



# Errata Sheet for Technical Support Materials: Developing Alternative Recreational Criteria for Waters Contaminated by Predominantly Non-Human Fecal Sources

**Issued July 31, 2024**

After publication of *Technical Support Materials: Developing Alternative Recreational Criteria for Waters Contaminated by Predominantly Non-Human Fecal Sources* in April 2024, an error in the code for the dose response function for adenovirus in Appendix E was identified. The code has been corrected in a revised version posted in July 2024. Additionally, a sentence on page 31 was edited for clarity. The specific revisions and corrections are described below.

**In version 2, Page 31, the first sentence of the second paragraph has been revised to:**

In gull feces, *Campylobacter* and *Salmonella* were considered to have a low fraction of human infectious strains (Schoen and Ashbolt, 2010; Soller et al., 2010b).

**In version 2, Page E-2, Appendix E. Example Code for Step 3: Approach 1, explanatory text has been revised to:**

```
### This code assumes the dataset includes columns labelled: sal_c, camp_c, aden_c, nov,
### gear1623, and cryp1623 that reflect the paired concentrations of Salmonella(culture),
### Campylobacter (culture), adenovirus (culture), norovirus, Giardia and
### Cryptosporidium in units of organisms/L. If any of these pathogens have not been measured,
### includes those columns in the test data spreadsheet and then represent their values with zero.
#####
```

**In version 2, Page E-2, Appendix E: Example Code for Step 3: Approach 1, example code for the adenovirus probability of illness given infection has been corrected to:**

```
#####
### Confluent Hypergeometric Expression of Beta Poisson
### Dose Response Function with Teunis Dose Dependent
### Parameters for infection and illness (Teunis 2016)
#####
pill_hyp <- function(alpha, beta, r, eta, d){
  return((1-(1+d/eta)**-r)*(1-genhypergeo(alpha, alpha+beta, -d)))
}
```

};

**In version 2, Page E-6, Appendix E: Example Code for Step 3: Approach 1, explanatory text has been added:**

```
### Caution: This code may produce negative illness estimates on rare occasions when the dose of adenovirus,  
### norovirus, or Campylobacter exceeds the computational bounds of the confluent hypergeometric  
### dose response function used to characterize these pathogens in the R code. Users are advised to treat  
### negative values for the minimum or mean illness rates in the simulation as an indication that some  
### concentrations are triggering false estimates when combined with high ingestion volumes in the  
### calculations; this eventuality is expected to be rare in surface waters with predominantly animal fecal  
### sources. The median and percentile estimates generated by the code will, however, be valid in these  
### circumstances.
```