

Table 1. Modeling approaches used to estimate the total number of illnesses for different types of data, United States

Pathogens for which laboratory-confirmed illnesses were scaled up			Pathogens for which US population was scaled down
Active surveillance data	Passive surveillance data	Outbreak surveillance data	
<i>Campylobacter</i> spp.	<i>Brucella</i> spp.	<i>Bacillus cereus</i>	Astrovirus
<i>Cryptosporidium</i> spp.	<i>Clostridium botulinum</i>	<i>Clostridium perfringens</i>	Norovirus
<i>Cyclospora cayetanensis</i>	<i>Giardia intestinalis</i>	ETEC [†]	Rotavirus
STEC* O157	Hepatitis A virus	<i>Staphylococcus aureus</i>	Sapovirus
STEC non-O157	<i>Mycobacterium bovis</i>	<i>Streptococcus</i> spp. group A	<i>Toxoplasma gondii</i>
<i>Listeria monocytogenes</i>	<i>Trichinella</i> spp.		
<i>Salmonella</i> spp., nontyphoidal*	<i>Vibrio cholerae</i> , toxigenic		
<i>S. enterica</i> serotype Typhi	<i>Vibrio parahaemolyticus</i>		
<i>Shigella</i> spp.	<i>Vibrio vulnificus</i>		
<i>Yersinia enterocolitica</i>	<i>Vibrio</i> spp., other		

*STEC = Shiga toxin-producing *Escherichia coli*.

[†]ETEC = Enterotoxigenic *Escherichia coli*; numbers of *Escherichia coli* other than STEC or ETEC assumed to be same as for ETEC.

*Includes all serotypes other than Typhi.