Foodborne Disease Estimates for the United Kingdom in 2018

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1. Executive summary

In February 2020 the FSA published two reports which produced new estimates of foodborne norovirus cases. These were the 'Norovirus Attribution Study' (NoVAS study) (O'Brien et al., 2020) and the accompanying internal FSA technical review 'Technical Report: Review of Quantitative Risk Assessment of foodborne norovirus transmission' (NoVAS model review), (Food Standards Agency, 2020). The NoVAS study produced a Quantitative Microbiological Risk Assessment model (QMRA) to estimate foodborne norovirus. The NoVAS model review considered the impact of using alternative assumptions and other data sources on these estimates. From these two pieces of work, a revised estimate of foodborne norovirus was produced.

The FSA has therefore updated its estimates of annual foodborne disease to include these new results and also to take account of more recent data related to other pathogens. The estimates produced include:

- Estimates of GP presentations and hospital admissions for foodborne norovirus based on the new estimates of cases. The NoVAS study only produced estimates for cases.
- Estimates of foodborne cases, GP presentations and hospital admissions for 12 other pathogens
- Estimates of unattributed cases of foodborne disease
- Estimates of total foodborne disease from all pathogens

Previous estimates

An FSA funded research project 'The second study of infectious intestinal disease in the community', published in 2012 and referred to as the IID2 study (Tam et al., 2012), estimated that there were 17 million cases of infectious intestinal disease (IID) in 2009. These include illness caused by all sources, not just food.

Of these 17 million cases, around 40% (around 7 million) could be attributed to 13 known pathogens. These pathogens included norovirus. The remaining 60% of cases (equivalent to 10 million cases) were unattributed cases. These are cases where the causal pathogen is unknown. Reasons for this include the causal pathogen was not tested for, the test was not sensitive enough to detect the causal pathogen or the pathogen is unknown to science.

A second project 'Costed extension to the second study of infectious intestinal disease in the community', published in 2014 and known as IID2 extension (Tam, Larose and O'Brien, 2014), estimated that there were 566,000 cases of foodborne disease per year caused by the same 13 known pathogens. Although a proportion of the unattributed cases would also be due to food, no estimate was provided for this in the IID2 extension.

New estimates

We estimate that there were 2.4 million cases of foodborne disease in the UK in 2018 (95% credible intervals 1.8 million to 3.1 million), with 222,000 GP presentations (95% Cred. Int. 150,000 to 322,000) and 16,400 hospital admissions (95% Cred. Int. 11,200 to 26,000). Of the estimated 2.4 million cases, 0.9 million (95% Cred. Int. 0.7 million to 1.2 million) were from the 13 known pathogens included in the IID2 extension and 1.4 million[1] (95% Cred. Int. 1.0 million to 2.0 million) for unattributed cases.

Norovirus was the pathogen with the largest estimate with 383,000 cases a year. However, this estimate is within the 95% credible interval for *Campylobacter* of 127,000 to 571,000. The pathogen with the next highest number of cases was *Clostridium perfringens* with 85,000 (95% Cred. Int. 32,000 to 225,000).

While the methodology used in the NoVAS study does not lend itself to producing credible intervals for cases of norovirus, this does not mean that there is no uncertainty in these estimates. There were a number of parameters used in the NoVAS study which, while based on the best science currently available, were acknowledged to have uncertain values. Sensitivity analysis undertaken as part of the study showed that changes to the values of these parameters could make big differences to the overall estimates.

Campylobacter was estimated to have the most GP presentations with 43,000 (95% Cred. Int. 19,000 to 76,000) followed by norovirus with 17,000 (95% Cred. Int. 11,000 to 26,000) and *Clostridium perfringens* with 13,000 (95% Cred. Int. 6,000 to 29,000).

For hospital admissions *Campylobacter* was estimated to have 3,500 (95% Cred. Int. 1,400 to 7,600), followed by norovirus 2,200 (95% Cred. Int. 1,500 to 3,100) and *Salmonella* with 2,100 admissions (95% Cred. Int. 400 to 9,900).

As many of these credible intervals overlap, any ranking needs to be undertaken with caution.

While the estimates provided in this report are for 2018 the methodology described can be applied to future years.

[1] Slight discrepancy due to rounding

2. Background to estimates of foodborne disease

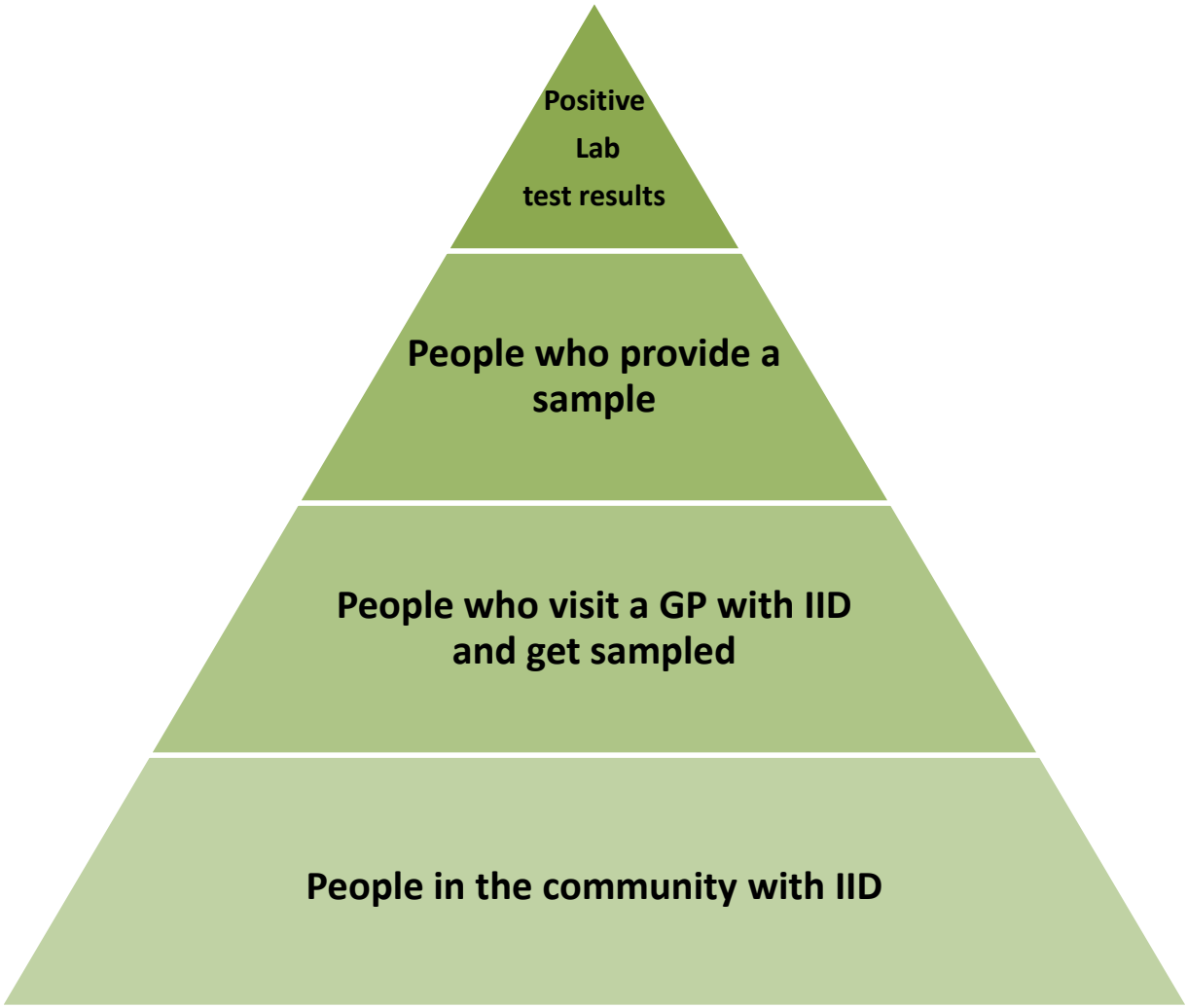
2.1 Surveillance pyramids

Infectious intestinal disease (IID) includes a range of possible infections which often result in diarrhoea and vomiting (more serious health problems are possible including a small number of fatalities). The term includes infections from a number of different pathogens which may be either bacteria, protozoa or viruses.

Foodborne disease (often referred to as food poisoning) is used to describe the proportion of these illnesses caused by contaminated food or drink. Non IID pathogens, such as *Listeria monocytogenes,* are also sometimes included under this term.

Confirmed laboratory reports, as recorded by the UK's four surveillance bodies (Public Health England, Public Health Wales, Health Protection Scotland and Public Health Agency for Northern Ireland), only make up a fraction of all cases of IID. The reasons for this are that not everyone who has an illness will seek medical help, not everyone who seeks medical help will have a sample taken and even when a sample is taken there will not always be a positive result identifying the causal pathogen. This under-ascertainment is illustrated in the surveillance pyramid below, where the positive laboratory test results are shown as a fraction of the cases in the community.

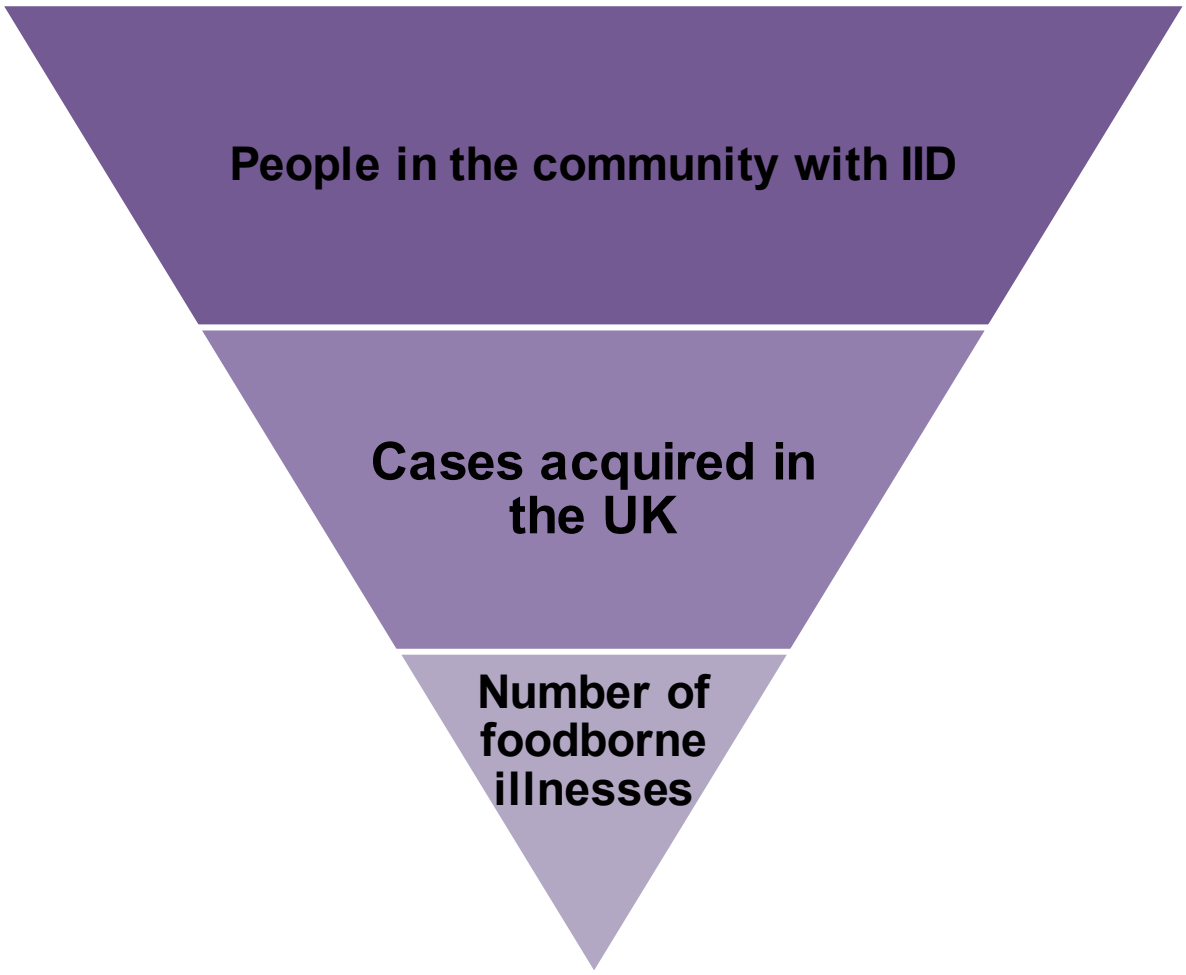
Figure 1: Surveillance pyramid illustrating under-ascertainment of cases of IID



At each stage there is under-ascertainment. The under-ascertainment differs by pathogen depending on various factors. These include severity (the more severe the pathogen the more likely the individual is to seek medical help) , whether the pathogen is routinely tested for (*Clostridium perfringens* for example is only tested for during outbreak investigations) and as a result of NHS advice (for instance norovirus sufferers are advised not to go their GP for fear of spreading the disease further).

For each pathogen not all cases will be attributed to food. There are several other possible sources (depending on the pathogen) such as person to person spread, contact with animals, the environment and recreational contact with water. In addition, not all cases will be acquired in the UK. Again, these factors differ by pathogen. Therefore, there is a second (inverted) pyramid that starts from the people in the community with IID and reduces this to those with domestically acquired foodborne disease (see below).

Figure 2: Surveillance pyramid illustrating stages from total IID to domestic foodborne disease



2.2 IID2 main study

"The second study of infectious intestinal disease in the community" (IID2 study) looked to estimate the overall level of IID in the community and how much was due to each pathogen. This study estimated that there were 274.3 cases per 1,000 person years (95% Confidence Interval 253.8 to 295.8). Based on the 2018 UK population estimate of 66 million this is equivalent to 18.2 million cases (95% CI 16.9 million to 19.7 million). To put this into context, this suggests that each year over a quarter of the UK population get IID.

The IID2 study also produced estimates for individual pathogens. Norovirus was the pathogen with the most cases with an estimated 47 cases per 1,000 person years (95% Credible Interval 39.1 to 56.5).

Only 40% of the IID cases were attributable to the 13 pathogens included in the IID2 extension. The other 60% of cases are referred to as unattributed cases. These are cases where the causal pathogen is unknown. Reasons for this include the causal

pathogen was not tested for, the test was not sensitive enough to detect the causal pathogen and the pathogen is unknown to science.

2.3 IID2 extension

The IID2 extension used the results from the IID study and supplementary data from outbreaks and a literature review to estimate the proportion of cases, GP presentations and hospital admissions due to food for each pathogen. The study provided an estimate of 566,000 foodborne cases from the 13 known pathogens considered. This was for the UK in 2009. No estimate was made for foodborne cases with an unattributed cause.

3. Methodology

The Foodborne Disease Estimation Model (FDEM) is a Monte Carlo simulation model built using Microsoft Excel and the @Risk add-in. It provides estimates for the total foodborne disease in the UK as well as individual estimates for the 13 pathogens included in the IID2 extension. The model is used by the FSA to produce annual estimates.

The model builds on the methodology used for model 1 in the IID2 extension and uses parameters produced in both the IID2 study and IID2 extension. A full description of model 1 can be found in section 3.6 in the IID2 extension.

3.1 IID2 extension model

The basic structure of model 1, as given in the IID2 extension, is as follows:

$$F_p = N \,.\, c_p \,.\, \pi_p \qquad \text{equation 1}$$

$$G_p = N \,.\, g_p \,.\, \pi_p \qquad \text{equation 2}$$

$$H_p = F_p \,.\, \gamma_p \qquad \text{equation 3}$$

Where:

F_p, is the estimated number of foodborne disease cases for pathogen p in 2009

G_p is the estimated number of GP consultations related to foodborne disease for pathogen p in 2009

H_p is the estimated number of hospital admissions related to foodborne disease for pathogen p in 2009

N is the mid 2009 population of the UK.

c_p is the UK rate of IID due to pathogen p

g_p is the UK rate of IID related GP presentations due to pathogen p.

π_p is the proportion of IID cases due to pathogen p that are attributable to foodborne transmission

γ_p is the hospital admission rate for pathogen p

3.2 Updating annual estimates of foodborne cases and GP presentations

One option to update the estimates for other years is to use equation 1 with N changed to the mid-year population for the relevant year. However, it is possible that rates of IID for some pathogens (expressed as a rate per 1,000 person years) may have changed since 2009. As it is not feasible to undertake such large pieces of research as the IID2 study every year we considered alternative methods to estimate cases.

The IID2 study provided the rates of IID cases and GP presentations per pathogen (with confidence intervals). It also provided under-ascertainment ratios (also with confidence intervals) for each pathogen[2] based on the overall estimates of IID for that pathogen for 2009 and the confirmed laboratory reports for 2009 (obtained from the UK's four surveillance bodies). Using the under-ascertainment ratios an alternative model to equations 1 and 2 is as follows:

$$F_p = lr_p.\ u_p\ .\pi_p \qquad \text{equation 4}$$

$$G_p = lr_p.\ gpu_p\ .\pi_p \qquad \text{equation 5}$$

Where:

lr_p is the number of confirmed laboratory report for pathogen p in the UK for the relevant year

u_p is the under-ascertainment ratio for pathogen p

gpu_p is the under-ascertainment ratio for GP presentations for pathogen P

Whether such a model is appropriate will vary by pathogen. For pathogens with large under-ascertainment ratios and small numbers of confirmed laboratory reports such a model is probably not appropriate. The large under-ascertainment ratios suggests the confirmed laboratory reports may be an unreliable indicator of trends and

[2] For *Shigella* under-ascertainment ratios from the IID2 study were not available, so data from the first study of infectious intestinal disease (IID1) was used instead (Food Standards Agency, 2000)

together with the small numbers overall estimates could swing widely from year to year. In such cases equations 1 and 2 are used.

For pathogens with smaller under-ascertainment ratios and larger numbers of confirmed laboratory reports using equations 4 and 5 is more appropriate.

Table 1 shows confirmed laboratory reports by pathogen for the UK from 2009 to 2018 and table 2 gives under-ascertainment ratios. These two tables show that for *Campylobacter*, *Salmonella*, *Shigella*, *Cryptosporidium* and *Giardia* the under-ascertainment ratios are relatively low, particularly in relation to the number of confirmed laboratory reports. For these pathogens equations 4 and 5 were used for the estimates. Despite the higher under-ascertainment ratios for rotavirus equations 4 and 5 were used, as the number of confirmed laboratory reports are considerably higher and the trend is clear. The fall in rotavirus numbers are likely to have been due to the introduction of an oral vaccine in 2013 making the use of equations 1 and 2 unsuitable (Thomas et al., 2017).

Table 1: Confirmed laboratory reports by pathogen 2009 to 2018

Pathogen	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018
Bacteria										
Campylobacter	65,164	70,329	72,249	72,577	66,584	68,471	61,588	59,253	64,227	69,636
Clostridium perfringens	389	110	46	43	43	39	130	91	117	108
E. coli O157	1,337	1,108	1,503	1,301	888	1,186	1,083	965	785	864
Listeria monocytogenes	248	191	174	195	162	188	173	195	162	172
Salmonella	10,083	9,374	9,456	8,804	8,461	9,074	8,630	9,253	10,061	10,124
Shigella	1,590	2,020	2,071	2,021	2,076	2,496	1,879	1,847	2,064	2,812
Protozoa										
Cryptosporidium	5,507	4,605	3,557	6,653	4,274	4,430	5,543	6,734	5,131	6,039
Giardia	3,571	4,037	3,942	4,128	3,838	4,227	4,073	4,742	5,256	6,216
Viruses										
Astrovirus	111	222	135	343	381	327	314	423	486	472
Norovirus	10,329	15,528	10,661	14,526	9,716	7,880	6,562	10,164	6,897	8,573
Rotavirus	17,495	18,446	18,068	17,136	16,958	5,011	4,721	3,061	4,400	2,651

Source: Public Health England, Public Health Wales, Health Protection Scotland and Public Health Agency for Northern Ireland

Table 2: Reporting ratios

Pathogen	Under-ascertainment ratios					
	Cases			GP presentations		
	Mean	Lower 95% CI	Upper 95% CI	Mean	Lower 95% CI	Upper 95% CI
Bacteria						
Campylobacter	9.3	6.0	14.4	1.3	0.9	1.8
Clostridium perfringens	2,518.7	890.7	7,179.4	419.1	181.9	962.8
Salmonella	4.7	1.2	18.2	1.4	0.6	3.3
Shigella	2.6	NA	NA	2.6	NA	NA
Protozoa						
Cryptosporidium	8.2	2.1	31.7	2.3	1.0	5.6
Giardia	14.0	4.0	49.0	1.5	0.5	4.5
Viruses						
Astrovirus	1,763.5	970.1	3,218.1	135.1	65.5	278.9
Rotavirus	42.9	29.5	62.4	4.6	3.0	7.0

Source: IID1 study for shigella, IID2 study for all other pathogens

The under-ascertainment ratios represent the ratio of rates in the community and presenting to general practice relative to the rate of reports to national surveillance.

For *Clostridium perfringens* and astrovirus under-ascertainment ratios were both very high and much larger than the number of confirmed laboratory reports. Adenovirus and sapovirus were omitted from the tables as data on these organisms were not routinely collected at a national level in all UK countries. For all four pathogens equations 1 and 2 were used to update the estimates.

For norovirus the new estimates provided from the NoVAS model review were used instead of either equations 1 or 4. To estimate the number of GP presentations we used equation 2 but updated π_p so that is was based on the new foodborne estimate of norovirus divided by an overall estimate of norovirus calculated using the IID2 study rate of norovirus scaled up by the UK 2018 population. This was calculated for each run of the model.

For *E. coli* O157 and *Listeria monocytogenes*, the four UK surveillance bodies undertake enhanced surveillance. This involves following up cases with questionnaires which provide more information on exposure to various risk factors and clinical details. From this dataset the numbers of cases, hospitalisations and deaths by pathogen were provided for 2018. While there may be some level of under-ascertainment, as these illnesses are relatively severe this is believed to be small. Therefore, for these two pathogens equation 4 and 5 are used but with an under-ascertainment ratio of 1 i.e. no under-ascertainment. All cases were assumed to consult their GP. For *E. coli* O157 the IID2 study did provide an estimate for under-ascertainment of 7.4 (95% CI 0.5 to 104.4). This was based on 1 positive sample (hence the large confidence intervals). Given the severity of this pathogen,

such a high under-ascertainment ratio is believed to be unlikely. The table in annex 2 shows which model each pathogen uses for cases and GP presentations with sources provided for each parameter.

3.3 Updating estimates of foodborne hospital admissions

Estimates were updated using equation 3 and the new estimates of foodborne cases. Parameter γ_p was updated using outbreak data from 2001 to 2016 (See section 4.3).

3.4 Estimating unattributed cases of foodborne disease

The IID2 study estimates that 60% of IID cases were unattributed to a known pathogen. For 2018 this would be equivalent to around 11 million cases per year. A proportion of these cases will be due to food. However, as the specific pathogen is unknown for each case this proportion is particularly difficult to estimate.

In order to estimate the number of unattributed cases of IID due to food we adopted a similar approach to that used in the USA (Scallan et al., 2011), Canada (Thomas et al., 2013) and Australia (Kirk et al., 2014).

For each run of the Monte Carlo simulation model, estimates for individual pathogens were produced as described in section 3.2 above. As well as producing the foodborne proportion, an estimate from all sources (not just food) for each pathogen was calculated by removing parameter π_p (the proportion of IID cases due to pathogen p that are attributable to foodborne transmission) from the equations. The total IID and foodborne IID for all the included known pathogens was then calculated by summing all the estimates for the individual pathogens together and the overall foodborne proportion calculated (π_t). *Listeria monocytogenes* was excluded from these calculations as it is not an IID pathogen, while *Clostridium difficile* was added as although it is understood to have no (or a very small) foodborne component it is an IID pathogen and was included in the IID study. In the case of *Clostridium difficile* $\pi_p$was given a value of 0 in each run of the model.

Total IID was sampled from a log normal distribution based on the mean rate and 95% confidence intervals given in the IID study. From this value the IID from the known pathogens was subtracted to provide an estimate of unattributed cases of IID and was then multiplied by the estimate of the proportion of IID due to food from the known pathogens – i.e. it is assumed the foodborne proportion of cases from the known pathogens and unattributed cases are the same.

This number of foodborne cases from all the known pathogens and the unattributed cases was then added to get an overall total estimate of IID cases due to food.

Estimates for GP presentations of unattributed cases were produced by first estimating overall GP presentations from IID (using a log normal distribution based

on the mean rate and 95% confidence intervals given in the IID study) and subtracting the GP presentations from all sources for each pathogen to get GP presentations of unattributed cases. This number was then multiplied by π_t, as calculated above, to get the proportion of foodborne GP presentations of unattributed cases. Again, the total from known pathogens and unattributed causes were added.

Estimates for hospital admissions used the same approach as for individual pathogens. This was based on equation 3 and the new estimates of foodborne unattributed cases. Parameter γ_u (the proportion of unattributed IID cases that are hospitalised) was updated using outbreak data from 2001 to 2016 (See section 4.3.2).

4. Setting the parameters used in the model

4.1 Incidence rate for cases and GP presentations (c_p and g_p)

Following the methodology of the IID2 extension, log-normal distributions for rates of IID and IID related to GP presentations based on means and confidence intervals were used to allow for uncertainty. These were based on the estimates from the IID2 study.

4.2 Under-ascertainment ratios for cases and GP presentations (u_p and gpu_p)

The under-ascertainment ratios are based on the those given in table 6.4 of the IID2 extension. Normal distributions were produced based on means and confidence intervals and used to model uncertainty.

The under-ascertainment ratio for cases was based on the ascertainment rates multiped by the proportion of cases that were indigenous (Adak et al., 2002). The same under-ascertainment ratio was used for GP presentations as the numbers were equal to those for cases in the same paper. No confidence intervals were available.

No under-ascertainment was assumed for *E. coli* O157 and *Listeria monocytogenes.* Although there is an under-ascertainment ratio for *E. coli* O157 given in the IID2 study, this is based on only 1 positive result from the 768 tested. This has caused the estimates to have extremely large confidence intervals and an unlikely median estimate given this pathogen causes severe symptoms likely to require medical help. It has therefore been decided to use the number of laboratory reports from enhanced surveillance data for the UK instead.

4.3 Proportion of foodborne cases and proportion of cases hospitalised (π_p and γ_p)

Outbreaks from 2001 to 2016 from PHE for England and Wales have been used to calculate the proportion of cases that are hospitalised, while data from 2001 to 2008 was used to calculate the proportion of cases from foodborne transmission. Outbreak data after 2008 was not used to estimate the proportion of cases due to foodborne transmission due to changes in 2017 which meant certain types of non-foodborne outbreaks were no longer recorded.

Section 3.4 of the IID2 extension describes the data that was used for the analyses and the method. The FSA have replicated this work and therefore used the same approach and assumptions for the data that is used. These are summarised as:

- Outbreaks involving contaminated food and outbreaks involving contaminated food with subsequent person-to-person transmission were considered to be foodborne.
- Waterborne outbreaks are considered to be foodborne.
- An outbreak where the source of illness is unknown is considered to be non-foodborne.
- Outbreaks that took place in the armed services were excluded.
- Outbreaks involving infected food handlers were not explicitly excluded. This is because evidence of infected food handler involvement in the outbreak data was largely speculative and often difficult to interpret.

For each outbreak, information was available on the following: outbreak setting, number of cases affected, number of cases hospitalised, main mode(s) of transmission, pathogen identified and, for outbreaks involving contaminated foods, the implicated food vehicle (where this was identified).

The outbreaks data is used to calculate the proportion of cases that are from foodborne transmission and the proportion of cases that are hospitalised. The method for calculating each one follows a two-step approach involving bootstrapping and fitting a beta distribution to the bootstrapped data and is described below.

4.3.1 Proportion of cases that are from foodborne transmission (π_p)

The proportion of cases involved in foodborne outbreaks is used as an estimate of the proportion of cases attributable to foodborne transmission. Using all the eligible outbreaks for each individual pathogen, the process to obtain a distribution of the percentage of cases that are foodborne used a bootstrapping approach as follows:

1. Repeatedly sample at random from all of the eligible outbreaks, with replacement.

2. Construct 4,999 sets of ‘n’ outbreaks from the data; with ‘n’ equalling the total number of outbreaks reported for each pathogen in the period 2001 to 2008.
3. For each of these sets calculate a percentage of foodborne cases. This gives an empirical distribution for the proportion foodborne.
4. Fit a beta distribution to these results.

For *Cryptosporidium* and *Giardia* we applied the approach of the IID2 extension which stated the following:

“the proportion of cases involved in foodborne outbreaks gave unrealistically high estimates for the proportion of cases attributable to foodborne transmission. This is because, while the number of reported outbreaks for these two pathogens was small, foodborne outbreaks were, on average, considerably larger than non-foodborne outbreaks. For these two pathogens, we used the same bootstrapping approach outlined above, but instead used the proportion of outbreaks that were foodborne as the estimate of the proportion of cases attributable to foodborne transmission.”

For adenovirus, there was no outbreak data available so the proportion that is foodborne is assumed to be the same as rotavirus. Similarly, there is no outbreak data available for sapovirus so the proportion foodborne for this pathogen is assumed to be the same as norovirus. This is consistent with the IID2 extension.

In order to set a distribution for the foodborne percentage for *Listeria monocytogenes*- where all the outbreaks were foodborne- it was assumed that the next outbreak to occur would be non-foodborne and would involve 2 cases. This is based on the definition for a general outbreak as an incident involving two or more epidemiologically-related cases. Similarly, for astrovirus where all of the outbreaks were non-foodborne the distribution was set by assuming that the next outbreak involved 2 cases and was foodborne.

4.3.2 Proportion of cases that are hospitalised (γ_p)

Using all of the eligible outbreaks for each individual pathogen, the process to obtain a distribution of the percentage of hospitalisations that are foodborne used the bootstrapping approach as follows:

1. Repeatedly sample at random from all of the eligible outbreaks, with replacement.
2. Construct 4,999 sets of ‘n’ outbreaks from the data; with ‘n’ equalling the total number of outbreaks reported for each pathogen in the period 2001 to 2016 (IID2 extension used data from 2001 to 2008, but this has since been updated).
3. For each of these sets, calculate a percentage of hospitalised cases from the total number of cases from the resampled outbreaks. This gives an empirical distribution for the proportion foodborne.

4. Fit a beta distribution to these results.

The exception to using this method was for *Listeria monocytogenes* and *E. coli* O157, where the total number of hospitalisations caused from all IID is available from enhanced surveillance data. In order to calculate the number of hospitalisations that are due to food, total hospital admissions from the enhanced surveillance data was multiplied by the distribution for the proportion that is foodborne (π_p).

As with the foodborne proportion (section 4.3.1) rotavirus was used as a proxy for adenovirus and norovirus as a proxy for sapovirus.

This approach was also undertaken for unattributed cases. This was based on outbreak data where the pathogen was either unknown or was one not included in the IID2 extension.

5. Results

Table 3 provides a summary of the estimates for 2018. The estimate for all foodborne disease is 2.4 million cases per year (95% Credible intervals 1.8 million to 3.1 million), with 222,000 GP Presentations (95% CI 150,000 to 322,000) and 16,400 hospital admissions (95% Cred. Int. 11,300 to 26,000).

Around 61% (1.4 million) of the estimated cases were unattributed cases. This figure was impacted by the new estimate of foodborne norovirus which was much higher than previously estimated by the IID2 extension, with a new median estimate of 383,000 compared to 73,000. As 44% of the known IID cases are norovirus, increasing the foodborne proportion also increases the overall percentage of all known pathogens that are foodborne. When this proportion was then applied to the estimate of unattributed cases the estimate for these also increased substantially.

The sum of the median estimates from the known pathogens excluding norovirus was 494,000. This was similar to the equivalent figure in the IID2 extension of 493,000 (note while these two numbers are very similar it should be noted that the UK population has increased by 6.7% over this period, so this represents a decrease per person). Therefore, the big increases in the estimates was the new foodborne norovirus estimate and the relating impact this had on the estimates of unattributed cases due to food. Both of these increases are due to changes in the estimated foodborne proportion rather than changes in the overall numbers who get ill from all sources.

Norovirus was the pathogen with the largest estimate with 383,000 cases a year. However, this estimate is within the 95% credible interval for *Campylobacter* of 127,000 to 571,000. The pathogen with the next highest cases was *Clostridium perfringens* with 85,000 (95% Cred. Int. 32,000 to 225,000).

While the methodology used in the NoVAS study does not lend itself to producing credible intervals for cases of norovirus, this does not mean that there is no uncertainty in these estimates. There were a number of parameters used in the NoVAS study which, while based on the best science currently available, were acknowledged to have uncertain values. Sensitivity analysis undertaken as part of the study showed that changes to the values of these parameters could make big differences to the overall estimates.

Campylobacter was estimated to have the most GP presentations with 43,000 (95% Cred. Int. 19,000 to 76,000) followed by norovirus with 17,000 (95% Cred. Int. 11,000 to 26,000) and *Clostridium perfringens* with 13,000 (95% Cred. Int. 6,000 to 29,000).

For hospital admissions *Campylobacter* was estimated to have 3,500 (95% Cred. Int. 1,400 to 7,600), followed by norovirus 2,200 (95% Cred. Int. 1,500 to 3,100) and *Salmonella* 2,100 (95% Cred. Int. 400 to 9,900).

As many of these credible intervals overlap any ranking needs to be undertaken with caution.

Table 3: Estimates of foodborne disease for 2018

Pathogen	Foodborne cases			Foodborne GP Presentations			Foodborne Hospitalisations		
	Median	Lower 95%	Upper 95%	Median	Lower 95%	Upper 95%	Median	Lower 95%	Upper 95%
Bacteria									
Campylobacter	299,392	127,128	571,332	42,506	18,683	75,857	3,505	1,352	7,641
Clostridium perfringens	84,854	32,044	224,637	13,458	6,145	29,327	376	104	1,250
E.coli O157	468	303	628	468	303	628	146	95	196
Listeria monocytogenes	162	146	170	162	146	170	139	126	146
Salmonella	31,601	6,781	147,158	11,484	4,590	28,620	2,097	444	9,904
Shigella	1,634	110	4,973	1,634	110	4,973	29	1	158
Protozoa									
Cryptosporidium	2,072	320	12,201	712	168	2,544	55	8	341
Giardia	13,142	2,034	71,127	1,512	269	6,830	28	1	328
Viruses									
Adenovirus	12,454	3,085	34,672	1,028	245	3,070	192	42	639
Astrovirus	2,552	573	7,993	192	41	659	36	1	274

Norovirus	383,182	NA	NA	16,915	11,206	25,544	2,167	1,467	3,061
Rotavirus	2,065	518	5,670	220	54	615	32	7	105
Sapovirus (SRSV)	43,621	28,934	64,705	2,625	1,606	4,224	245	141	419
Total	909,375	702,281	1,225,152	96,884	67,218	135,872	9,731	6,157	18,120
Unattributed cases	1,449,168	1,046,506	1,991,612	124,102	70,914	201,947	6,439	4,347	9,429
Total IID including unattributed cases	2,362,095	1,794,915	3,149,584	222,046	149,799	322,179	16,301	11,271	25,981
Total (IID plus *Listeria monocytogenes*)	2,362,262	1,795,083	3,149,740	222,207	149,964	322,347	16,439	11,410	26,119

Note:

1. Credible intervals for norovirus were not possible for cases due to the modelling approach. This does not mean that there is no uncertainty in these estimates. There were a number of parameters used in the NoVAS study which, while based on the best science currently available, were acknowledged to have uncertain values. Sensitivity analysis undertaken as part of the study showed that changes to the values of these parameters could make big differences to the overall estimates.

2. As with all other results presented in table 3 the median estimates for the totals are based on distributions derived from running the model. This gives slightly different numbers to what you would get summing the median estimates from individual pathogens.

6. Validation

The methodology used to model the estimates for the number of foodborne cases, foodborne GP presentations and hospitalisations was largely replicated from the IID2 extension. This meant that outputs of the model could be validated against the results presented in Model 1 of the IID2 extension for 2009. The results were comparable to the median estimates and 95% intervals presented in that report.

Steps in validation included replicating distributions created using the available data and carrying out sensitivity analyses to test the impact of changing data. Replicating distributions included setting the incidence rate for the overall level of IID and bootstrapping outbreaks data to create beta distribution for the proportion of cases attributable to foodborne transmission.

7. Further work

The estimate of both the overall number of unattributed cases and the proportion of these cases due to food has a major impact on these estimates, contributing 60% of the total. Since they are unknown it makes it very difficult to estimate them with certainty.

The FSA is planning to commission the third study of infectious intestinal disease in the community. Since 2009, when the last such study was undertaken, diagnostic techniques have improved and whole genome sequencing is much more common. This should help with reducing the size of this unknown element along with improved attribution to sources for all cases. This in turn will lead to more accurate foodborne disease estimates. This study will also provide updated estimates for some of the parameters used in the models, such as the level of under-ascertainment for each pathogen, as such values may have changed over time.

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Annex 1: Data sources used in model

Data Required	Purpose	Dates data available for	What is available?	What is to be included in the model estimates?
Outbreak data for 13 pathogens and unknowns	Determine distributions for: • % foodborne • % hospitalisations	1992 to 2016	England and Wales data available from 1992 to 2016 (only foodborne outbreaks available up to 2009).	2001 – 2008 for % foodborne 2001 – 2016 for % hospitalisations
Confirmed laboratory reports for 13 pathogens	Update 2009 estimates to different years	2009 to 2018	Confirmed laboratory reports for all major pathogens requested from UK surveillance bodies to use with old methodology. Confirmed laboratory reports for adenovirus are not available.	Latest available data.
Enhanced Surveillance data including cases, hospitalisations and deaths for *Listeria monocytogenes* and *E.coli O157*	Estimates for E.coli O157 and Listeria updated using actuals due to huge uncertainties in data.	2009 to 2018	Enhanced surveillance figures available for all four UK countries.	Latest available data.
Community rate of IID cases and GP presentation rate for individual pathogens	Calculate the total IID cases and GP presentations caused by each pathogen based on population before applying % foodborne.	2009	IID2 study was carried out in 2009 and covered the UK.	IID2 study for all pathogens

Under-ascertainment rates for cases and GP presentations for individual pathogens	Calculate the total IID cases and GP presentations caused by each pathogen based on confirmed laboratory reports before applying % foodborne. Alternative method to row above	2009	IID2 study was carried out in 2009 and covered the UK.	IID2 study for all pathogens except: Shigella (IID1 study), *Listeria monocytogenes* and *E.coli O157*
Foodborne norovirus estimate	Estimate of rate of norovirus due to food used in model	Rate per population so can be adjusted for year	Foodborne norovirus estimate	Rate per population with variation based on Poisson distribution
Population Estimate	Estimate of the UK mid-year population by year used in the IID2 Extension.	Estimates and projections available from ONS	Population estimates for UK are available from ONS.	Latest year for which other data is available

Annex 2: model and parameters used for cases and GP presentations for the known pathogens

Method for cases and GP presentations	Pathogens	Parameters	Source
Method 1- (UK rate & UK population)	Astrovirus, Adenovirus, *Clostridium perfringens,* Sapovirus	Foodborne proportion	IID2 extension
		Population	ONS 2018 mid-year population
		UK rate of IID	IID2 study
		UK rate of IID related GP presentations	IID2 study
Method 2- (Laboratory reports & ascertainment ratio)	*Campylobacter*, *Cryptosporidium*, *Giardia*, *Salmonella*, *Shigella*, Rotavirus	Foodborne proportion	IID2 extension
		Confirmed laboratory reports	UK's four surveillance bodies
		under-ascertainment ratio for cases	IID2 (apart from Shigella, using the figure from IID1)
		Under-ascertainment ratio for GP presentations	IID2 study
Enhanced surveillance	*E.coli* O157*, Listeria monocytogenes*	Foodborne proportion	IID2 extension
		Confirmed laboratory reports	UK's four surveillance bodies
		Under-ascertainment ratio for cases	Assume there is no under-ascertainment (=1)
		Under-ascertainment ratio for GP presentations	Assume there is no under-ascertainment (=1)
NoVAS model review	Norovirus	Foodborne proportion	NoVAS model review and IID2 study
		Confirmed laboratory reports	UK's four surveillance bodies

		Under-ascertainment ratio for GP presentations	IID2 study