean for the number of symptomatic infections per year in the total population, accounting for intrinsic and acquired immunity.

For the first set of results (original NoVAS risk assessment run to convergence, section 6.1), we also report the arithmetic mean of the expected number of infections per 1000 person-years in an individual sampled at random from the population (i.e. not assuming intrinsic susceptibility) who has no acquired immunity, to allow comparison with the estimate given in the original report. However, as this does not take account of acquired immunity it is not a relevant value for estimating pathogen burden.

Convergence of all distributions was monitored, with the risk assessment being run for 150,000 iterations or until mean convergence was achieved (tolerance 5%, confidence level 95%); this value ensured full convergence.

Results are presented for the following models and scenarios:

1. Rerun of original NoVAS risk assessment (using original files and original parameter values, but running to convergence)
2. Reformatted NoVAS risk assessment (original immunity component and original parameters, only changes are cosmetic)
3. Revised immunity component risk assessment (as detailed in section 3) using original parameters
4. FSA risk assessment (revised immunity component detailed in section 3 and revised parameters detailed in section 4)
5. Scenarios (all using FSA risk assessment as above):
    i. Exploration of the effect of increasing the duration of immunity using a PERT(6, 9, 24) distribution;
    ii. Exploration of the effect of using the significantly lower infectivity estimate assumed in Stals et al.;
    iii. Exploration of using the more recent FSA Food and You produce washing data;
    iv. Exploration of doubling the adult and whole-population rate of asymptomatic carriage.

For the FSA risk assessment, the decision was made to ignore estimated norovirus doses per meal below 10^{-6} infectious units for all food types, as the model was returning a proportion of estimated doses per meal as low as 10^{-30} infectious particles and this was slowing down the simulation.

6.1 Original NoVAS risk assessment run to convergence

Exposure model

Pathway	Infection per meal, arithmetic mean	Infection per meal, 5th percentile	Infection per meal, 95th percentile	Expected number of meals per infectious exposure
Oyster	0.00691	0	0.0311	145
Lettuce	0.0000770	0	0.0000517	12,987
Raspberry	0.0000995	0	0.0000428	10,050
Catered	0.000809	0	0.00297	1,236
Takeaway	0.000815	0	0.00296	1,227

These mean values were extremely close to the values given in the NoVAS final report (the percentiles are not equivalent to the credible intervals calculated in the NoVAS report and should not be directly compared).

Risk model

Pathway	Risk via pathway
Oyster	3.08%
Lettuce	15.89%
Raspberry	2.96%
Catered	43.79%
Takeaway	34.29%

The expected rate of infection from all sources in a randomly-selected individual ignoring acquired immunity was estimated as 22.09 infections per 1000 person-years, compared to a value of 23.76 in the original report.

The expected rate of symptomatic infection in intrinsically susceptible individuals via all pathways when acquired immunity was included was estimated as 9.49 per 1000 person-years (5th and 95th percentile values of 0.29 and 34.80 respectively). When scaled to reflect the rate in an individual sampled at random this yields an estimate of 7.12, compared to the value in the original report of 7.65.

This translates to an estimated average of 501,376 cases in the population as a whole per year.

6.2. Reformatted model with original parameters

Exposure model

Pathway	Infection per meal, arithmetic mean	Infection per meal, 5th percentile	Infection per meal, 95th percentile	Expected number of meals per infectious exposure
Oyster	0.007	0	0.03	143
Lettuce	0.0000825	0	0.0000527	12,121
Raspberry	0.000102	0	0.0000437	9,804
Catered	0.000812	0	0.00294	1,232
Takeaway	0.000813	0	0.00296	1,230

Risk model

Pathway	Risk via pathway
Oyster	2.94%
Lettuce	15.96%
Raspberry	2.30%
Catered	45.08%
Takeaway	33.73%

The expected rate of symptomatic infection was estimated as 9.89 per 1000 person-years (5th and 95th percentile values of 0.31 and 36.55 respectively), translating to an estimated 522,508 cases in the population as a whole per year.

This was judged to be sufficiently close to the values from the original risk assessment model above (9.49 and 501,376) to conclude that reformatting the model did not introduce any errors into the risk assessment calculation process.

6.3 Original risk assessment with changed immunity representation

As described in section 3, the risk assessment was modified with two changes made to the immunity component. The first was to calculate new infections each day as the average number of all infections per day (food and non-foodborne, symptomatic and asymptomatic). This removed the complexity of having to estimate a value for food infections prior to running the model. The second change was to modify the way the parameters "Estimated incidence of symptomatic" and "Symptomatic incidence" are calculated to reflect the assumption that intrinsically non-susceptible individuals cannot develop infection, which is more consistent with the reported data but increases the infection rate for susceptible individuals.

The exposure assessment for this scenario is unchanged, and therefore exposure results are not reported.

Risk model

Pathway	Risk via pathway
Oyster	2.77%
Lettuce	15.96%
Raspberry	2.27%
Catered	44.99%
Takeaway	34.01%

The expected rate of symptomatic infection was estimated as 6.88 per 1000 person-years (5^{th} and 95^{th} percentile values of 0.149 and 26.7 respectively), translating to an estimated 363,484 cases in the population as a whole per year.

This reflects the fact that, with these modifications to the model, the proportion of susceptible individuals in the population who happen to have acquired immunity at the time of exposure is higher. As expected, there are no changes to the proportion of risk via each pathway as the exposure component is unchanged.

6.4 FSA risk assessment (model changes as detailed in section 3 and updated parameters as detailed in section 4)

Exposure model

Pathway	Infection per meal, arithmetic mean	Infection per meal, 5^{th} percentile	Infection per meal, 95^{th} percentile	Expected number of meals per infectious exposure
Oyster	0.00631	0	0.0278	158
Lettuce	0.0000679	0	0.0000386	14,728
Raspberry	0.0000804	0	0.0000247	12,438

Pathway	Infection per meal, arithmetic mean	Infection per meal, 5th percentile	Infection per meal, 95th percentile	Expected number of meals per infectious exposure
Catered	0.000495	0	0.0011	2,020
Takeaway	0.000491	0	0.00109	2,037

Risk model

Pathway	Risk via pathway
Oyster	2.71%
Lettuce	30.43%
Raspberry	3.92%
Catered	36.94%
Takeaway	25.99%

The expected rate of symptomatic infection was estimated as 7.21 per 1000 person-years (5th and 95th percentile values of 0.212 and 27.0 respectively) in intrinsically susceptible individuals, translating to an estimated 380,919 cases in the population as a whole per year.

Collectively, the changes recommended in this review increase the risk per meal for all pathways but when combined with the effect of changed representation of immunity there is a net reduction in the estimated total cases compared to the original NoVAS model. The lettuce pathway becomes relatively more important but otherwise a similar general pattern is seen: the catered and takeaway pathways between them account for well over half of the risk, while oysters and raspberries are responsible for a very small fraction of overall risk (even though the risk per meal from oysters is highest, reflecting that they are consumed infrequently).

6.5 Scenario modelling

6.5.1 duration of immunity 6, 9, 24

The exposure assessment for this scenario is unchanged, and therefore exposure results are not reported.

Risk model

Pathway	Risk via pathway
Oyster	2.65%
Lettuce	30.38%
Raspberry	3.88%
Catered	37.06%
Takeaway	26.02%

The expected rate of symptomatic infection was estimated as 5.69 per 1000 person-years (5th and 95th percentile values of 0.129 and 22.3 respectively), translating to an estimated 300,711 cases in the population as a whole per year.

As expected, the total rate of infection is reduced, reflecting the fact that increasing the average duration of immunity increases the proportion of individuals with acquired immunity at the time of exposure. The relative risk via each pathway remains unchanged.

6.5.2 Stals et al. infectivity

Exposure model

Pathway	Infection per meal, arithmetic mean	Infection per meal, 5th percentile	Infection per meal, 95th percentile	Expected number of meals per infectious exposure
Oyster	0.000128	0	0.000402	7,813
Lettuce	0.00000095	0	0.00000047	1,052,632
Raspberry	0.00000123	0	0.000000296	813,008
Catered	0.0004	0	0.000826	2,500
Takeaway	0.000397	0	0.000818	2,519

As might be expected, reducing the assumed infectivity of non-faecally derived contaminating virus increases the expected number of meals required to cause an infection in a susceptible individual very significantly for the first three pathways (oysters, lettuces and raspberries). The effect on the catered and takeaway pathways is far less pronounced, reflecting that a proportion of the exposures via this pathway are assumed to be recent contaminations from asymptomatically-infected food preparation workers and this virus is assumed to be fully infectious.

Risk model

Pathway	Risk via pathway
Oyster	0.10%
Lettuce	0.66%
Raspberry	0.10%
Catered	58.2%
Takeaway	41.0%

The expected rate of symptomatic infection was estimated as 3.66 per 1000 person-years (5th and 95th percentile values of 0.0193 and 15.8 respectively), translating to an estimated 193,365 cases in the population as a whole per year.

The significant reduction in exposure via the first three pathways means that the catered and takeaway pathways represent virtually all (99%) of the infection risk in this scenario.

6.5.3 FSA Food and You produce washing data

Exposure model

Pathway	Infection per meal, arithmetic mean	Infection per meal, 5th percentile	Infection per meal, 95th percentile	Expected number of meals per infectious exposure
Oyster	0.63%	0.00%	2.78%	158
Lettuce	0.01%	0.00%	0.01%	7,576
Raspberry	0.02%	0.00%	0.00%	6,579
Catered	0.05%	0.00%	0.11%	2,020
Takeaway	0.05%	0.00%	0.11%	2,037

This scenario describes an alternative assumption about consumer produce washing habits. As such, the oyster, catered and takeaway pathways are unaffected, while the rate of infection per lettuce and raspberry meal increases.

Risk model

Pathway	Risk via pathway
Oyster	2.04%
Lettuce	44.2%
Raspberry	5.65%
Catered	28.3%
Takeaway	19.8%

The expected rate of symptomatic infection was estimated as 9.52 per 1000 person-years (5th and 95th percentile values of 0.316 and 33.8 respectively), translating to an estimated 502,961 cases in the population as a whole per year.

The results of this scenario illustrate that the total burden of norovirus and the importance of lettuce as an exposure pathway is sensitive to our assumptions about the frequency with which consumers wash purchased produce.

6.5.4 doubled duration of excretion

Exposure model

The exposure assessment for this scenario is unchanged, and therefore exposure results are not reported.

Risk model

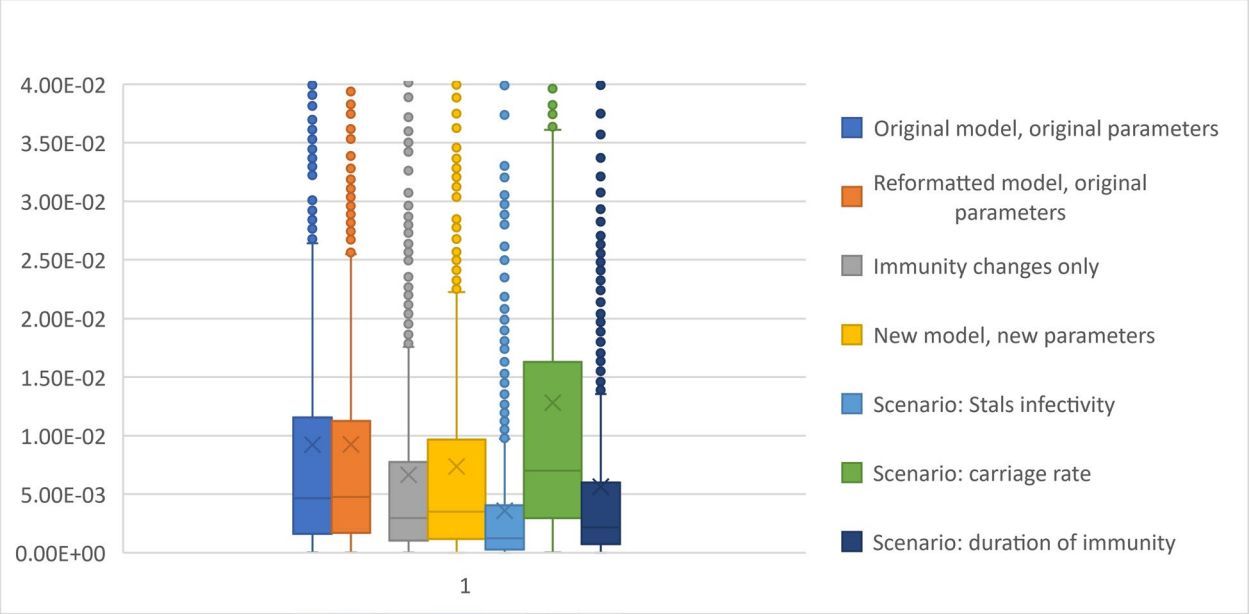
Pathway	Risk via pathway
Oyster	1.12%
Lettuce	42.5%
Raspberry	5.26%
Catered	29.7%
Takeaway	21.4%

The expected rate of infection was estimated as 12.5 infections per 1000 person-years (5th and 95th percentile values of 0.572 and 42.6 respectively), translating to an estimated 657,801 cases in the population as a whole per year.

6.6 Model comparison

Estimated mean risk per thousand person-years

Model	Expected potential infections per thousand person-years
Original NoVAS RA	9.49
Reformatted NoVAS, original parameters	9.89
Reformatted plus immunity changes	6.88
FSA RA, new parameters	7.21
Scenario 1: immunity 6, 9, 24	5.69
Scenario 2: Stals infectivity	3.66
Scenario 3: less food-washing	9.52
Scenario 4: doubled carriage duration	12.5



N.B. mean (in table above) shown as “X”.

Total annual symptomatic infections in the population, accounting for intrinsic and acquired immunity and using the estimated 2018 population of 66,432,000[3]

Model	Mean expected infections per year
Original NoVAS RA	504,352
Reformatted NoVAS, original parameters	525,610
Reformatted plus immunity changes	365,642
FSA RA, new parameters	383,180
Scenario 1: immunity 6, 9, 24	302,496
Scenario 2: Stals infectivity	194,513
Scenario 3: less food-washing	505,946
Scenario 4: doubled carriage duration	661,705

[3] Figures in text use the 2017 population estimates to calculate the totals, for comparability to the NoVAS results

6.7. Sensitivity analysis results

Built-in @Risk Sensitivity analysis functionality: Exposure component

The Exposure model required 1.5 million iterations to converge. The results are shown below. Parameters are colour-coded by pathway (yellow: oyster pathway, green: lettuce pathway, pale red: raspberry pathway, blue: catered and takeaway pathways); unshaded parameters are shared between all pathways. Parameters in bold represent variability, italics represents uncertainty. Values given are regression coefficients.

Rank	Dose/oyster meal		Dose / lettuce meal		Dose / raspberry meal		Dose / catered meal		Dose / takeaway meal	
1	**Concentration of gene copy norovirus in gland**	**0.106**	**Original Concentration in lettuce/gram (log)**	**0.055**	**Original Concentration in Rasp/gram (log)**	**0.047**	**Number of times food touched**	**0.049**	**Number of times food touched**	0.049
2	**Proportion of viable particles**	**0.091**	**Proportion of viable particles**	**0.05**	**Proportion viable particles**	**0.043**	Probability that food item touched is NOT subsequently heated after touch	0.031	Probability that food item touched is NOT subsequently heated after touch	0.032
3	**Is the oyster contaminated ?**	**0.04**	**Probability of washing fruit or veg**	**-0.039**	**Weight of raspberry meal/grams**	**0.033**	Log Proportion of Noro viable in food (mean)	0.018	Log Proportion of Noro viable in food (mean)	0.018
4	**Weight of oyster meal eaten g**	**0.034**	**Weight of lettuce meal/grams**	**0.025**	**Probability of washing fruit or veg**	**-0.032**	Proportion of virus transferred by each touch (alpha)	0.005	Proportion of virus transferred by each touch (beta)	-0.006
5	**Proportion of oyster that is composed of digestive gland**	**0.024**	**Proportion removed by washing (log)**	**-0.012**	**Proportion removed by washing (log)**	**-0.01**	Proportion of virus transferred by each touch (beta)	-0.003	Proportion of virus transferred by each touch (alpha)	0.005
6	-	-	-	-	-	-	Mean proportion of virus on	0.003	Mean proportion of virus on	0.003

							hands directly from human rather than via food (max)		hands directly from human rather than via food (max)	
7	-	-	-	-	-	-	Proportion viable when direct from human	0.003	Proportion viable when direct from human	0.002

Built-in @Risk Sensitivity analysis functionality: Risk component

The Risk model required 0.8 million iterations to converge. The results are shown below. Values given are regression coefficients.

Rank	Risk in susceptible, oyster		Risk in susceptible, lettuce		Risk in susceptible, raspberry		Risk in susceptible, catered		Risk in susceptible, takeaway		Adjusted risk > Intrinsic susceptible	
1	**Number of oyster meals in a year?**	**0.163**	**Number of lettuce meals in a year?**	**0.055**	**Number of raspberry meals in a year?**	**0.035**	**Number of catered meals in a year?**	**0.174**	**Number of takeaway meals in a year?**	**0.185**	**Individual susceptibility**	0.198
2	Dose-response model, alpha	0.005	Dose-response model, alpha	0.014	Dose-response model, alpha	0.009	Dose-response model, alpha	0.034	Dose-response model, beta	-0.028	**Duration of immunity**	-0.106
3			Dose-response model, beta	-0.014	Dose-response model, beta	-0.008	Dose-response model, beta	-0.031	Dose-response model, alpha	0.028	**Number of catered meals in a year?**	0.043
4											**Number of takeaway**	0.033

Rank	Risk in susceptible, oyster	Risk in susceptible, lettuce	Risk in susceptible, raspberry	Risk in susceptible, catered	Risk in susceptible, takeaway	Adjusted risk > Intrinsic susceptible	
						meals in a year?	
5						Norovirus genotype diversity	0.031
6						Proportion population intrinsically susceptible	0.031
7						**Number of lettuce meals in a year?**	0.029
8						**Number of oyster meals in a year?**	0.026
9						Dose-response model, beta	-0.024
10						Duration of carriage	0.023
11						Dose-response model, alpha	0.022
12						Carriage rate in asymptomatics from IID1/person	-0.021
13						Relative change in	-0.012

Rank	Risk in susceptible, oyster		Risk in susceptible, lettuce		Risk in susceptible, raspberry		Risk in susceptible, catered		Risk in susceptible, takeaway		Adjusted risk > Intrinsic susceptible	
											background incidence	
14											**Number of raspberry meals in a year?**	0.007

Combined regression analysis in R

The results are shown below. Parameters are shaded to make it easier to track individual parameters across the sensitivity analyses. Only six parameters are shown for illustrative purposes and because no multiple hypothesis testing correction was applied to the results, meaning the model is likely to be overfitted and the borderline results should be treated with caution.

Rank	Untransformed risk, all individuals	Untransformed risk, susceptible individuals only	Log-transformed risk, all individuals	Log-transformed risk, susceptible individuals only	Rank-transformed risk, all individuals	Rank-transformed risk, susceptible individuals only
1	b-parameter, load of virus on hand	b-parameter, load of virus on hand	Original concentration in lettuce (gram)	Original concentration in lettuce (gram)	Original concentration in lettuce (gram)	Original concentration in lettuce (gram)
2	a-parameter, load of virus on hand	a-parameter, load of virus on hand	b-parameter, load of virus on hand	b-parameter, load of virus on hand	Original concentration in raspberry	b-parameter, load of virus on hand
3	Duration of immunity	Duration of immunity	a-parameter, load of virus on hand	a-parameter, load of virus on hand	b-parameter, load of virus on hand	a-parameter, load of virus on hand

Rank	Untransformed risk, all individuals	Untransformed risk, susceptible individuals only	Log-transformed risk, all individuals	Log-transformed risk, susceptible individuals only	Rank-transformed risk, all individuals	Rank-transformed risk, susceptible individuals only
4	Number of takeaway meals	Number of times food touched, takeaway	Original concentration in raspberry	Original concentration in raspberry	a-parameter, load of virus on hand	Original concentration in raspberry
5	Number of times food touched, takeaway	Number of takeaway meals	Number of oyster meals in a year	Number of oyster meals in a year	Number of oyster meals in a year	Number of oyster meals in a year
6	Probability that food is not heated after touching	Probability that food is not heated after touching	Probability that food is not heated after touching	Probability that food is not heated after touching	Proportion of population intrinsically susceptible	Probability that food is not heated after touching

The two parameters related to the load of norovirus on hand (a-parameter, load of virus on hand and b-parameter, load of virus on hand) were among the top four factors in all the tornado plots.

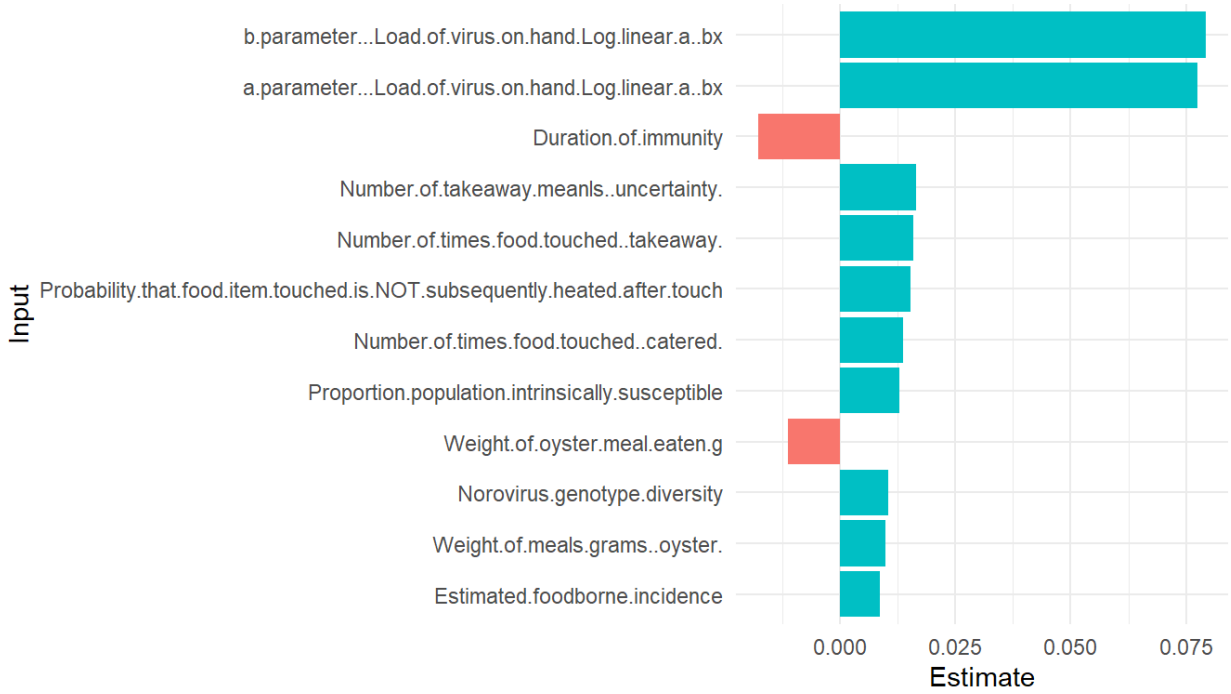
The original concentrations of norovirus in lettuce and raspberries had the two largest Standardised Rank Risk Coefficient (SRRC) parameters.

Other inputs related to catering and takeaways featured highly in all the tornado plots.

Other parameters identified as important included the number of takeaway meals consumed in a year, the duration of immunity, and the proportion of the population that is intrinsically susceptible.

Excluding non-susceptible individuals did not change the results much, although as might be expected the proportion of the population that is intrinsically susceptible was no longer a significant input in any results (since it no longer had an effect).

SA of Untransformed adjusted risk, all individuals



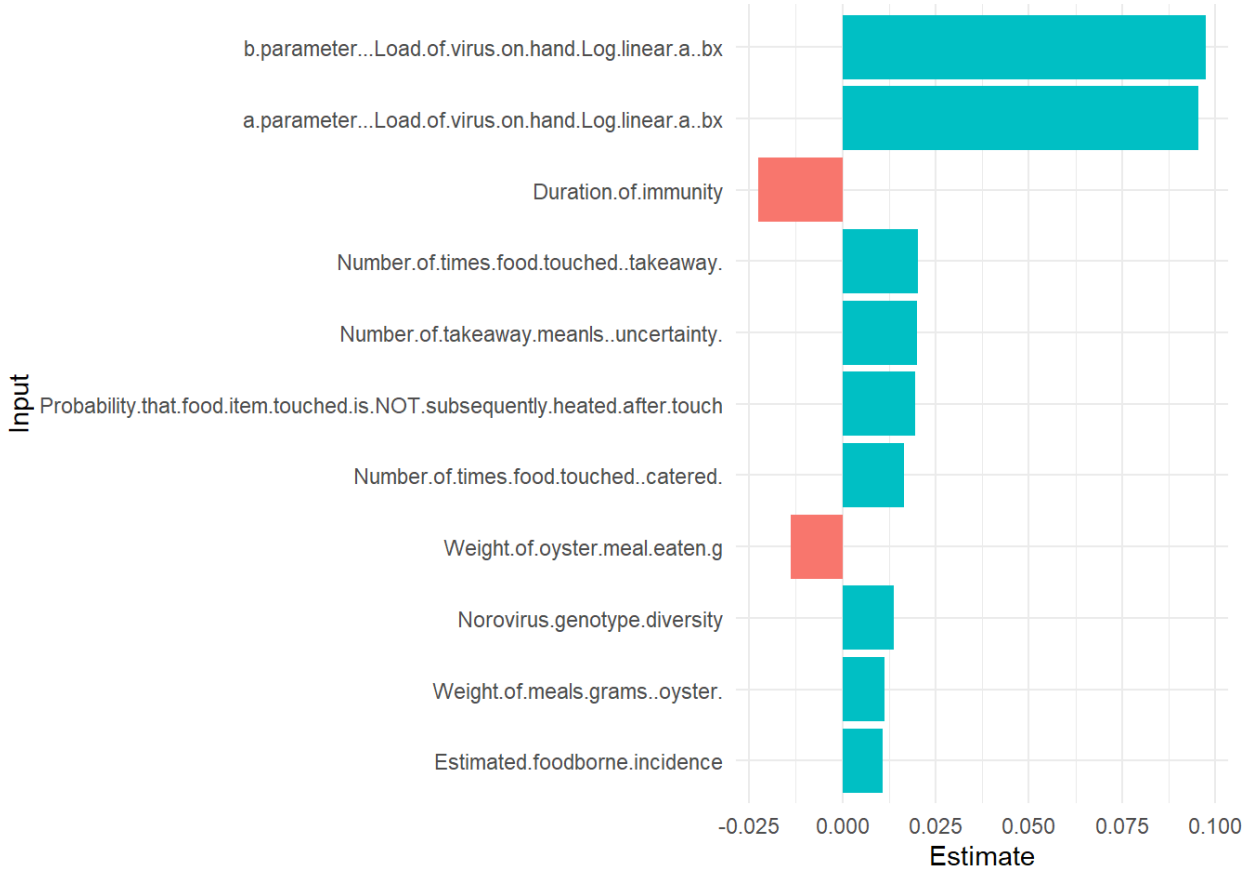
The tornado plot for the untransformed adjusted risk shows that that the two parameters related to the Load of virus on hand to have a much larger Standardised Risk Coefficient (SRC) than any of the other inputs.

Duration of immunity had the third largest SRC in magnitude. The SRC was negative indicating that the risk decreased with increased duration. The next four five largest SRC were all positive and related to takeaway and or catered food. The proportion of the population that is intrinsically susceptible had the eight largest SRC.

Sensitivity analysis of the untransformed risk should be directly related to the expected number of norovirus cases. However, the regression model may be particularly influenced by the extreme risk values. This is because the regression model assumes its residuals will be Normally adjusted whereas the distribution of the adjusted risk is very asymmetric. (Firstly, there are many simulated people with zero risk, mainly because they are not susceptible to norovirus. Furthermore, the remaining risks are roughly log-Normally distributed.)

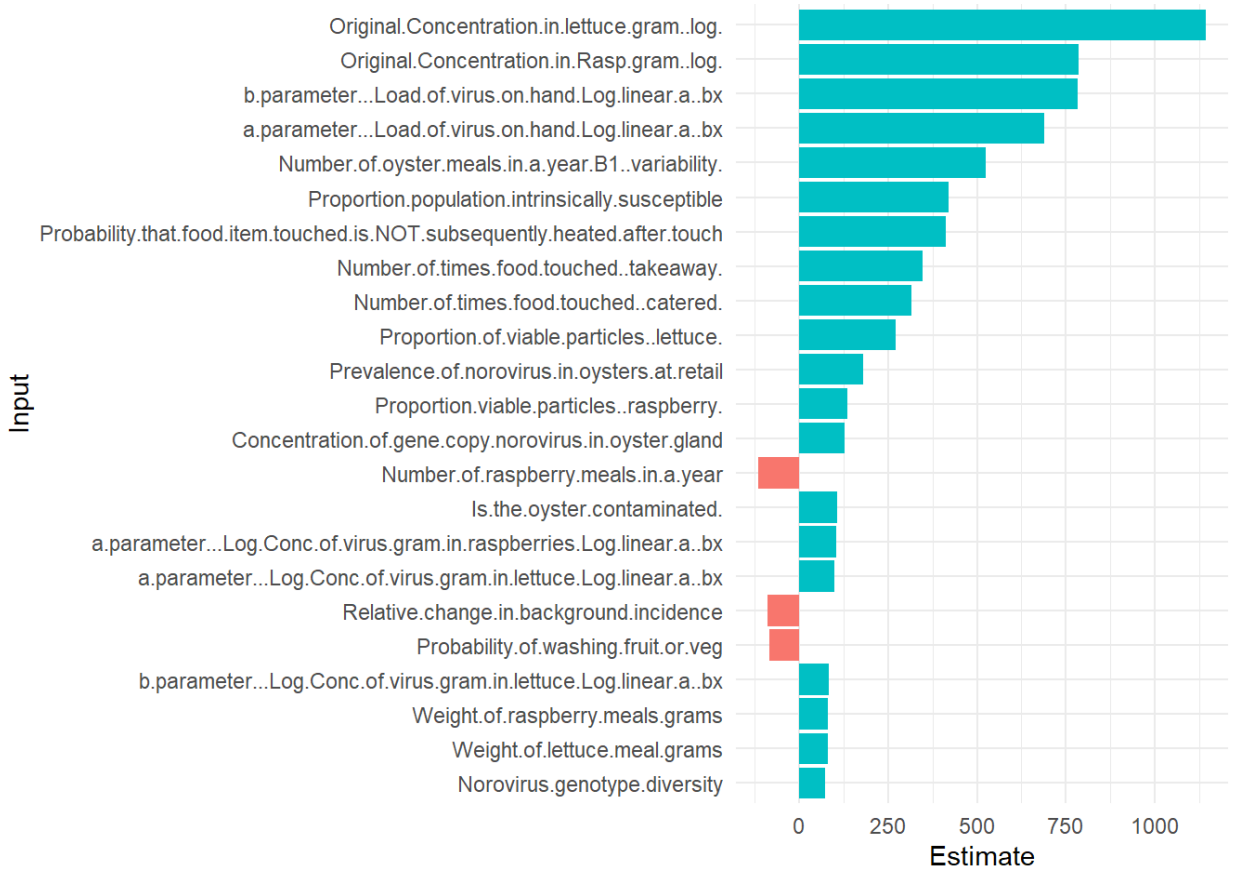
The SRC (and later SRRC) values used for this and other tornado plots in this section have not been corrected to reflect multiple comparisons, hence coefficients with relatively low values should be treated with caution as they may reflect spurious associations.

SA of Untransformed adjusted risk, susceptible individuals only



Removing individuals simulated to be non-susceptible led to a very similar tornado plot as before. However, the input determining the proportion of the population that is intrinsically susceptible was longer found to be significant in the model. This is to be expected since this input can only influence who is susceptible not the level of risk for those known to be susceptible.

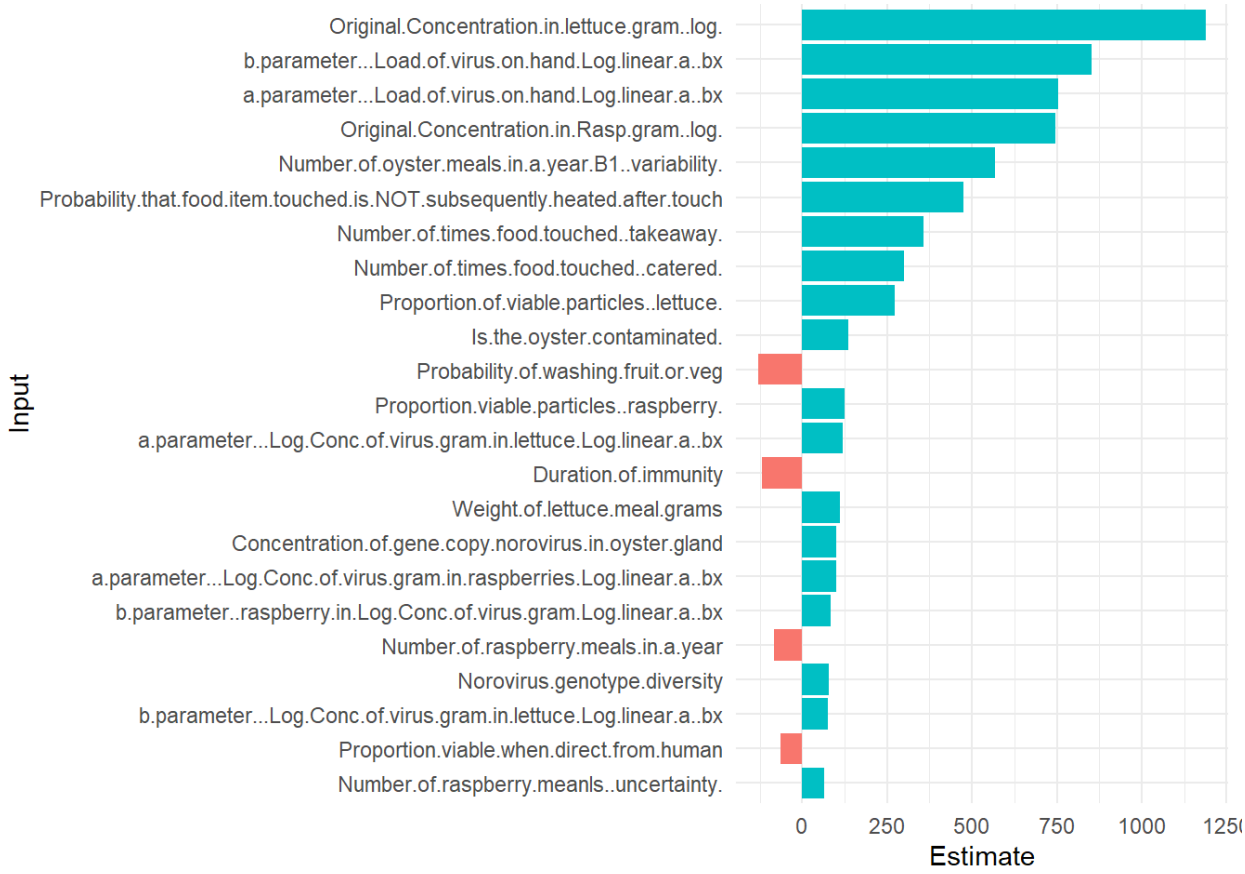
SA of the rank of the adjusted risk, all individuals



The tornado plot for the rank of the adjusted risk shows that that the original concentrations of norovirus in lettuce and raspberries have the two largest Standardised Rank Risk Coefficient (SRRC) parameters. They are followed by the parameters related to the load of virus on hand (which were identified in as most important using the untransformed risk.)

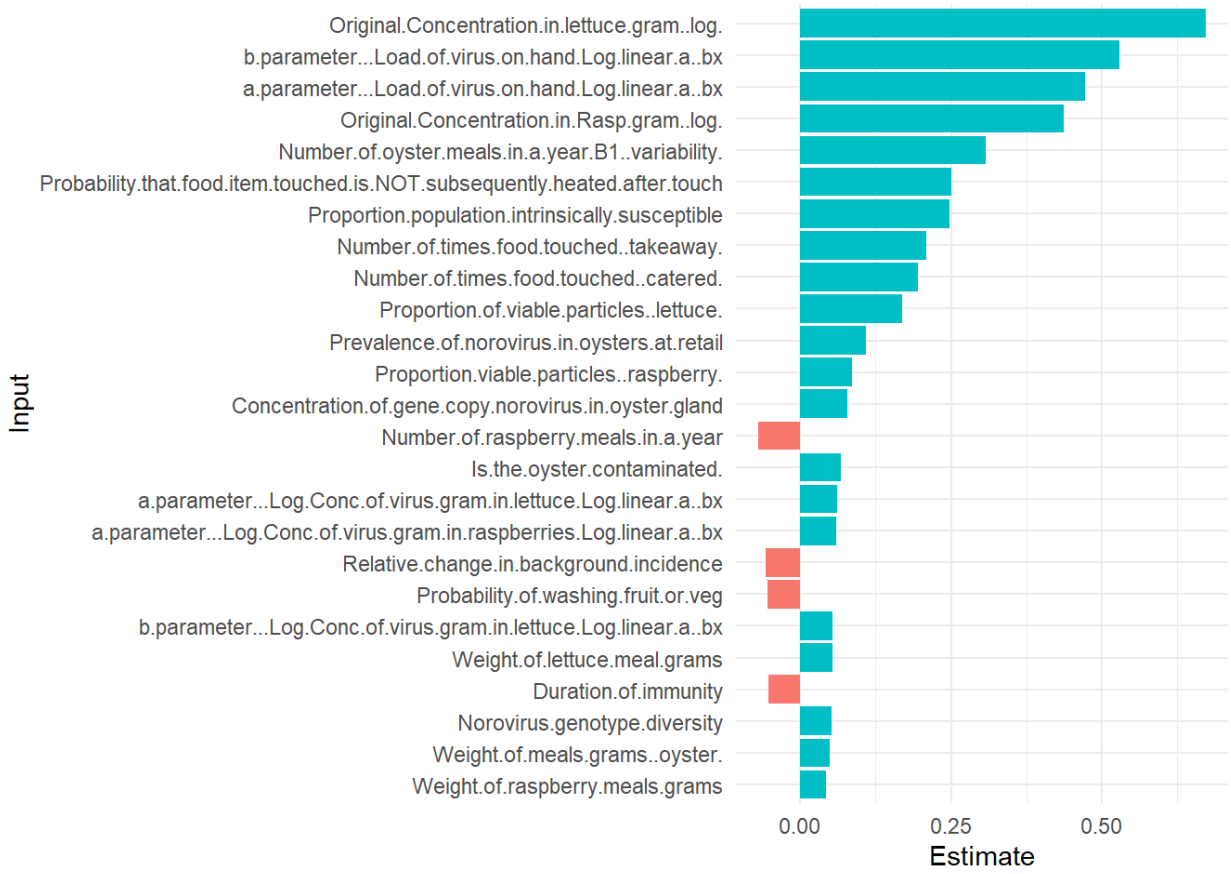
The next five largest SRRC includes the proportion of population that is intrinsically susceptible, and some factors related to takeaways and catering also identified by the sensitivity analysis on the untransformed risk. However, factors related to oyster consumption were also had large SRRC values.

SA of the rank of the adjusted risk, susceptible individuals only

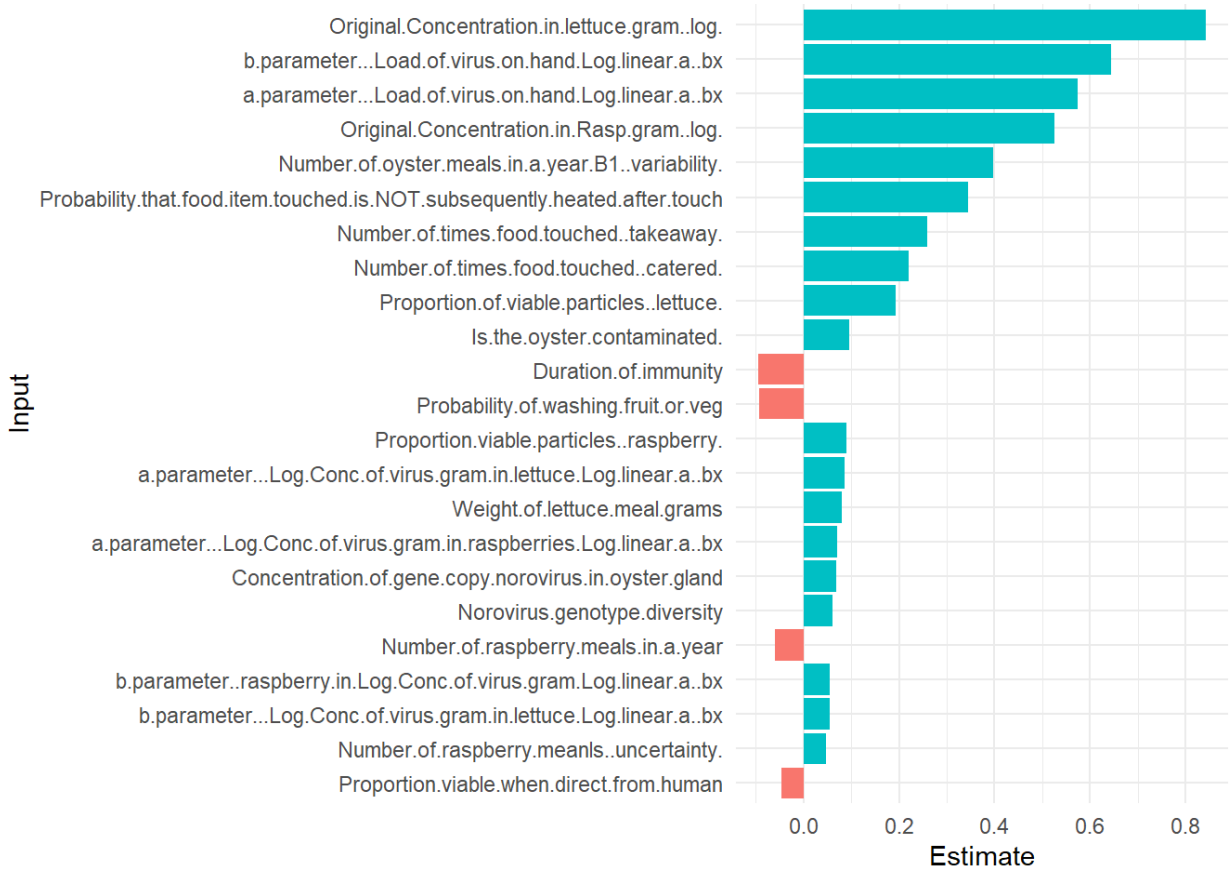


The nine inputs with the highest SRRC values after excluding non-susceptible individuals were all from the top 10 when all individuals were included. (The inputs had similar SRRC in much the same order.) The one exception was again the proportion of the population that is intrinsically susceptible, which was longer found to be significant in the model.

SA of the log-transformed adjusted risk to all individuals



SA of the log-transformed adjusted risk to susceptible individuals only



The inputs with the ten highest SRC for the log-risk were the same as the those with the ten highest SRRC (in a similar order). Again, the proportion of the population that is intrinsically susceptible which was only found to be significant when including non-susceptible individuals.

7. Risk assessment conclusions

The estimated number of symptomatic infections according to the revised risk assessment using the revised parameter estimates (section 6.4) is approximately 25% lower than that estimated using the original risk assessment with the original parameter estimates (section 6.1). The results from section 6.3 demonstrate that this most of this reduction is attributable to the modifications to the immunity component, which mean that the proportion of susceptible individuals in the population who happen to have acquired immunity at the time of infection, and are therefore not protected from developing disease, is higher. The use of the revised parameter estimates makes relatively little difference to the estimated total number of symptomatic infections beyond the changes resulting from these modifications.

However, the use of the revised parameter estimates does increase the proportion of infections acquired via the lettuce pathway. The average exposure per meal actually decreases relative to that in the original NoVAS assessment, as it does for all pathways (compare exposure results for section 6.4 against 6.1 and 6.2), but the estimated consumption frequency of lettuce is 23% higher, increasing from 72.1 to 88.9 meals per year; the original NoVAS estimate was estimated indirectly based on total lettuce

consumption and average portion size, but the updated estimate is taken directly from survey data available to the FSA and is likely to be more accurate.

The result obtained from the alternative scenarios reinforce our conclusion that small changes in the assumed duration of immunity, a value associated with a high level of uncertainty, can have substantial effects on the total estimated burden, although as the exposure remains unchanged the relative importance of the five pathways is also unchanged. They also indicate that the total estimated burden is again highly dependent on assumptions about the proportion of contaminating virus that remains infectious, another parameter associated with a high level of uncertainty, and that in this case the relative importance of each pathway may also be affected by changes to this assumption (assuming, as our assessment and the original NoVAS assessment do, that the infectivity of virus originating from asymptomatic carriers is higher). Our third scenario demonstrates that the frequency with which consumers wash produce purchased at retail before consumption is another relatively important factor. This is an area where improved data could feasibly be obtained relatively cost-effectively.

8. Conclusions to this review

Fitness for purpose of the model

Our review recommended few significant changes to the approach used during the NoVAS project, which has resulted in a novel and useful quantitative framework for estimating the relative contribution of different pathways to the burden of UK foodborne norovirus and to estimating the overall burden. The framework allows additional pathways to be added and it is straightforward to update parameters and investigate their impact.

One area not considered in this review is the issue of broader model uncertainty. It is important to acknowledge that gaps exist in the science underlying our understanding of norovirus transmission and epidemiology. Although these uncertainties are difficult to assess formally for complex numerical models, some initial approaches to assessing the sensitivity of risk estimates to deeper uncertainty are discussed in e.g. Spiegelhalter & Riesch (2011).

Scope of appropriate model usage

Although several parameters in the risk assessment are likely to vary between seasons, available data are not sufficient to allow a risk assessment that fully reflects the effects of seasonality. As a result, the model should be used for long-term estimates rather than season-specific estimates.

Similarly, although norovirus genotypes and strains within genotypes vary in traits such as bioaccumulation efficiency and seasonality, the known data gaps and uncertainties in these differences are such that current EFSA guidance is not to attempt modelling of strain-specific differences in these traits.

Modelling control measures

The risk assessment has been developed so that estimating the impact of control measures for the different food pathways on the number of infections before acquired immunity is taken into account should be relatively straightforward, although this will depend on the nature of the control measures to be investigated. For instance, investigating the impact of changing the percentage of lettuces or raspberries washed after purchase requires a single parameter value change, while reducing the number of touches in food preparation, for instance by the use of gloves, would require a minor change to the formulae.

Estimating the impact on total infections once acquired immunity is taken into account is more complicated. There are two main reasons for this. Firstly, while the reduction in food associated number of infections on symptomatic cases will be modelled, the impact on asymptomatic cases attributable to food (which are not differentiated from fully-resisted infectious exposures) will not. All other things being equal it would be expected that any control measures which impact on symptomatic cases will similarly impact asymptomatic cases and thus reduce the number of people who are immune. Secondly, the risk assessment only considers infection by primary infection (directly from the food) and not secondary spread (food then person to person). Therefore, any person to person spread (either symptomatic or asymptomatic) that will be prevented due to the first person no longer being infected via food is not captured by the risk assessment.

The fact that asymptomatic carriage is not divided into food and non-food elements, although not important for estimating the current foodborne burden of norovirus, would also be an issue if the risk assessment was later to be used to estimate the impact of reducing foodborne exposure since no reduction to the asymptomatic carriage rate would be made reflecting the reduction in the foodborne component. To address this either significant additional complexity would be required, or some of the input parameters could be adjusted to compensate (although this would be less precise). Ideally there should also be a further adjustment increasing non-food symptomatic and asymptomatic infections as a result of the reduction in herd immunity from reduced total infections.

Both these factors are a reflection of the dynamic nature of norovirus infection and ideally would require feedback loops that this risk assessment has not been designed to include. A pragmatic approach to approximate the impact may be the best option to account for first of these issues. Firstly, the risk assessment could be run to produce a baseline of both the number and proportion of norovirus infections due to food. Using the second of these figures the number of asymptomatic infections due to food and non-food can be estimated, as well as non-food symptomatic cases. Next the risk assessment is run with the control measures and the results compared to the baseline results and a new estimated of number of symptomatic and asymptomatic cases due to food produced. These figures are added to non-food symptomatic and asymptomatic cases to obtain an estimate for overall infection numbers and the risk assessment is then run again with these new parameters and the controls measured. These last two steps may need to be repeated until the proportion of cases due to food is similar at the start and end of the runs.

Because the model does not dynamically model the full process of norovirus transmission such as non-food pathways, independent strain circulation, age-structured exposure, and contact networks, we do not recommend that it should be used in its current form for predicting medium to long-term changes to overall norovirus disease burden as a result of control strategies.

Priority areas for future research

The assessed individual risk is relatively sensitive to several parameters, including the load of virus on the hand of individuals involved in food preparation, the level of contamination of lettuce and raspberries, the frequency of consumption of oysters, the number of times food is touched during preparation and the probability that the food is not heated after touching. Duration of immunity and the frequency of eating takeaway meals appear only in the sensitivity analysis for the untransformed data, suggesting they affect the extreme values but are less important when the influence of these is reduced via data transformation.

Many of these parameters were investigated directly during NoVAS and further research is unlikely to be cost-effective unless there is reason to expect significant variability between groups for these parameters. The exception, for reasons discussed earlier in this report, would be a survey of contamination levels on pre-washed leafy green vegetables. One concern raised during this exercise was the extent to which other leafy green vegetables (such as spinach, rocket etc) or other soft fruit (strawberries and blueberries) should be considered a risk, and exploratory retail surveys of these products could be useful.

Also for reasons discussed above, the frequency of oyster consumption is difficult to estimate with the sample size used for the National Diet and Nutrition Survey, and targeted surveillance of oyster consumers could be useful.

Although not the most highly-scoring parameters, improved estimates of the number of times takeaway food is touched during preparation, and the probability that it is heated after touching, are likely to be relatively cost-effective. This part of the model is likely to benefit from more complexity, and it seems likely that these parameters would vary substantially between different types of takeaway businesses (for example sandwich delicatessens versus fish and chip shops).

The scenario analysis suggests that other priority areas for future research should be the duration of acquired immunity, the estimation of infectivity (particularly at low exposure), the frequency with which consumers wash their leafy green vegetables and soft fruit, and the duration of asymptomatic carriage. Of these, improved estimates of the first and last should be achieved via the FSA's next Infectious Intestinal Diseases (IID) project, which is likely to start during 2020. The estimation of infectivity for low-dose exposure is extremely difficult for pathogens where a laboratory model does not exist; although there are some promising developments in this area, this is unlikely to be achievable with currently validated methods for some time. The most cost-effective is likely to be improving our estimation of the frequency with which consumers wash their leafy green vegetables and soft fruit.

It may be possible to represent the evolution of the system through time in a more realistic fashion, particularly if data were incorporated on relative strain diversity or changing strain diversity and cross-protection, but at the expense of significantly greater complexity. It is also possible that such an approach would still oversimplify other factors such as differing levels of cross immunity between different strains. There might also be advantages to adding seasonality to a dynamic model as mentioned earlier in this report, but this would further increase the complexity of the model and require data on the seasonality of individual parameters, for example food consumption rates, which are not currently available.

9. References

Additional references for Immunity component not in NoVAS report

A report of the Study of Infectious Intestinal Disease in England

The Second Study of Infectious Intestinal Disease in the Community

Barker SF, O'Toole J, Sinclair MI, Leder K, Malawaraarachchi M, Hamilton AJ (2013) A probabilistic model of norovirus disease burden associated with greywater irrigation of home-produced lettuce in Melbourne, Australia. Water Research Volume 47, Issue 3, 1 March 2013, Pages 1421-1432;

de Wit MA, Koopmans MP, Kortbeek LM, van Leeuwen NJ, Vinje J, van Duynhoven YT (2001) Etiology of gastroenteritis in sentinel general practices in The Netherlands. Clin Infect Dis 33:280 – 288

de Wit MA, Koopmans MP, Kortbeek LM, Wannet WJB, Vinje J, van Leusden F, Bartelds AIM, van Duynhoven YT (2001) Sensor, a population-based cohort study on gastroenteritis in The Netherlands: incidence and etiology. Am J Epidemiol 154:666 – 674

Hall AJ, Eisenbart VG, Etingüe AL, Gould LH, Lopman BA, Parashar UD. Epidemiology of foodborne norovirus outbreaks, United States, 2001-2008. Emerg Infect Dis. 2012;18(10):1566–1573.

Lawrence, L., E. Kerrod, R. Gani and S. Leach. 2004. Microbiological risk assessment for norovirus infection – Contribution to the overall burden afforded by foodborne infections Food Standards Agency: London.

Lowther JA, Cross L, Stapleton T, Gustar NE, Walker DI, Sills M, Treagus S, Pollington V, Lees DN (2019) Use of F-Specific RNA Bacteriophage to Estimate Infectious Norovirus Levels in Oysters. Food Environ Virol. 2019 Sep;11(3):247-258. doi: 10.1007/s12560-019-09383-3. Epub 2019 May 21.

Phillips G, Tam CC, Conti S, Rodrigues LC, Brown D, Iturriza-Gomara M, Gray J, Lopman B (2010). Community incidence of norovirus-associated infectious intestinal disease in England: improved estimates using viral load for norovirus diagnosis. Am J Epidemiol. 2010 May 1;171(9):1014-22.

Phillips G, Tam CC, Rodrigues LC, Lopman B (2010). Prevalence and characteristics of asymptomatic norovirus infection in the community in England. Epidemiol Infect. 2010 Oct;138(10):1454-8. doi: 10.1017/S0950268810000439. Epub 2010 Mar 3.

Spiegelhalter D. J. and H Riesch (2011) Don't know, can't know: embracing deeper uncertainties when analysing risks 369 (1956) Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences

Stals A, Jacxsens L, Baert L, Van Coillie E, Uyttendaele M (2015) A quantitative exposure model simulating human norovirus transmission during preparation of deli sandwiches. International Journal of Food Microbiology Volume 196, 2 March 2015, Pages 126-136.

Teunis, P., Sukhrie, F., Vennema, H., Bogerman, J., Beersma, M., & Koopmans, M. (2015). Shedding of norovirus in symptomatic and asymptomatic infections. *Epidemiology and Infection, 143*(8), 1710-1717. doi:10.1017/S095026881400274X

Van Abel N, Schoen ME, Kissel JC, Meschke JS (2017) Comparison of Risk Predicted by Multiple Norovirus Dose–Response Models and Implications for Quantitative Microbial Risk Assessment. Risk Analysis Volume 37, Issue 2

Appendix 1: Risk Assessment Model Framework

The risk assessment is divided into several different components. The first component is the Exposure Model which estimates the number of infectious particles per meal.

Exposure component data inputs:

Input data description	Symbol	Definition	Value	Unit	References
Log Proportion of Noro viable in food	D3	Mean	-1.58		
	D4	Std Dev	0.705		
	D5	Max	0		
	D6	Min	-10		
Probability washing	D7	Mean	0.6	%	Barker et al. 2013
Log Proportion removed by washing	D8	Min	0.1		Barker et al. 2013
	D9	Mod	1		
	D10	Max	2		
Weight of meals/grams	D11	Mean	37.2	g	
	D12	Std Dev	14.7	g	
	D13	Min	0	g	
	D14	Max	1000	g	
Digestive gland proportion of whole Oyster	D15	min	0.017		
	D16	most likely	0.0476		
	D17	max	0.158		
Log number of Gene copies in gland/gram	D18	Mean	1.27	ct/g	Research Project
	D19	Std Dev	0.762	ct/g	
Probability of an oyster at retail testing positive	D20	Number	630		Research project
	D21	Successes	433		

Input data description	Symbol	Definition	Value	Unit	References
Weight of meals/grams	D22	Mean	3.23	g	
	D23	Std Dev	0.83	g	
	D24	Min	-	g	
	D25	Max	-	g	
Log concentration of virus/gram Log linear=a +bx	D26	A	-23.2	where x varies from 0 to 1	
	D27	b	24.2		
Weight of raspberry meals/grams	D28	Mean	3.42	g/meal	
	D29	Std Dev	1.01	g/meal	
	D30	Min	-	g/meal	
	D31	Max	-	g/meal	
Log concentration of virus/gram Log linear=a +bx	D32	a	-28.1	ct/g	
	D33	b	28.9	where x varies from 0 to 1	
Number of times food in meal is touched	D34	Mean	7.8	N	Stals et al. 2015
Load of virus on hand Log linear=a +bx	D35	a	-88.4		REF
	D36	b	91.1		
Proportion of virus transferred by each touch	D37	alpha	0.76		Stals et al. 2015
	D38	beta	1.04		
	D39	min	0.026		
	D40	max	0.46		
Probability that food item touched is NOT subsequently heated after touch	D41	Mean	0.5		
Mean proportion of virus on hands directly from human rather than via food	D42	Min	0		
	D43	Mod	0.12		
	D44	Max	1		
Proportion viable when direct from human	D45	point value	1		

Input data description	Symbol	Definition	Value	Unit	References
Dose response curve	D46	alpha	0.349		Van Abel et al. 2016
	D47	beta	357		

Exposure component data inputs

Parameter	Symbol	Dist used	Uncertainty or Variability	Iterative value	Unit
Oyster model					
Proportion of viable particles	O1	Normal	Variability btw individuals	10^Normal(D3,D4, Truncate(D6,D5))	
Prevalence of norovirus in oysters at retail	O2	Beta	Variability btw years	Beta(D21+1,D20-D21+1)	
Is the oyster contaminated?	O3	Bernoulli	Variability btw individuals	Binomial(1,Beta(S+1,N-S+1))	Binary
Concentration of gene copy norovirus in gland	O5	Normal	Variability btw individuals	10^Normal(D18,D19)	ct/g
Proportion of oyster that is composed of digestive gland	O6	Pert	Variability btw individuals	Pert(D15,D16,D17)	
Final infectious concentration	O7	Calc	Calc	O1*O3*O5*O6	i/g
Weight of oyster meal eaten g	O8	Gamma	Variability btw individuals	Normal(D11,D12,Truncate(D13,D14))	g
Dose / oyster meal	O9	Calc	Calc	O7*O8	i/meal
Infection / oyster meal		Calc	Calc	1-(1+O9/D47)^-D46	inf/meal
Lettuce model					
Proportion of viable particles	L1	Normal	Variability btw individuals	10^Normal(D3,D4, Truncate(D6,D5))	
Probability of washing fruit or veg	L2	Binomial	Variability btw individuals	Binomial(1,D7)	Binary
Proportion removed by washing (log)	L3	Pert	Variability btw individuals	Pert(D8,D9,D10)	
Original Concentration in lettuce/gram (log)	L4	Uniform	Variability btw individuals	D26+(D27*Uniform(0,1)	ct/g
Concentration after washing (log)	L5	Calc	Calc	IF(L2=1,L4-L3,L4)	

Final viable concentration Lettuce	L6	Calc	Calc	(10^L5)*L1	i/g
Weight of lettuce meal/grams	L7	Normal	Variability btw individuals	Lognorm2(D22,D23)	g
Dose / lettuce meal	L8	Calc	Calc	L6*L7	i/meal
Infection / lettuce meal		Calc	Calc	1-(1+L8/D47)^-D46	inf/meal
Raspberry model					
Proportion viable particles	R1	Normal	Variability btw individuals	10^Normal(D3,D4, Truncate(D6,D5))	
Probability of washing fruit or veg	R2	Binomial	Variability btw individuals	Binomial(1,D7)	Binary
Proportion removed by washing (log)	R3	Pert	Variability btw individuals	Pert(D8,D9,D10)	
Original Concentration in Rasp/gram (log)	R4	Uniform	Variability btw individuals	10^D32+(D33*Uniform(0,1))	ct/g
Concentration after washing (log)	R5	Calc	Calc	IF(R2=1,R4-R3,R4)	
Final viable concentration Rasp	R6	Calc	Calc	(10^R5)*R1	i/g
Weight of raspberry meal/grams	R7	Normal	Variability btw individuals	Lognorm2(D28,D29)	g
Dose / raspberry meal	R8	Calc	Calc	R6*R7	i/meal
Infection / raspberry meal		Calc	Calc	1-(1+R8/D47)^-D46	inf/meal

Appendix 2: UK norovirus outbreak data from 1992-2016 provided by Public Health England.

Only primary food vehicles are reported.

Food vehicle category	Vehicle description	No. of outbreaks	No. associated with infected food handler
Composite | mixed foods	A selection of sandwiches	1	0
Composite | mixed foods	All buffet foods	1	1
Composite | mixed foods	Buffet meal	8	5
Composite | mixed foods	Chinese - various foods	2	0
Composite | mixed foods	Cold buffet foods - mainly sandwiches	1	0
Composite | mixed foods	Cold food	1	1
Composite | mixed foods	Cold starters	1	1
Composite | mixed foods	Egg mayonnaise sandwiches	1	0
Composite | mixed foods	Ham + pease pudding sandwiches	1	0
Composite | mixed foods	Italian - pasta dish	1	1
Composite | mixed foods	Mexican grill with various chipotle containing ingredients	1	0
Composite | mixed foods	Mixed or buffet meals	1	0
Composite | mixed foods	Pasta salad	1	0
Composite | mixed foods	Pizza	1	1
Composite | mixed foods	Potato salad	1	0
Composite | mixed foods	Quiche - quiche Lorraine	1	0
Composite | mixed foods	Rice salad	1	1
Composite | mixed foods	Salad	3	1
Composite | mixed foods	Salad + rolls	1	1
Composite | mixed foods	Salad bar	1	0
Composite | mixed foods	Sandwiches	8	6
Composite | mixed foods	Sausage rolls and Cajun chicken strips	1	1
Composite | mixed foods	Supermarket foods used to make buffet of sandwiches, quiche and sausage roll but no specific item identified as vehicle	1	1
Composite | mixed foods	Three bean salad	1	0

Food vehicle category	Vehicle description	No. of outbreaks	No. associated with infected food handler
Composite | mixed foods	Turkey sandwiches	1	0
Composite | mixed foods	Various foods	1	1
Condiments + sauces	Mayonnaise	2	2
Crustacea + shellfish	Crab - claws	1	1
Crustacea + shellfish	Lobster - tail	1	0
Crustacea + shellfish	Mussels and cockles (octopus frumenty, roast halibut, cod in cider)	1	1
Crustacea + shellfish	Oysters	50	2
Crustacea + shellfish	Oysters eaten raw	1	0
Crustacea + shellfish	Oysters served with lemon on ice prepared by outside caterers	1	0
Crustacea + shellfish	Prawn cocktail	1	0
Crustacea + shellfish	Prawns - with mayonnaise	1	1
Crustacea + shellfish	Raw oysters	2	0
Desserts, cakes + confectionery	Cakes with icing	1	0
Desserts, cakes + confectionery	Cake - christening	2	1
Desserts, cakes + confectionery	Gateau - peach + raspberry	1	0
Desserts, cakes + confectionery	Meringue - fresh fruit salad + cream	1	1
Desserts, cakes + confectionery	Profiteroles	1	0
Desserts, cakes + confectionery	Slices - custard	1	1
Desserts, cakes + confectionery	Syllabub - raspberry	1	0
Finfish	Fish	1	1
Finfish	Salmon	1	1

Food vehicle category	Vehicle description	No. of outbreaks	No. associated with infected food handler
Milk + dairy products	Margarine	1	1
Mixed finfish + crustacea | shellfish	Seafood - prawn + salmon starter	1	1
Mixed finfish + crustacea | shellfish	Seafood platter	2	0
Not known	Not known	178	61
Other foods	Cold food buffet	1	0
Other foods	Vegetable soup	1	1
Potable water	Private drinking water - well	1	0
Poultry meat	Chicken	1	1
Poultry meat	Chicken - coronation	2	1
Poultry meat	Chicken - drumsticks	2	1
Poultry meat	Chicken - nuggets	2	2
Poultry meat	Chicken stick, nibbles, burgers	1	0
Poultry meat	Chicken tikka	1	1
Poultry meat	Chilli chicken tostada	1	0
Poultry meat	Turkey	2	1
Poultry meat	Turkey - roast	1	1
Red meat	Beef	1	0
Red meat	Ham	2	2
Red meat	Ham hock	1	1
Red meat	Meats - pie	1	1
Red meat	Sausages	1	0
Vegetables + fruit	Carrots - raw	1	1
Vegetables + fruit	Fresh herbs - watercress	1	0
Vegetables + fruit	Fruit salad - raspberries, blueberries, blackberries and melon (sliced at hotel)	1	0
Vegetables + fruit	Lettuce - green salad	1	1

Food vehicle category	Vehicle description	No. of outbreaks	No. associated with infected food handler
Vegetables + fruit	Lettuce, cucumber (open salad bar for self service)	1	1
Vegetables + fruit	Melon + papaya cocktail	1	1
Vegetables + fruit	Mixed vegetables - salad	1	1
Vegetables + fruit	Mixed vegetables - tomato + cucumber	1	0
Vegetables + fruit	Mixed vegetables - salad	1	0
Vegetables + fruit	Mushrooms - raw	1	1
Vegetables + fruit	Orange juice	2	1
Vegetables + fruit	Salads	1	1
Vegetables + fruit	Side salads	1	1
Total		**322**	**119**

Appendix 3: RASFF data from 1979 to 2017 concerning norovirus

Adapted from Papapanagiotou (2017).

	Alert	Border rejection
Food	**107**	**42**
Bivalve Molluscs	**61**	**37**
Oyster	51	0
Clams	4	35
Mussels	4	0
Scallops	1	2
Fruit and Veg	**46**	**5**
Raspberries	31	1
Strawberries	5	3
Tomatoes	3	0
Blueberries	2	0
Lettuce	2	0
Blackberries	1	1
Lingonberries	1	0
Forest fruit mix	1	0

Appendix 4: Food pathways excluded from the risk assessment

Food pathway category	Rationale for excluding from risk assessment
Foods of animal origin (FoAO)	
Poultry *(chicken, turkey, duck, goose, pigeon, etc.)*	Poultry is not known to be a reservoir for norovirus and there is no UK data on norovirus contamination of retail poultry. Poultry will undergo cooking and other processing (e.g. defeathering, evisceration, skin removal, etc) which may reduce or eliminate any norovirus that may be present. Norovirus outbreaks associated with poultry are rare in the UK, with only 17 outbreaks reported between 1992 to 2016. This data can be found in Table 4, Appendix 1. Six were associated with infected food handlers. In many cases the food vehicle descriptive text provided was ambiguous in terms of whether other ingredients may be involved (e.g. did chicken burgers include salad?), meaning poultry could not be definitively identified as the vehicle in any of these outbreaks.
Red meat *(beef, pork, lamb, goat, veal, venison, etc.)*	Red meat is not considered a reservoir for norovirus and we are not aware of any UK data on norovirus contamination in retail meat. Red meat will undergo cooking and other processing (e.g. hide removal, evisceration, etc) which may reduce or eliminate any norovirus that may be present. Norovirus outbreaks associated with red meat are rare in the UK with only 10 outbreaks reported between 1992 to 2016 of which 5 were associated with infected food handlers. This data can be found in Table 4, Appendix 1.
Fish *(freshwater and marine varieties)*	Although the majority of fish are fished from deeper cleaner waters, it is plausible that some fish may be sourced or farmed from waters (includes coastal waters, rivers and lakes) which may be contaminated with norovirus from human sewage and sewage effluent. However, we are not aware of any UK data on norovirus contamination in retail fish. Fish generally tend to be descaled, gutted, cleaned, possibly filleted, cooked and to a lesser extent smoked before being consumed. These will help to remove or eliminate any norovirus contamination that may be present. Average adult consumption of raw fish in the UK is less than 0.3g per person per day. There were only 2 norovirus outbreaks which were linked with fish in the UK between 1992 and 2016, one of which was associated with an infected food handler. This data can be found in Table 4, Appendix 1.
Other bivalve molluscs excluding oysters *(mussels, cockles, clams and scallops)*	This category of food would include the other types of bivalve molluscs, typically mussels, cockles, clams and scallops. These may be sourced from fresh and marine waters (e.g. coastal waters, rivers and lakes) which may be contaminated with norovirus from human sewage and sewage effluent. Most of these bivalve molluscs will tend to be cooked before being consumed which should eliminate the risk of norovirus. However, some of the methods used to cook these bivalve molluscs (e.g.

Food pathway category	Rationale for excluding from risk assessment
Foods of animal origin (FoAO)	
	steaming mussels) may potentially lead to some of these food products being undercooked and therefore norovirus surviving. RASFF data from 1979 to 2017 (Table 5, Appendix 2) contains 51 alerts for norovirus in oysters and 10 for other bivalve molluscs including clams, mussels and scallops. UK outbreak data between 1992 and 2016 details two outbreaks, one in clams and the other in mussels and cockles. Therefore, outbreaks for this type of bivalve molluscs do occur although they are lower in comparison to oysters. This data can be found in Table 4, Appendix 1. UK Consumption of bivalve molluscs (other than oysters) that are eaten raw is low (adult population mean < 0.1g per day).
Cephalopods *(squid, cuttlefish, octopus, etc.)*	Although most squid and octopus are fished from deeper cleaner waters, it is plausible that some may be sourced from waters (includes coastal waters, rivers and lakes) which may be contaminated with norovirus from human sewage and sewage effluent. There is no data on norovirus contamination in UK retail cephalopods. Squid, cuttlefish and octopus are generally prepared and cleaned (I.e. highest-risk parts removed) and tend to be cooked before being consumed which will reduce or eliminate any norovirus contamination that may be present. The consumption of squid and octopus in the UK is low (adult population mean is 0.2g per person per day). Data between 1992 and 2016 suggest that squid, octopus and other cephalopods are not a main cause of norovirus illness in the UK as there were only one outbreaks involving a dish which consisted of octopus amongst other seafood ingredients. This data can be found in Table 4, Appendix 1.
Crustacea *(prawns, shrimps, crabs, lobster, etc.)*	It is plausible that some crustacea may be sourced or farmed from waters (includes coastal waters, rivers and lakes) which may be contaminated with norovirus from human sewage and sewage effluent. We are not aware of any UK data on norovirus contamination in retail crustacea. Generally, most prawns, shrimps, crabs, lobsters tend to be cooked before being consumed which will reduce or eliminate any norovirus contamination that may be present. No crustacea were recorded as being eaten raw in the NDNS, however some raw dishes may be consumed in the UK such as ceviche. There were only 6 norovirus outbreaks which were linked with crustacea in the UK between 1992 and 2016, two of which were associated with an infected food handler. It should be noted that two of these outbreaks were associated with composite/mixed foods containing prawns. This data can be found in Table 4, Appendix 1.
Eggs	Eggs are derived from poultry which are not considered a reservoir for norovirus. There is UK data on norovirus

Food pathway category	Rationale for excluding from risk assessment
Foods of animal origin (FoAO)	
	contamination found on retail hen, duck or other types of poultry. Generally, eggs (both in terms of individually of part of a composite meal), tend to be cooked before being consumed which will reduce or eliminate any norovirus which may be present. Consumption of raw eggs in the UK is low (adult population mean < 0.1g per person per day). Table 1.5 of the Wave 5 Food and You report states that 7% of respondents consume raw or under-cooked eggs at least once a month, with another 8% sometimes consuming such eggs less frequently. In terms of UK outbreak data, there were no norovirus outbreaks associated with eggs between 1992 and 2016 suggesting that eggs are not a vehicle for norovirus illness in the UK. This data can be found in Table 4, Appendix 1.
Milk and dairy products *(cheese, yoghurt, cream, ice cream, butter, margarine, etc.)*	Milk and dairy products are produced from animals (e.g. cows, goats, etc) which are not considered a reservoir for norovirus and there is no UK data on the norovirus contamination in retail milk or other dairy products. Most milk and products derived from milk will tend to undergo a pasteurisation (heat) process which would eliminate norovirus contamination that may be present. The consumption of raw drinking milk in the UK is low (adult population mean = 0.1g per person per day). There were only two UK norovirus outbreaks associated with cheese and margarine between 1992 and 2016, one of which was linked to an infected food handler. This data can be found in Table 4, Appendix 1. This suggest that milk and dairy products are not a major vehicle for norovirus illness in the UK.
Foods of non-animal origin (FoNAO)	
Other types of berries (strawberries, blueberries, blackberries)	Norovirus in strawberries, blueberries and blackberries were not identified in the EFSA opinion on FoNAO as one of the top pathogen-food combinations often linked to foodborne humans cases. Despite the large 2012 German norovirus outbreak linked to imported strawberries, norovirus outbreaks linked to strawberries are rare and occur much less frequently then those associated with raspberries. A EFSA opinion on berries found that between 2007 and 2011, there was only one norovirus outbreak associated with strawberries in the EU and no outbreaks associated with blueberries and blackberries. UK outbreak data from 1992 to 2016 found three norovirus outbreaks associated with berries one of which was associated with a fruit salad consisting of raspberries, blueberries, blackberries and sliced melons. RASFF data from 1979-2017 (Table 5, Appendix 2) reported that of the 63 alerts and border rejections raised for norovirus in fruit and

Food pathway category	Rationale for excluding from risk assessment
Foods of animal origin (FoAO)	
	vegetables, 8 were for strawberries, 2 for blueberries, 2 for blackberries, 1 to Lingonberries and finally 1 to forest fruit mix. The NDNS adult consumption data for raw strawberries in the UK is over three times greater than that of raspberries. Despite strawberries being consumed more frequently that raspberries, we rarely see norovirus outbreaks associated with strawberries. Post-purchase, strawberries may undergo a washing process to remove other bacterial contamination whereas raspberries are washed less frequently as they are more fragile. This washing step may remove norovirus from the more uniform surface of strawberries hence may partly explain why they tend to be less associated with outbreaks in comparison to raspberries. Consumption of blueberries/bilberries exceed that of raspberries, whereas the consumption of blackberries is a third of the quantity of raspberries. There has been no routine/regular monitoring of berry fruits for the presence of norovirus in most of the EU Member States and there is very limited prevalence data on the rates of contamination of berries (not involved in foodborne outbreaks) by norovirus in the peer-reviewed literature. Maunula et al. (2013) did not find norovirus in 21 fresh strawberries samples at retail in Czech Republic, Poland and Serbia. There is no data on the prevalence and titres of norovirus RNA found on strawberries, blueberries and blackberries on retail sale in the UK. A farm-to-fork quantitative microbial risk assessment for norovirus in frozen strawberries has been previously carried out which involve building a simulation model to replicate the largest known 2012 norovirus outbreak in Germany where about 11,000 people were affected linked to contaminated frozen strawberries imported from China. The input that had the greatest effect on increasing in the number of infections was a high NoV concentration in the water (8 log Genome Copies/L) when compared to the baseline scenario.
Tropical fruit (melons, pineapple, papaya, dates, bananas, oranges, etc.)	Tropical fruits such as melons and pineapples may pose a potential risk as they are grown on the ground and their surface could potentially become contaminated with norovirus in human faeces as a result of 'run-off' etc. The norovirus contamination on the surface of the fruit can be introduced into the fruit flesh during handling and cutting by consumers and food manufacturers. Other fruits, such as bananas, dates, oranges and papaya pose less of a risk as they grow on trees and therefore less likely to be contaminated with norovirus other than via handling.

Food pathway category	Rationale for excluding from risk assessment
Foods of animal origin (FoAO)	
	UK outbreak data from 1992 to 2016 found only three norovirus outbreaks associated with tropical fruits which were orange juice, a melon and papaya cocktail and a fruit salad consisting of a range of berries and melon which was sliced at a hotel. There is a lack of UK data on the prevalence of norovirus in tropical fruits.
Tomatoes	The EFSA opinion on norovirus in tomatoes identified one outbreak between 2007 and 2012 (linked to an infected food handler) and no outbreak was specifically linked to tomatoes in UK outbreak data from 1992 to 2016. This data can be found in Table 4, Appendix 1. Between 1979 and 2017, three RASFF alerts were raised for presence of norovirus in tomatoes (Table 5, Appendix 2). The EFSA opinion notes a lack of information on occurrence and viral load in tomatoes.
Bulb and stem vegetables and carrots (onions, garlic, leek, fennel, asparagus, celery and carrots)	The EFSA opinion on norovirus in bulb and stem vegetables and carrots covers onions, garlic, leek, fennel, asparagus, celery and carrots. There is limited data on the occurrence (prevalence and titres) of norovirus in or on these vegetables. Only three outbreaks were identified in the opinion covering 2007-2012, with two likely to be linked to an infected food handler. No contributory factor information was reported for the third. There was one outbreak in the UK data covering 1992-2016 attributed to raw carrot. This data can be found in Table 4, Appendix 1.
Other foods	
Mixed or composite foods (foods consisting of multiple ingredients such as ready meals, sandwiches, etc.)	These foods consist of multiple ingredients which would make attributing to source of norovirus contamination difficult. A huge number of food types would be included in this food category each of which would have a different set of risk factors associated with them, pathways by which norovirus can contaminate the food, the way they are consumed (i.e. require cooking versus ready-to-eat), etc which would make modelling very difficult.
Natural mineral water	Natural mineral water is source from deep aqua fills from the ground, are sourced from bore holes and bottled without any further processing. This water source is unlikely to be contaminated with norovirus as the water is deep underground and therefore unlikely to come in contact with human faecal waste which is on the surface for the ground. There is a potential for the top of the bore hole to become contaminated with norovirus as a result of flooding events but providing that good hygiene practices are applied during the extraction of the water from the bore hole then the risk is minimal. There is minimal handling of natural mineral water during its extraction therefore the risk of cross-contamination from food handlers with norovirus is low. There is a lack of evidence suggesting that people becoming ill with norovirus through consuming natural mineral water. Similarly,

Food pathway category	Rationale for excluding from risk assessment
Foods of animal origin (FoAO)	
	there is a lack of data on norovirus contamination in retail natural mineral water.

Appendix 5: NDNS data for Leafy Greens

Identifying NDNS food codes that fall within the definition of uncooked leafy greens

Step 1: Identify non-composite food codes that qualify as uncooked leafy greens.
A 2014 EFSA scientific opinion on the microbiological risk posed by leafy greens contains varying but similar definitions of leafy greens (see below). A set of keywords were derived from these definitions for use as a criterion to identify appropriate food codes.

EFSA definitions of leafy greens

beet greens, bitterleaf, bok choy, cabbage, celery, celtuce, Ceylon spinach, chard, chicory, Chinese cabbage, collard greens, cress, endive, epazote, garden cress, garden rocket, komatsuna, lamb's lettuce, land cress, lettuce, mizuna greens, mustard, New Zealand spinach, pak choy, radicchio, rapini, spinach, tatsoi, watercress, water spinach and wrapped heart mustard cabbage among others.

A 2014 EFSA scientific opinion on the microbiological risk posed by leafy greens (EFSA, 2014): "The main species produced in EU are Lactuca sativa, Cichorium endivia, Beta vulgaris, Valerianella locusta, Cichorium intybus, Eruca vesicaria subsp. sativa, Spinacea oleracea, Brassica rapa, Brassica oleracea and Nasturtium officinale. Apart for Spinacea oleracea (spinach), Cichorium intybus (Belgian endive) and Brassica spp. (cabbage), these leafy greens are mostly consumed fresh-cut and raw.

'lettuce' types (Lactuca sativa L.- iceberg and romaine lettuce; Cichorium endivia L. - endive; Beta vulgaris L. - chard; Valerianella locusta (L.) Betcke - lambs lettuce; Cichorium intybus L.- red chicory; Eruca vesicaria subsp. sativa (Mill.) Thell. - rucola and Spinacia oleracea L. - spinach);
leafy brassicas (Brassica rapa L. - Chinese cabbage, and Brassica oleracea L.- kale);
cabbage (Brassica oleracea L. - green red and savoy cabbage);
Belgian endive (Cichorium intybus L.)

Keywords used to identify non-composite foods (keywords with any matches shown in bold)

bitterleaf, bok choy, **cabbage, celery**, celtuce, **chard, chicory, cress, endive**, epazote, **greens**, iceberg, **iceberg, kale**, komatsuna, **lettuce, mustard, pak choi,** pak choy, **raddiccio**, rapini, **rocket**, rocula, romaine, sativa, **spinach**, tatsoi, **watercress**

The following criteria were used to identify applicable NDNS food codes:

1. **Include** foods whose name contains one or more keywords unless clearly irrelevant i.e. pilCHARDs plus liqueurs and supplements containing the letters GREENS.
2. **Exclude** foods whose name indicates cooking or other processing i.e. CANNED, BOILED, STEAMED or DRIED plus MUSTARD POWDER.

3. **Exclude** foods with multi-ingredient recipes (as they will be identified at the next step.

This identified the non-composite foods listed below. All were from the “36B Salad and other raw vegetables” food group. The keywords identified some leafy green foods from “37D Leafy green vegetables not raw” and “37M Other vegetables (including homemade dishes)”, but they were excluded due to cooking or canning.

Food Code	Food Name
1700	CABBAGE - RED RAW
1703	CABBAGE - SAVOY FRESH RAW
1706	CABBAGE, WHITE, FRESH, RAW
1707	CABBAGE - WINTER KALE RAW
1725	CELERY, FRESH RAW
1728	CHICORY FRESH RAW
1742	ENDIVE FRESH RAW
1762	LETTUCE UNSPECIFIED RAW
1782	MUSTARD CRESS RAW
1914	SPINACH FRESH RAW
1947	WATERCRESS RAW
7844	CABBAGE-JANUARY KING-RAW
7846	CABBAGE-SUMMER RAW
7853	LETTUCE-BUTTERHEAD-RAW
7854	LETTUCE-COS-RAW
7855	LETTUCE-ICEBERG RAW
7856	LETTUCE-WEBB
8283	RADDICCIO UNCOOKED
11100	SPINACH RAW NOT BABY SPINACH
11101	SPINACH RAW BABY SPINACH ONLY
11114	ROCKET RAW
11376	SPINACH FRESH RAW (PUREED) FS PROJECT-NDB-YR9
30022	WATERCRESS RAW (PUREED) FF PROJECT

Step 2: Identify all relevant food codes that are or contain uncooked leafy greens.
The following criteria were used to identify applicable NDNS food codes:

1. **Include** all foods comprised in whole or part of one of 23 NDNS food codes identified in Step 1.
2. **Exclude** foods whose name suggests that the Step 1 ingredient might be processed.
3. **Exclude** foods in which the Step 1 ingredient comprises less than 5% of the total weight (to reduce the risk of including consumers with minimal exposure).

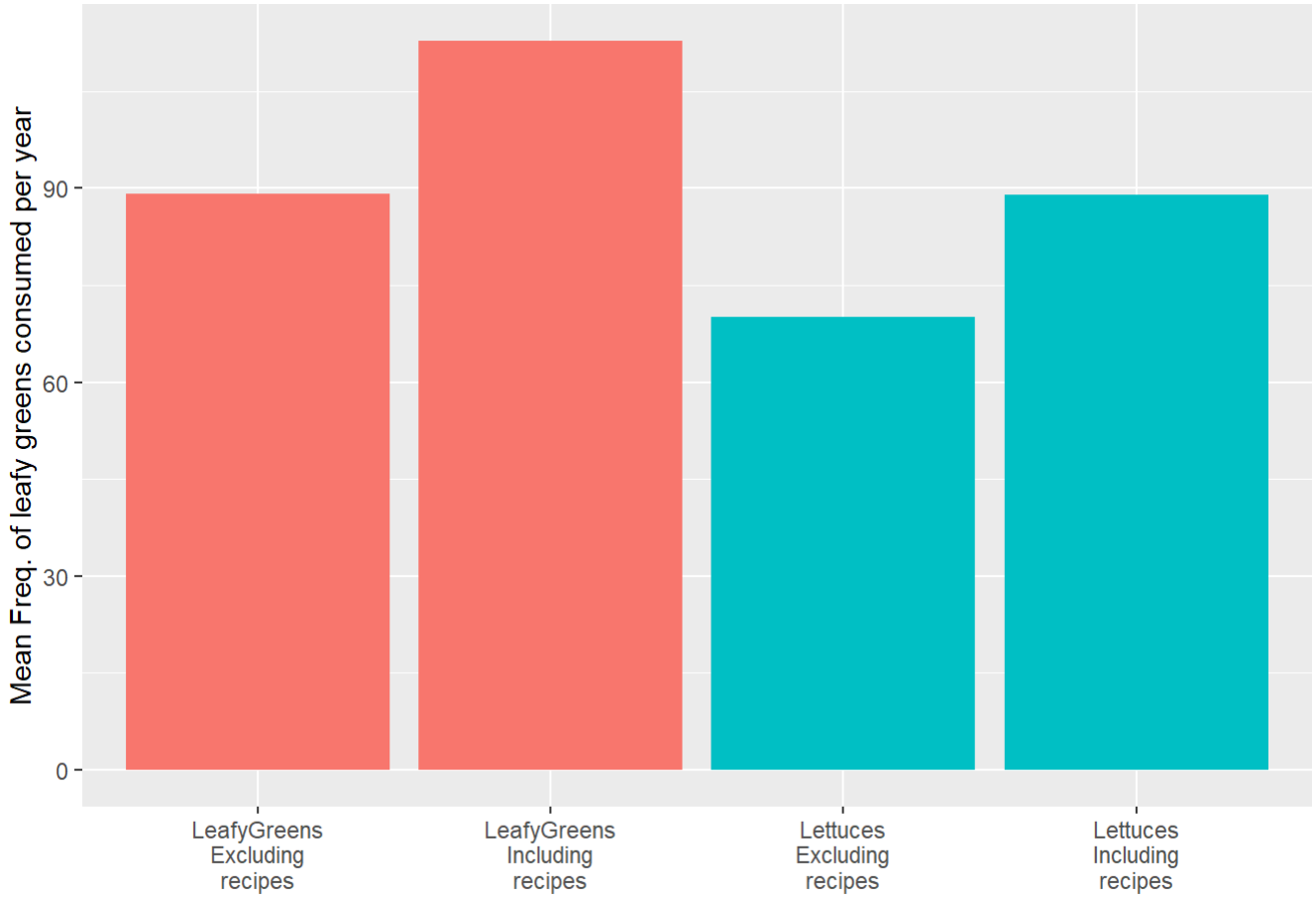
There were 57 relevant food codes (34 composite codes plus the 23 codes listed above). Most of the composite codes were either salads, kebabs and burgers served with cabbage or lettuce or sauerkraut and coleslaw made with cabbage.

Comparing frequency of consumption

In the original NoVAS risk assessment, the frequency of lettuce meals is modelled by a single-parameter model. The **mean** number of meals per year is assumed to vary between people following a Poisson distribution. This rate is then used to determine the **actual** number of meals in a given period (again Poisson distributed).

The rate currently used in the spreadsheet model is 72.1 meals per year. This is based on lettuce (not including recipes) consumed by all adults in NDNS Years 1 to 6. This is close to 70.1 meals per year for lettuce excluding recipes based on NDNS Years 1 to 8. Including recipes in Years 1 to 8 would increase this to 88.9.

If we consider all leafy greens consumed by adults in NDNS Years 1 to 8, then the rate becomes 89.2 meals per year excluding recipes and 112.8 when including recipes.



Comparing quantity consumed on each occasion

In the risk assessment, the size of a lettuce meal is modelled by a truncated Normal distribution. The mean of the distribution currently used in the spreadsheet model is 24.5g per meal. This is based on lettuce (not including recipes) consumed by all adults in NDNS Years 1 to 6. This is close to 25.4 g per meal for lettuce excluding recipes based on NDNS Years 1 to 8. Including recipes in Years 1 to 8 would change this to 24.3 g per meal.

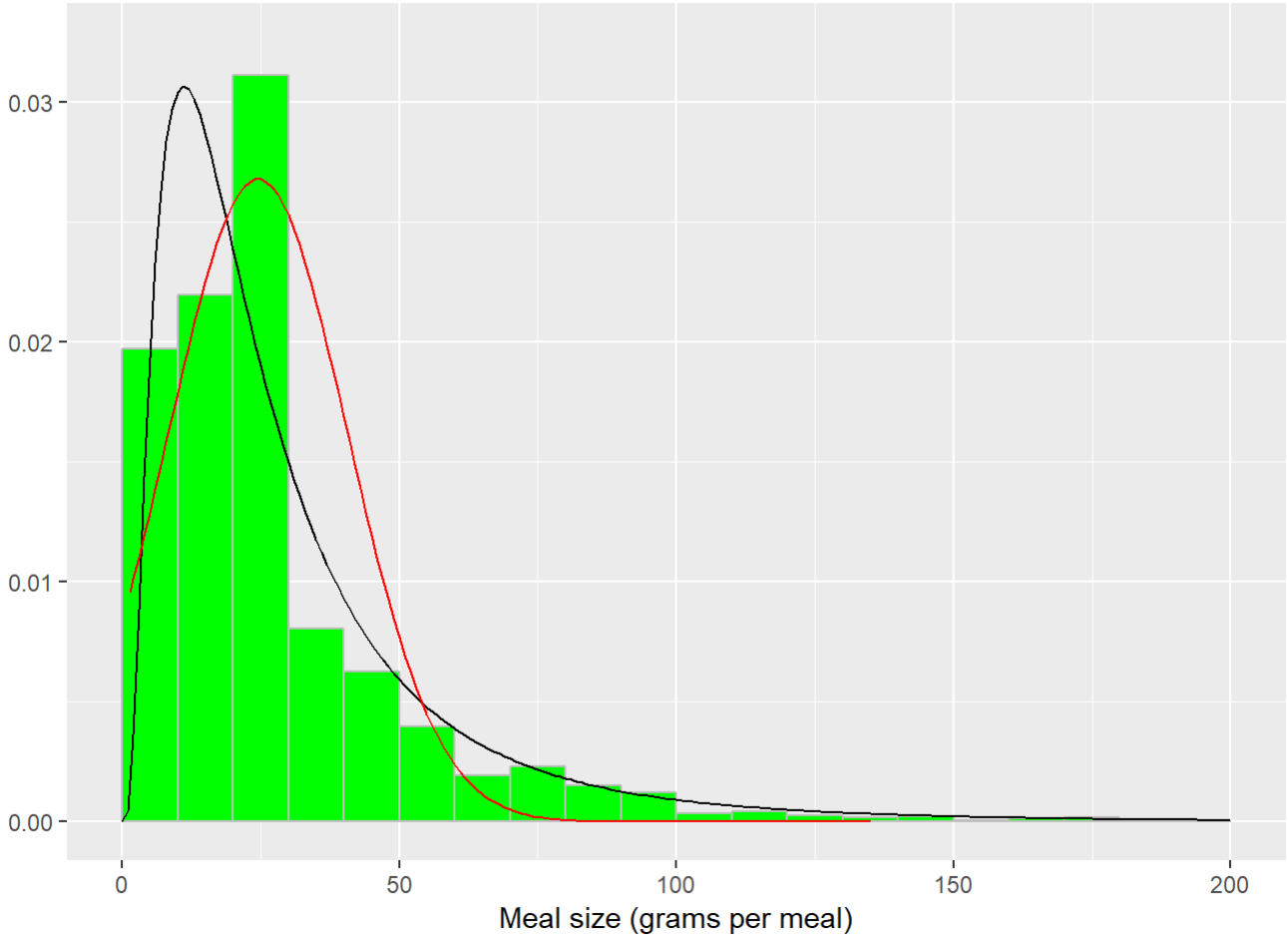
Considering all leafy greens consumed by adults in NDNS Years 1 to 8, then there are more of the larger meal sizes. The mean becomes 29.9 g per meal excluding recipes and 34.1 g per meal ` when including recipes.

	Mean	StdDev	Median.50%	LowPc.5%	HighPc.95%	logMean	logsd
Lettuces excluding recipes	25.43	19.47	22.50	7.40	60.00	3.01	0.69
Lettuces including recipes	24.34	18.65	22.50	6.30	55.57	2.97	0.69
Leafy greens excluding recipes	29.95	25.64	24.75	5.81	80.00	3.10	0.83
Leafy greens including recipes	34.08	28.25	27.00	7.20	86.80	3.23	0.83

The histograms below show how different definitions lead to different quantities of leafy greens consumed. The truncated Normal distribution for the current risk assessment (based just on lettuce) is shown in red. The blue line shows a logNormal distribution to fitted to meal size for leafy greens.

Quantity consumed on each occasion (in grams) of leafy greens (EXCLUDING recipes)

(Adults aged 19+, Years 1 to 8)



Quantity consumed on each occasion (in grams) of leafy greens (INCLUDING recipes)

(Adults aged 19+, Years 1 to 8)

Norovirus Risk assessment - NDNS data for Leafy Greens - Advanced fits

Identifying NDNS food codes that fall within the definition of uncooked lettuce

Step 1: Identify non-composite food codes that qualify as uncooked lettuce.

The following criteria were used to identify applicable NDNS food codes:
1. **Include** ingredients whose name contains “LETTUCE”.
2. **Exclude** foods whose name indicates cooking or other processing i.e. CANNED, BOILED, STEAMED or DRIED plus MUSTARD POWDER.
3. **Exclude** foods with multi-ingredient recipes (as they will be identified at the next step).

This identified the non-composite foods listed below. All were from the “36B Salad and other raw vegetables” food group. The keywords identified some leafy green foods from “37D Leafy green vegetables not raw” and “37M Other vegetables (including homemade dishes)”, but they were excluded due to cooking or canning.

FoodCode	FoodName	IngredientCode	IngredientName	IngredientFraction
1762	LETTUCE UNSPECIFIED RAW	1762	LETTUCE UNSPECIFIED RAW	1
7853	LETTUCE-BUTTERHEAD-RAW	7853	LETTUCE-BUTTERHEAD-RAW	1
7854	LETTUCE-COS-RAW	7854	LETTUCE-COS-RAW	1
7855	LETTUCE-ICEBERG RAW	7855	LETTUCE-ICEBERG RAW	1
7856	LETTUCE-WEBB	7856	LETTUCE-WEBB	1

Step 2: Identify all relevant food codes that are or contain uncooked lettuce.

The following criteria were used to identify applicable NDNS food codes:
1. **Include** all foods comprised in whole or part of one of 5 NDNS food codes identified in Step 1.
2. **Exclude** foods whose name suggests that the Step 1 ingredient might be processed.
3. **Exclude** foods in which the Step 1 ingredient comprises less than 5% of the total weight (to reduce the risk of including consumers with minimal exposure).

FoodCode	FoodName	IngredientCode	IngredientName	IngredientFraction
1762	LETTUCE UNSPECIFIED RAW	1762	LETTUCE UNSPECIFIED RAW	1.00
7853	LETTUCE-BUTTERHEAD-RAW	7853	LETTUCE-BUTTERHEAD-RAW	1.00
7854	LETTUCE-COS-RAW	7854	LETTUCE-COS-RAW	1.00
7855	LETTUCE-ICEBERG RAW	7855	LETTUCE-ICEBERG RAW	1.00
7856	LETTUCE-WEBB	7856	LETTUCE-WEBB	1.00
1763	LETTUCE (OIL & VINEGAR DRESSING)	1762	LETTUCE UNSPECIFIED RAW	0.90
8096	KFC CAESAR SALAD	7855	LETTUCE-ICEBERG RAW	0.28
8084	MIXED LEAF SALAD	7854	LETTUCE-COS-RAW	0.25
8084	MIXED LEAF SALAD	7855	LETTUCE-ICEBERG RAW	0.25
3363	KFC CHICKEN AND SALAD IN TORTILLA WRAP	7855	LETTUCE-ICEBERG RAW	0.19
1344	SHISH KEBAB	7855	LETTUCE-ICEBERG RAW	0.18
1342	DONER KEBAB	7855	LETTUCE-ICEBERG RAW	0.14
1602	FISH IN BUN TAKEAWAY (NOT MCDONALDS)	1762	LETTUCE UNSPECIFIED RAW	0.14
5930	LAMB KEBAB HOMEMADE WITH LAMB MINCE ONIONS GARLIC	7855	LETTUCE-ICEBERG RAW	0.14
8037	SALMON AND NEW POTATO STEAMED READY MEAL	1762	LETTUCE UNSPECIFIED RAW	0.13

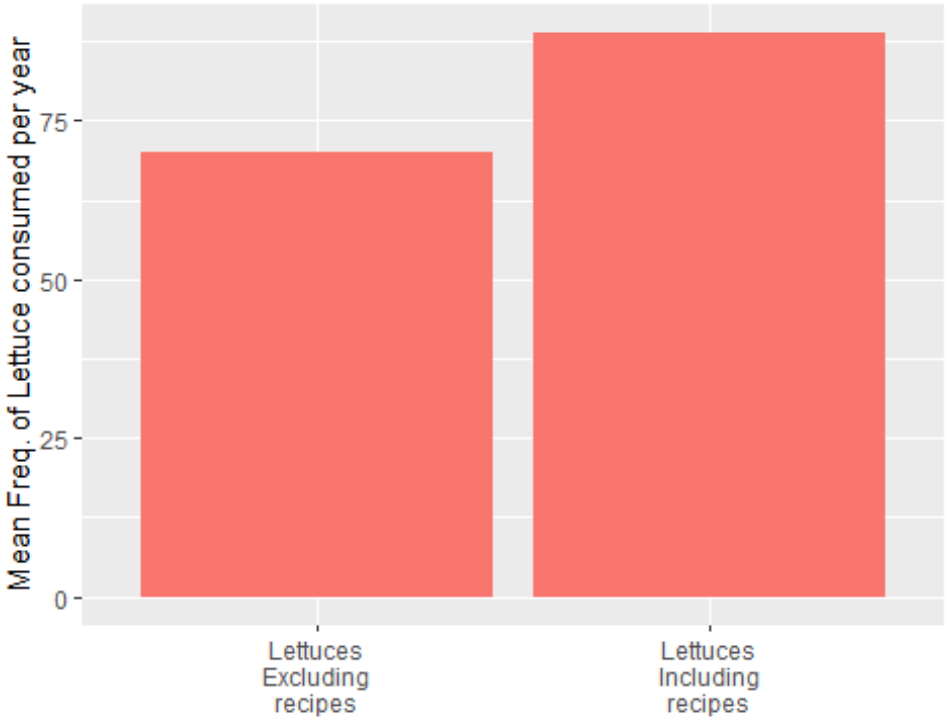
FoodCode	FoodName	IngredientCode	IngredientName	IngredientFraction
8097	MCDONALDS CAESAR SALADS	1762	LETTUCE UNSPECIFIED RAW	0.10
6109	VEGEMINCE STIR FRY RICE ONION PEAS LETTUCE & PUFA	7853	LETTUCE-BUTTERHEAD-RAW	0.08
5304	BURGER KING WHOPPER ONLY	7855	LETTUCE-ICEBERG RAW	0.08
5305	BURGER KING WHOPPER WITH CHEESE ONLY	7855	LETTUCE-ICEBERG RAW	0.07
5306	BURGER KING DOUBLE WHOPPER ONLY	7855	LETTUCE-ICEBERG RAW	0.06
5307	BURGER KING DOUBLE WHOPPER WITH CHEESE ONLY	7855	LETTUCE-ICEBERG RAW	0.06
6330	OLD CODE BURGER KING DOUBLE SUPREME	7855	LETTUCE-ICEBERG RAW	0.05

There were 22 relevant food codes (17 composite codes plus the 5 codes listed above). Most of the composite codes were mixed salads or salads served with other foods.

Comparing frequency of consumption

In the current risk assessment, the frequency of lettuce meals is modelled by a single-parameter model. The **mean** number of meals per year is assumed to vary between people following a Poisson distribution. This rate is then used to determine the **actual** number of meals in a given period (again Poisson distributed).

The rate currently used in the spreadsheet model is 72.1 meals per year. This is based on lettuce (not including recipes) consumed by all adults in NDNS Years 1 to 6. This is similar to 70.1 meals per year for lettuce excluding recipes based on NDNS Years 1 to 8. Including recipes in Years 1 to 8 would increase this to 88.9.



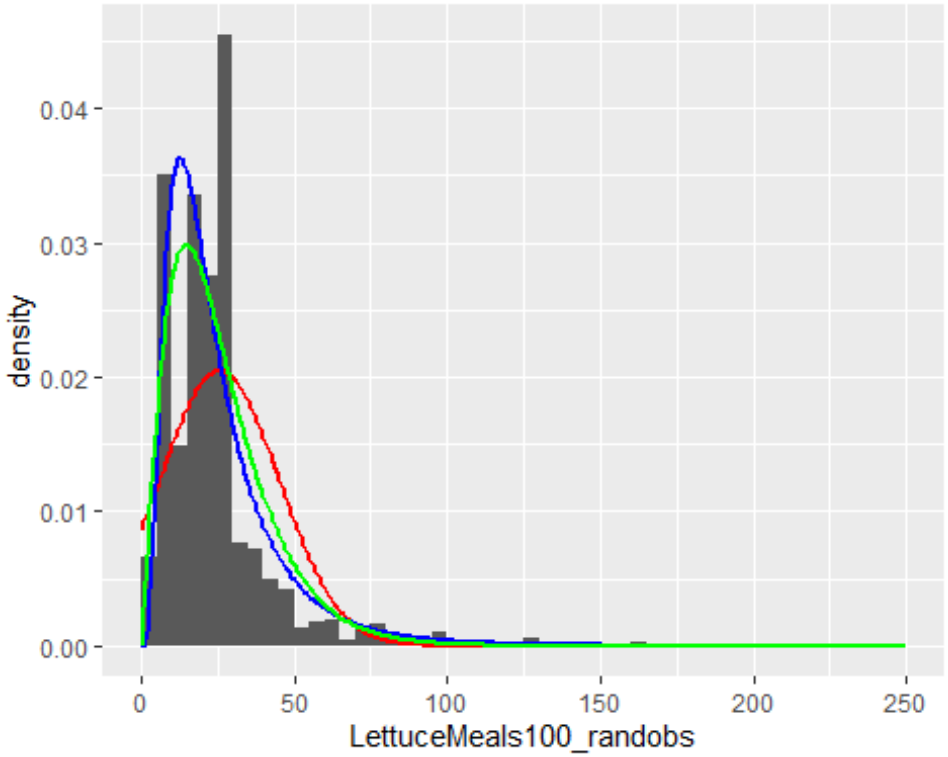
Comparing quantity consumed on each occasion

In the risk assessment, the size of a lettuce meal is modelled by a truncated Normal distribution. The mean of the distribution currently used in the spreadsheet model is 24.5g per meal. This is based on lettuce (not including recipes) consumed by all adults in NDNS Years 1 to 6. This is similar to 25.4 g per meal for lettuce excluding recipes based on NDNS Years 1 to 8. Including recipes in Years 1 to 8 would change this to 24.3 g per meal .

	Mean	StdDev	Median.50%	LowPc1%	HighPc99%	logMean	logsd
Lettuces excluding recipes	25.43	19.47	22.5	3.6	105	3.01	0.69
Lettuces including recipes	24.34	18.65	22.5	3.6	100	2.97	0.69

Comparing distribution fits for meal size

Quantity consumed on each occasion (in grams) of lettuce (EXCLUDING recipes)
(Adults aged 19+, Years 1 to 8)



	0.1th%ile	1th%ile	2.5th%ile	97.5th%ile	99th%ile	99.9th%ile
Normal	-34.7	-19.8	-12.7	63.6	70.7	85.5
LnNormal	2.40	4.07	5.24	78.0	100.	170
Gamma	0.897	2.51	3.86	66.9	79.0	108

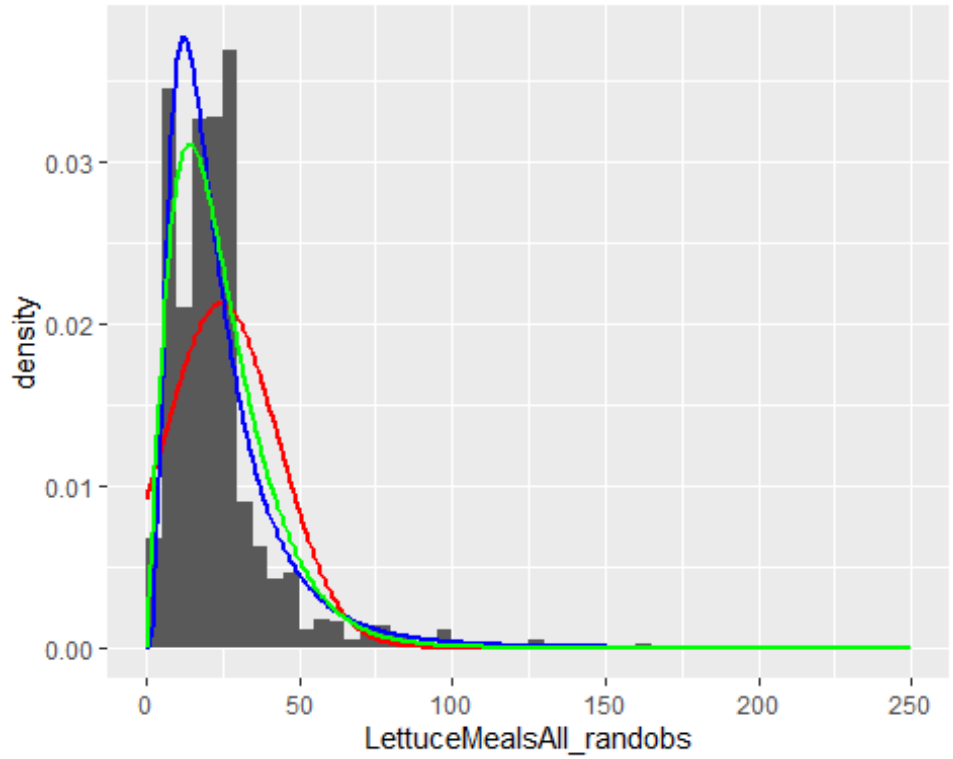
The plot above shows the fit for three different distributions to the meals size for leafy greens.

1. The Normal distribution is shown in red (mean = 25.42, sd = 19.46). It is centred near to the mode and seems to fit the bottom half of the distribution. However, it does not fit the long upper tail well, having fewer high values than seen in the NDNS.

2. The logNormal distribution is shown in blue (meanlog = 3.01, sdlog = 0.69). Its skewed shape is a better fit than the Normal distribution.
3. The gamma distribution is shown in green (shape = 2.33, rate = 0.09). It is similar to the logNormal distribution, but it is slightly less skewed.

Comparing distribution fits for meal size

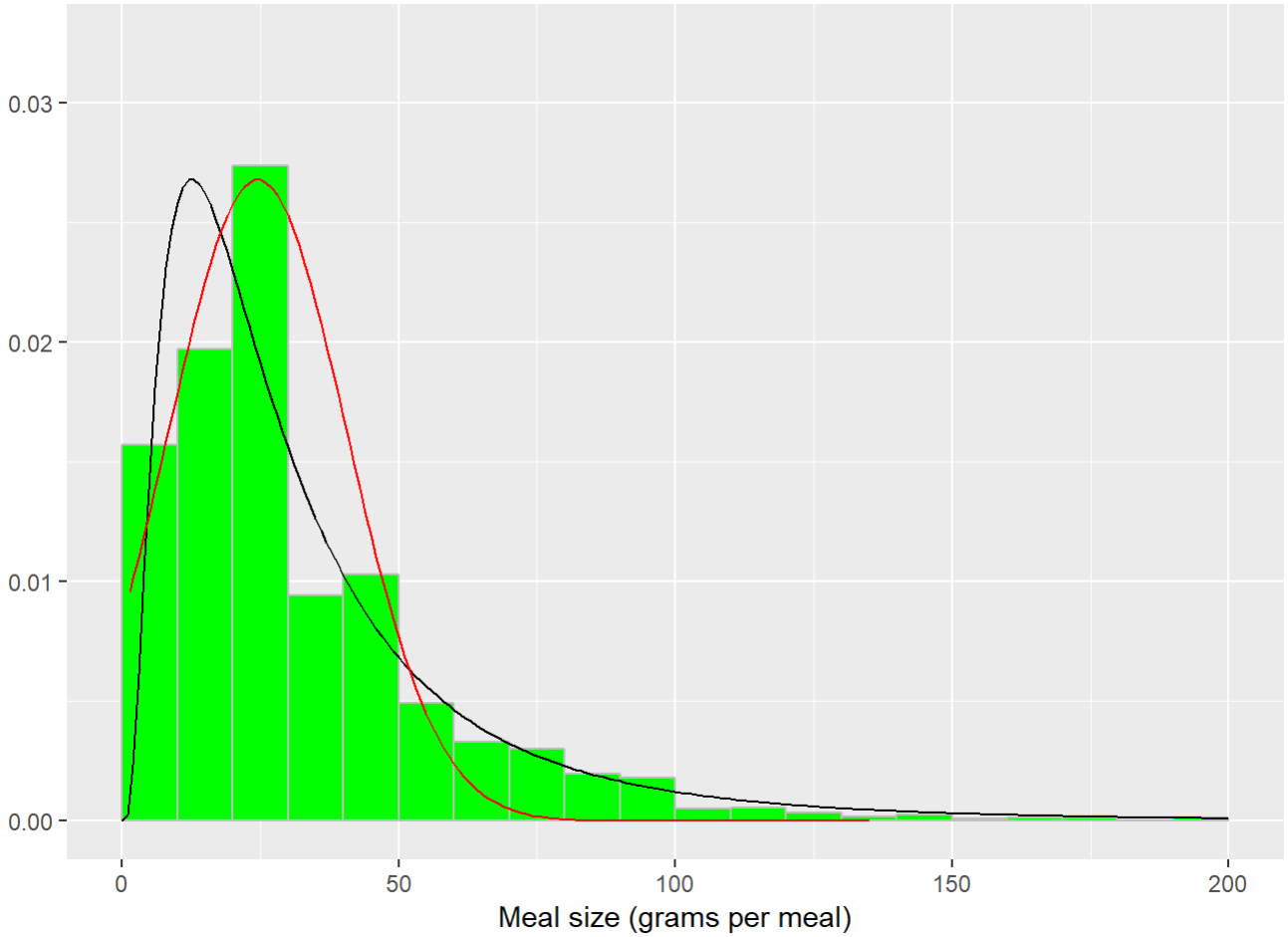
Quantity consumed on each occasion (in grams) of lettuce (INCLUDING recipes)
(Adults aged 19+, Years 1 to 8)



	0.1th%ile	1th%ile	2.5th%ile	97.5th%ile	99th%ile	99.9th%ile
Excluding Recipes Normal	-33.6	-19.2	-12.4	61.1	68.0	82.3
LnNormal	2.31	3.91	5.03	74.9	96.5	163
Gamma	0.875	2.44	3.73	64.0	75.5	103

The plot above shows the fit for three different distributions to the meals size for lettuce.

1. The Normal distribution is shown in red (mean = 24.37, sd = 18.75). It is centred near to the mode and seems to fit the bottom half of the distribution. However, it does not fit the long upper tail well, having fewer high values than seen in the NDNS.
2. The logNormal distribution is shown in blue (meanlog = 2.97, sdlog = 0.69). Its skewed shape is a better fit than the Normal distribution.
3. The gamma distribution is shown in green (shape = 2.35, rate = 0.1). It is similar to the logNormal distribution, but it is slightly less skewed.


0.03
0.02
0.01
0.00
0
50
100
150
200
Meal size (grams per meal)

Appendix 6: Norovirus Risk assessment - NDNS data for Raspberries

Identifying NDNS food codes that fall within the definition of uncooked raspberries

Step 1: Identify non-composite food codes that qualify as uncooked raspberries.

The following criteria were used to identify applicable NDNS food codes:

1. **Include** foods whose name contains the string “RASPBERR”.
2. **Exclude** foods whose name indicates cooking or being a supplement i.e. that contained STEWED, CANNED or KETONE.
3. **Exclude** foods with multi-ingredient recipes (as they will be identified at the next step.

FoodCode	FoodName
2143	RASPBERRIES RAW
2147	RASPBERRIES FROZEN NO ADDED SUGAR
8091	DRIED RASPBERRIES
10689	RASPBERRY PUREE, HOMEMADE, 100% FRESH RAW FRUIT NAS
20079	RASPBERRY PUREE, HOMEMADE (JUICE) FS PROJECT
30070	DRIED RASPBERRIES(PUREED)-FS PROJECT

This identified the 6 non-composite foods listed above. All were from the “40R Other fruit not canned” group”.

Step 2: Identify all relevant food codes likely contain uncooked raspberries.

The following criteria were used to identify applicable NDNS food codes. Eligible foods had to comprised in whole or part of one of 6 NDNS food codes identified in Step 1 and to be in one of the following food groups.

1. **Either** uncooked fruit (specifically in 40R Other fruit not canned)
2. **Or** breakfast cereals (“5 High fibre breakfast cereals” and “6 Other breakfast cereals”)
3. **Or** uncooked puddings (explicitly “9G Other cereal based puddings (manufactured)”, “9H Other cereal based puddings (homemade)” and “16C Manufactured egg products including ready meals” (which included pavlova).

Furthermore, **exclude** foods in which the Step 1 ingredient comprises less than 5% of the total weight (to reduce the risk of including consumers with minimal exposure).

There were 8 relevant food codes (2 composite codes plus the 6 codes listed above).

Food Code	Food Name
2143	RASPBERRIES RAW
2147	RASPBERRIES FROZEN NO ADDED SUGAR
5474	CHEESECAKE LOW FAT FRUIT TOPPING PURCHASED
5581	PAVLOVA / MERINGUE WITH FRUIT AND CREAM PURCHASED
8091	DRIED RASPBERRIES
8208	FRUIT CUP JELLY WITH FRUIT
8211	FROZEN SUMMER MIXED FRUITS
10689	RASPBERRY PUREE, HOMEMADE, 100% FRESH RAW FRUIT NAS

The food group criteria exclude the following food types even when the relevant recipe mentions uncooked raspberries as an ingredient. These foods include:

- Sugar-based foods such as jam, preserves, sugar confectionary and chocolate confectionary. In such highly processed foods, it is assumed that any fruit would be cooked or preserved in some way.
- Baked goods such as Biscuits, Buns, cakes, pastries and fruit pies plus Sponge puddings – such foods are assumed to always be cooked. (Where uncooked raspberries are included as an ingredient, it is often in the form of jam.)
- Dairy desserts such as Ice cream, yogurt, fromage frais and other dairy desserts. The fruit content of these processed products is assumed to be either cooked or pasteurised.
- Drinks including soft drinks, fruit juice, smoothies and commercial toddler drinks. Again, the fruit content of these processed products is assumed to be either cooked or pasteurised.
- Commercial toddler foods. Again, this would be highly processed. In any case, most of these categories would have been excluded because none of the foods exceeded 5% raspberry (whether uncooked or not).

Furthermore, it is not easy to reliably include many of these foods in the analysis. Many NDNS codes are for generic composite foods whose descriptions often do not specify the nature of the fruit content. For example:

- 324 DOUGHNUTS JAM FILLED, WITH OR WITHOUT GLAZE, PURCHASED
- 704 YOGURT LOW FAT FRUIT
- 725 ICE CREAM, STANDARD DAIRY, FLAVOURED, NOT VANILLA OR CHOCOLATE OR NUTS ETC, SOFT SCOOP
- 8444 FRUIT JUICE DRINK CARBONATED NOT LOW CAL NOT CANNED
- 10747 SMOOTHIES RED, PURCHASED, FRUIT/JUICE BLEND (MAX 2 PORTIONS)

So, although the presence/absence and quantity of uncooked raspberries is assumed in the recipes, this will not always reflect what was eaten. In several cases, the recipe used is an average of several products. If some contained raspberries and others did not, then this will tend to increase the number of eating occasions but reduce the portion size.

Comparing frequency of consumption

In the current risk assessment, the frequency of raspberry meals is modelled by a single-parameter model. The **mean** number of meals per year is assumed to vary between people following a Poisson distribution. This rate is then used to determine the **actual** number of meals in a given period (again Poisson distributed).

The rate currently used in the spreadsheet model is 7.99 meals per year. This is based on raspberries (not including recipes) consumed by all adults in NDNS Years 1 to 6. This is close to 9.1 meals per year for lettuce excluding recipes based on NDNS Years 1 to 8. Including recipes in Years 1 to 8 would increase this to 10.7.

Comparing quantity consumed on each occasion

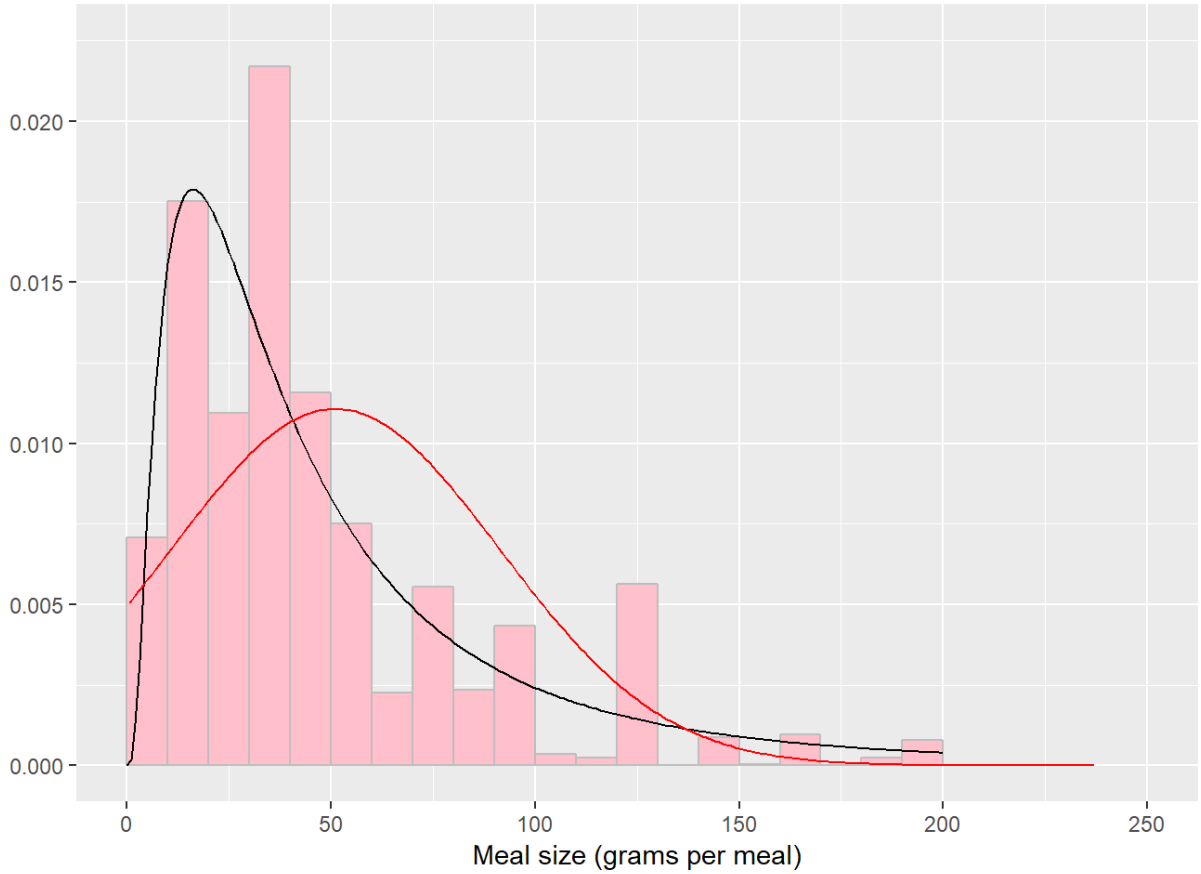
In the risk assessment, the size of a raspberry meal is modelled by a truncated Normal distribution. The mean of the distribution currently used in the spreadsheet model is 50.98 per meal. This is based on raspberries (not including recipes) consumed by all adults in NDNS Years 1 to 6. This is close to 52.5 g per meal for raspberries excluding recipes based on NDNS Years 1 to 8. Including recipes in Years 1 to 8 would change this to 46.6 g per meal.

	Mean	StdDev	Median.50%	LowPc.5%	HighPc.95%	logMean	logsd
Excluding recipes	52.5	46.3	40.0	7.00	125	3.61	0.91
Including recipes	46.6	45.0	32.5	3.79	125	3.42	1.01

The histograms below show how different definitions lead to different quantities of raspberries consumed. The truncated Normal distribution for the current risk assessment is shown in red. The black line shows a log Normal distribution to fitted to meal size.

Quantity consumed on each occasion (in grams) of raspberries (EXCLUDING recipes)

(Adults aged 19+, Years 1 to 8)



Quantity consumed on each occasion (in grams) of raspberries (INCLUDING recipes)

(Adults aged 19+, Years 1 to 8)