Safely-Managed Hygiene: A Risk-Based Assessment of Handwashing Water Quality Supporting Information

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Pages: 25
Figures: 3
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Table S1. Data sources used in the model

ID	Description	References
D_1	Compilation of data on the efficacy of handwashing for different waterborne pathogens (compiled from various sources by authors)[1]	Ansari SA, Sattar SA, Springthorpe VS, Wells GA, Tostowaryk W. In vivo protocol for testing efficacy of hand-washing agents against viruses and bacteria: experiments with rotavirus and Escherichia coli. *Appl Environ Microbiol.* 1989; 55(12):3113-8. Edmonds SL, McCormack RR, Zhou SS, Macinga DR, Fricker CM. Hand hygiene regimens for the reduction of risk in food service environments. *J Food Prot.* 2012; 75(7):1303-9 Liu P, Yuen Y, Hsiao HM, Jaykus LA, Moe C. Effectiveness of liquid soap and hand sanitizer against Norwalk virus on contaminated hands. *Appl Environ Microbiol.* 2010; 76(2):394-9 Manthriratna GA. *Efficacy of handwashing as an aid in the control of rotavirus and Giardia transmission:* University of Arizona; 1989 Pickering AJ, Davis J, Walters SP, Horak HM, Keymer DP, Mushi D, et al. Hands, water, and health: Fecal contamination in Tanzanian communities with improved, non-networked water supplies. *Environ Sci Technol.* 2010; 44:3267-72 Schurmann W, Eggers HJ. An experimental study on the epidemiology of enteroviruses: water and soap washing of poliovirus 1--contaminated hands, its effectiveness and kinetics. *Med Microbiol Immunol.* 1985; 174(5):221-36 Sickbert-Bennett EE, Weber DJ, Gergen-Teague MF, Rutala WA. The effects of test variables on the efficacy of hand hygiene agents. *Am J Infect Control.* 2004; 32(2):69-83 Sickbert-Bennett EE, Weber DJ, Gergen-Teague MF, Sobsey MD, Samsa GP, Rutala WA. Comparative efficacy of hand hygiene agents in the reduction of bacteria and viruses. *Am J Infect Control.* 2005; 33(2):67-77
D_2	Transfer of bacteriophages between the fingers of volunteers and water or saliva[2]	Pitol, A. K., Bischel, H. N., Kohn, T., & Julian, T. R. (2017). Virus Transfer at the Skin–Liquid Interface. *Environmental Science & Technology*, 51(24), 14417-14425.
D_3	*E. coli* in handwashing water and hands (Harare, Zimbabwe)[3]	Paired samples of the concentration of E. coli in handwashing water sources and on the hands of volunteers (before and after handwashing) from Harare, Zimbabwe. The data are primary data collected, analyzed, and reported as described in: Navab-Daneshmand, T., Friedrich, M. N., Gächter, M., Montealegre, M. C., Mlambo, L. S., Nhiwatiwa, T., Mosler, H.-J., Julian, T. R. (2018). Escherichia coli Contamination across Multiple Environmental Compartments (Soil, Hands, Drinking Water, and Handwashing Water) in Urban Harare: Correlations and Risk Factors. *The American Journal of Tropical Medicine and Hygiene*, 98(3), 803
D_4	Hand and palm surface areas measured (cm^2)[4]	Table 1 from: Joo-Young Lee, Jeong-Wha Choi, Ho Kim, Determination of Hand Surface Area by Sex and Body Shape using Alginate, *Journal of Physiological Anthropology*, 2007, Volume 26, Issue 4, Pages 475-483, Released August 15, 2007, Online ISSN 1880-6805, Print ISSN 1880-6791

Electronic Retrieval Locations for Datasets:
[1] http://hydro.sdsu.edu/~verbyla/wordpress/wp-content/uploads/2018/10/hw_data.csv
[2] http://doi.org/10.25678/000099
[3] http://doi.org/10.25678/000088
Electronic Retrieval Locations for Datasets:
[4] http://doi.org/10.2114/jpa2.26.475

D_5	Dose-response data for select pathogens (compiled from various sources by authors)[5]	The data were compiled (mostly via QMRAwiki) from various sources by the authors: Center for Advancing Microbial Risk Assessment (CAMRA) Dose Response. Quantitative Microbial Risk Assessment (QMRA) Wiki http://qmrawiki.canr.msu.edu/index.php/Dose_Response (25 June 2018). Atmar RL, Opekun AR, Gilger MA, Estes MK, Crawford SE, Neill FH, Ramani S, Hill H, Ferreira J, Graham DY. Determination of the human infectious dose-50% for Norwalk virus. Journal of Infectious Diseases, 2014; 209(7):1016–1022. Bieber D, et al. (1998) Type IV pili, transient bacterial aggregates, and virulence of enteropathogenic Escherichia coli. Science (New York, N.Y.). 280(5372), pp.2114-2118. Chappell CL, Okhuysen PC, Langer-Curry R, Widmer G, Akiyoshi DE, Tanriverdi S, Tzipori S. (2006). Cryptosporidium hominis: Experimental challenge of healthy adults. American Journal of Tropical Medicine and Hygiene, 75(5):851– 857. Chappell CL, Okhuysen PC, Langer-Curry R, Lupo PJ, Widmer G, Tzipori S. (2015). Cryptosporidium muris: Infectivity and illness in healthy adult volunteers. American Journal of Tropical Medicine and Hygiene, 92:50–55. DuPont HL, et al. (1971) Pathogenesis of Escherichia coli diarrhea. The New England Journal of Medicine. 285(1), pp.1-9. DuPont HL, et al., (1972) Immunity in shigellosis. II. Protection induced by oral live vaccine or primary infection. The Journal of Infectious Diseases, 125(1), pp.12-16. Ferguson WW & June RC (1952) Experiments on feeding adult volunteers with Escherichia coli 111, B4, a coliform organism associated with infant diarrhea. American Journal of Hygiene. 55(2), pp.155-169. Frenck R, Bernstein DI, Huang P, Zhong W, Parker S, Dickey M, McNeal, M, Jiang X. Predicting susceptibility to Norovirus GII.4 by use of a challenge model involving humans. Journal of Infectious Diseases, 2012; 206:1386–1393. Hornick RB, et al. (1966) Study of induced typhoid fever in man. I. Evaluation of vaccine effectiveness. Transactions of the Association of American Physicians. 79, pp.361-367. Hornick RB, et al. (1970) Typhoid fever: pathogenesis and immunologic control. The New England Journal of Medicine. 283(13), pp.686-691. Hornick, R.B., Music, S.I., Wenzel, R., Cash, R.A., Libonati, J.P., Snyder, M.J., Woodward, T.E. (1971) The Broad Street Pump Revisited: Response of Volunteers to Ingested Cholera Vibrios Bulletin New York Academy of Medicine 47(10): 1181-1191. June RC, Ferguson WW & Worfel MT (1953) Experiments in feeding adult volunteers with Escherichia coli 55, B5, a coliform organism associated with infant diarrhea. American Journal of Hygiene. 57(2), pp.222-236. Levine MM, et al. (1977) Diarrhea caused by Escherichia coli that produce only heat-stable enterotoxin. Infection and Immunity. 17(1), pp.78-82 Levine MM, et al. (1978) Escherichia coli strains that cause diarrhoea but do not produce heat-labile or heat-stable enterotoxins and are non-invasive. Lancet. 311(8074), pp.1119-1122 Messner, M.J., Chappell, C.L., Okhuysen, P.C. (2001). Risk assessment for Cryptosporidium: A hierarchical Bayesian analysis of human dose response data. Water Research, 35(16):3934–3940. Okhuysen PC, Rich SM, Chappell CL, Grimes KA, Widmer G, Feng X, Tzipori S. (2002). Infectivity of a Cryptosporidium parvum isolate of cervine origin for healthy adults and interferon-γ knockout mice. Journal of Infectious Diseases, 185(9):1320–1325. Rendtorff, R.C., 1954. The experimental transmission of human intestinal protozoan parasites. II. Giardia lamblia cysts given in capsules. American Journal of Epidemiology, 59(2), pp.209-220.

[5] http://hydro.sdsu.edu/~verbyla/wordpress/wp-content/uploads/2018/09/dose_response_data.csv

		Seitz SR, Leon JS, Schwab KJ, Lyon GM, Dowd M, Mc- Daniels M, Abdulhafid G, Fernandez ML, Lindesmith LC, Baric RS, Moe CL. Norovirus infectivity in humans and per- sistence in water. Applied and Environmental Microbiology, 2011; 77:6884–6888. Tacket CO, et al. (2000) Role of EspB in experimental human enteropathogenic Escherichia coli infection. Infection and Immunity. 68(6), pp.3689-3695. Teunis PFM, Moe CL, Pengbo L, Miller SE, Lindesmith L, Baric RS, Le Pendu J, Calderon RL. Norwalk virus: How infectious is it? Journal of Medical Virology, 2008; 80: 1468–1476. United States Environmental Protection Agency (USEPA). (2005). Economic Analysis for the Final Long Term 2 Enhanced Surface Water Treatment Rule; EPA 815-R-06-001 Washington, DC: U.S. Environmental Protection Agency, Office of Water. Ward RL, Bernstein DI, Young EC, Sherwood JR, Knowlton DR, Schiff GM. Human rotavirus studies in volunteers: determination of infectious dose and serological response to infection. J. Infect. Dis. 1986 Nov;154(5):871-880.
D_6	Worldwide trends in body-mass index, underweight, overweight, and obesity from 1975 to 2016[6]	Abarca-Gómez, L., Abdeen, Z.A., Hamid, Z.A., Abu-Rmeileh, N.M., Acosta-Cazares, B., Acuin, C., Adams, R.J., Aekplakorn, W., Afsana, K., Aguilar-Salinas, C.A. and Agyemang, C., 2017. Worldwide trends in body-mass index, underweight, overweight, and obesity from 1975 to 2016: a pooled analysis of 2416 population-based measurement studies in 128· 9 million children, adolescents, and adults. *The Lancet*, 390(10113), 2627-2642.
D_7	A century of trends in adult human height[7]	NCD Risk Factor Collaboration. (2016). A century of trends in adult human height. *Elife*, *5*, e13410.
D_8	Population figures for countries, regions (e.g. Asia) and the world[8]	The World Bank: Population figures for countries, regions (e.g. Asia) and the world. Data sources: (1) United Nations Population Division. World Population Prospects: 2017 Revision; (2) Census reports and other statistical publications from national statistical offices; (3) Eurostat: Demographic Statistics; (4) United Nations Statistical Division. Population and Vital Statistics Reprot (various years); (5) U.S. Census Bureau: International Database; (6) Secretariat of the Pacific Community: Statistics and Demography Programme
D_9	Population, female (% of total)[9]	

Electronic Retrieval Locations for Datasets:

[6] http://www.ncdrisc.org/downloads/bmi/NCD_RisC_Lancet_2017_BMI_age_standardised_country.csv

[7] http://www.ncdrisc.org/downloads/height/NCD_RisC_eLife_2016_height_age18_countries.csv

[8] http://datahub.io/core/population/r/population.csv

Electronic Retrieval Locations for Datasets:

[9] http://datahub.io/world-bank/sp.pop.totl.fe.zs/r/data.csv

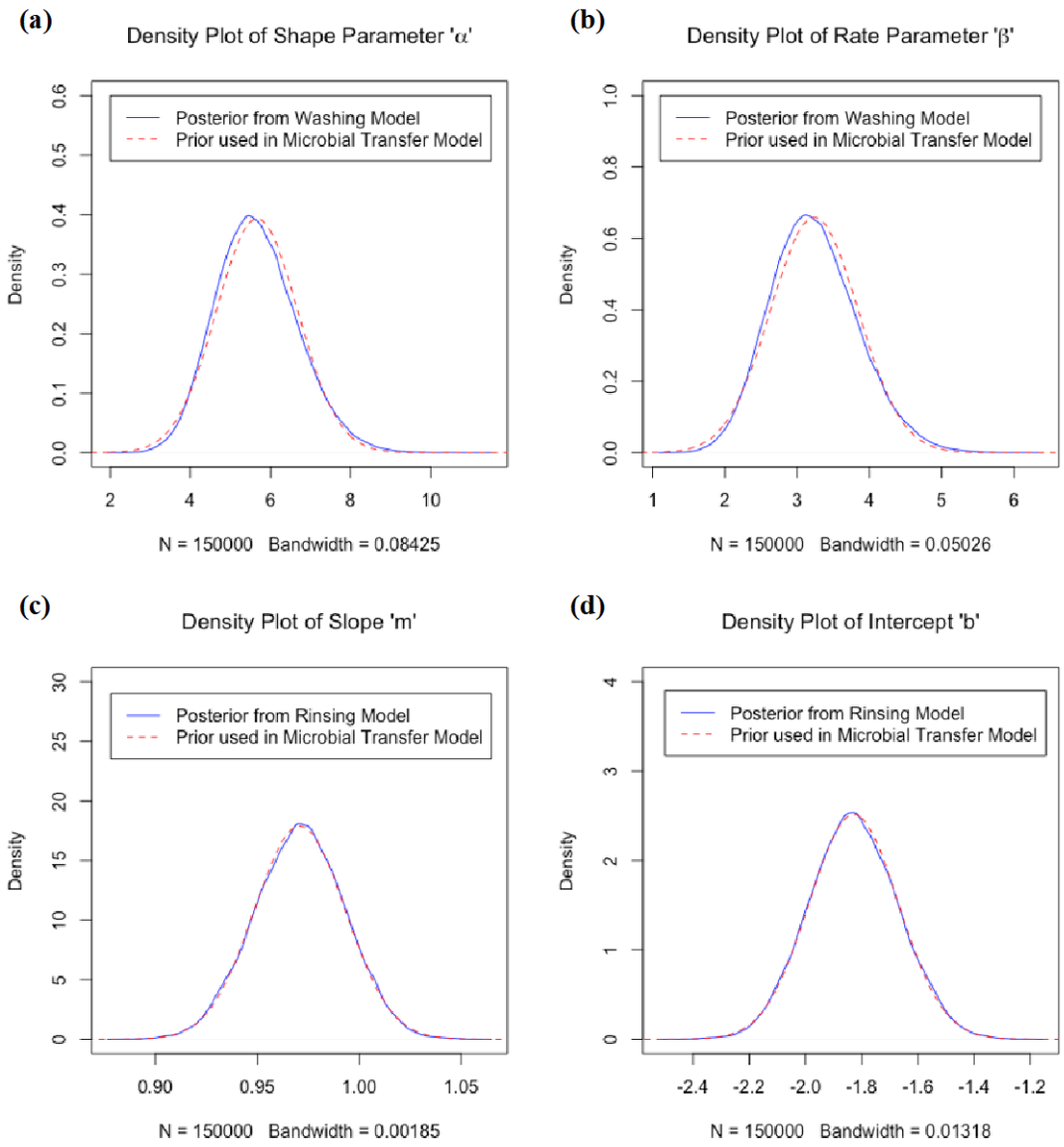

Figure S1. Comparison between posterior distributions for a) the shape (α) and b) rate (β) parameters derived in the Washing Model, and c) the slope (*m*) and d) intercept (*b*) parameters derived in the Rinsing Model, as well as the corresponding prior distributions used in the Microbial Transfer Model.

a)

	V. cholerae	*S. flexneri*	*S. enterica* (Typhi)	*E. coli* (ETEC)	*E. coli* (EPEC)	*Giardia*	*Cryptosporidium*	Norovirus	Rotavirus
Rinsing Model Slope (m)	-0.011	-0.014	-0.009	-0.009	-0.005	-0.017	-0.015	-0.016	-0.013
Rinsing Model Intercept (b)	0.030	0.032	0.024	0.021	0.027	0.033	0.033	0.034	0.031
Washing Model Log Reduction Value (LRV)	-0.004	-0.007	-0.002	-0.004	-0.004	-0.007	-0.007	-0.007	-0.006
Precision of Rinsing Model	0.015	0.019	0.012	0.010	0.014	0.020	0.020	0.020	0.018
Hand Surface Area Model Slope (β_1)	0.007	0.000	0.004	0.005	0.001	0.000	-0.001	0.000	-0.002
Hand Surface Area Model Intercept (β_0)	-0.007	0.000	-0.003	-0.004	-0.002	0.000	0.001	0.000	0.002
Precision of Hand Surface Area Model	0.002	0.003	0.001	0.006	0.004	0.002	0.003	0.002	0.002
Average Number of Times Hands Washed Daily (λ)	0.046	0.047	0.037	0.031	0.033	0.050	0.049	0.051	0.047
Number of Times Hands Washed Daily (κ)	0.060	0.063	0.049	0.043	0.044	0.066	0.064	0.067	0.063
Hand-to-Mouth Transfer Efficiency (TE)	0.028	0.032	0.025	0.026	0.020	0.032	0.031	0.032	0.031
Hand-to-Mouth Contact Fraction (f)	0.028	0.029	0.024	0.023	0.019	0.027	0.026	0.029	0.027
Dose-Response Model Parameter (α)	0.181	0.132	0.209	0.156	0.207	-	0.018	-	0.096
Dose-Response Model Parameter (β)	0.022	0.021	-0.009	-0.017	-0.012	-	-0.008	-	0.003
Dose-Response Model Parameter (Φ)	-	-	-	-	-	-	-	-0.008	-
Dose-Response Model Parameter (a)	-	-	-	-	-	-	-	-0.036	-
Dose-Response Model Parameter (r)	-	-	-	-	-	0.028	-	-	-

b)

Rinsing Model Slope (m)	-0.008	-0.011	-0.008	-0.006	-0.004	-0.015	-0.014	-0.014	-0.012
Rinsing Model Intercept (b)	0.022	0.031	0.022	0.024	0.020	0.031	0.030	0.032	0.027
Washing Model Log Reduction Value (LRV)	0.001	0.000	0.000	-0.003	-0.001	0.001	0.000	0.000	0.000
Precision of Rinsing Model	0.010	0.017	0.010	0.013	0.011	0.017	0.017	0.018	0.015
Hand Surface Area Model Slope (β_1)	0.001	0.003	0.002	0.006	0.001	0.002	0.003	0.002	0.004
Hand Surface Area Model Intercept (β_0)	0.000	-0.003	-0.003	-0.006	-0.001	-0.002	-0.003	-0.002	-0.004
Precision of Hand Surface Area Model	-0.001	0.000	0.004	0.003	-0.004	0.000	0.000	0.000	0.001
Average Number of Times Hands Washed Daily (λ)	0.039	0.045	0.038	0.032	0.038	0.048	0.048	0.049	0.045
Number of Times Hands Washed Daily (κ)	0.053	0.058	0.052	0.045	0.046	0.063	0.062	0.065	0.058
Hand-to-Mouth Transfer Efficiency (TE)	0.027	0.033	0.027	0.025	0.026	0.033	0.031	0.033	0.031
Hand-to-Mouth Contact Fraction (f)	0.030	0.034	0.028	0.024	0.027	0.035	0.035	0.037	0.032
Dose-Response Model Parameter (α)	0.234	0.131	0.208	0.163	0.200	-	0.003	-	0.093
Dose-Response Model Parameter (β)	0.031	0.025	-0.002	-0.008	-0.023	-	0.006	-	0.000
Dose-Response Model Parameter (Φ)	-	-	-	-	-	-	-	-0.008	-
Dose-Response Model Parameter (a)	-	-	-	-	-	-	-	-0.035	-
Dose-Response Model Parameter (r)	-	-	-	-	-	0.025	-	-	-

Figure S2. Heat map showing Spearman's correlation coefficients between model inputs and the model outputs (*i.e.*, the annual probability of infection for all reference pathogens) under the following assumptions: a) that each handwashing event represents an independent probability of infection; and b) that all handwashing events in a day represent a cumulative dose, with 365 independent probabilities of infection per year.

Table S2. Maximum tolerable pathogen concentrations (per 100 mL) in handwashing water for the annual probability of infection (P_{inf}) threshold of 1:100 and 1:10,000, under the assumptions that 1) hands did not contain any pathogens prior to handwashing, and 2) each handwashing event represents an independent dose with an independent probability of infection. The concentrations correspond with a 95% probability that the risk level for the population will be equal to or below the specified thresholds.

Reference Pathogen	Units	Pathogen concentration (per 100 mL) corresponding to the following threshold with 95% probability	
		$P_{inf} \leq$ 1:100	$P_{inf} \leq$ 1:10,000
V. cholerae	CFU	$<2\times10^{-3}$	$<1\times10^{-5}$
S. flexneri	CFU	$<2\times10^{-3}$	$<1\times10^{-5}$
S. enterica Typhi	CFU	$<5\times10^{-3}$	$<4\times10^{-5}$
E. coli (ETEC)	CFU	$<2\times10^{-2}$	$<1\times10^{-4}$
E. coli (EPEC)	CFU	$<4\times10^{-3}$	$<3\times10^{-5}$
Giardia	Cysts	$<2\times10^{-4}$	$<1\times10^{-6}$
Cryptosporidium	Oocysts	$<1\times10^{-4}$	$<8\times10^{-7}$
Norovirus	GC	$<4\times10^{-3}$	$<3\times10^{-5}$
Rotavirus [a]	FFU	$<3\times10^{-5}$	$<2\times10^{-7}$

[a] Rotavirus is primarily a risk for unvaccinated children <5 years, as most older children and adults have acquired immunity due to exposure and/or vaccinations

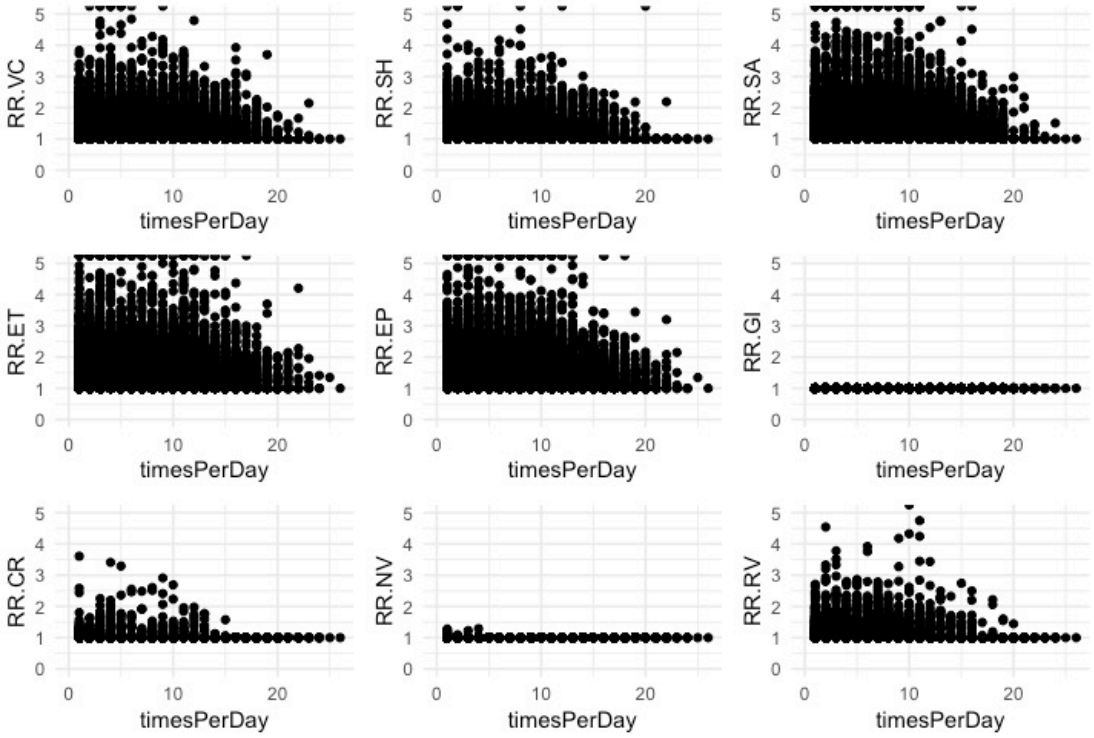

Figure S3. Plots of the risk ratios for the different pathogens (the probability of infection when not washing hands relative to the probability of infection when washing hands using water with no pathogens) relative to the number of times per day hands are washed. Initial concentrations of pathogens on hands are assumed to be uniformly distributed between 1 and 10^{10} per cm^2. Risk ratios >1.0 indicate handwashing reduces risk (a risk ratio of 2 indicates that the risk of infection is twice as high if hands are not washed).

Section S1. Complete R and JAGS Script

The following script can be copied and pasted into R and used to reproduce the figures and tables contained within the manuscript. Note that it is necessary to have JAGS installed in order for the script to run within R. JAGS can be downloaded from http://mcmc-jags.sourceforge.net/.

```
#############################################################################################################

rm(list=ls())
require(rjags)
require(coda)
require(reshape2)
require(svDialogs)
require(ggplot2)
require(gridExtra)
require(grid)
require(NADA)

############### - Choose assumptions about the number of doses - ###################
IIPperDay <- as.numeric(dlgInput(message=c("Enter the number 1 or 2",
                                  "1: assumes a daily accumulated dose and a single independent
infection probability per day.",
                                  "2: assumes multiple independent infection probabilities per day)"),
default = 1,
                        Sys.info()["user"])$res)
if ((IIPperDay!=1 & IIPperDay!=2) || !length(IIPperDay)) { # The user did not enter a valid option
  dlg_message("You did not enter a valid option.\nClick OK to assume a single independent infection
probability per day.", "ok")$res
  IIPperDay <- 1
} else {
  if (IIPperDay==1) {
    dlg_message("You selected option 1 (a single independent infection probability per day).",
"ok")$res
  } else {
    dlg_message("You selected option 2 (multiple independent infection probabilities per day).",
"ok")$res
  }
}

####----FIRST THE USER NEEDS TO CHOOSE IF THEY WILL OPTIMIZE FOR MAX CONCENTRATION ON HANDS OR WATER
  ##-- handsorwater=1 --> water has some pathogens, hands have some pathogens
  ##-- handsorwater=2 --> water has no pathogens, hands have some pathogens
  ##-- handsorwater=3 --> water has some pathogens, hands have no pathogens
handsorwater <- as.numeric(dlgInput(message=c("Enter the number 1, 2, or 3.",
                                          "1: Assume both water and hands have some pathogens",
                                          "2: Assume water has no pathogens (optimize for the maximum
concentration on unwashed hands)",
                                          "3: Assume hands have no pathogens (optimize for the maximum
concentration in handwashing water)"), default = 1,
                                  Sys.info()["user"])$res)
if ((handsorwater!=1 & handsorwater!=2 & handsorwater!=3) || !length(handsorwater)) { # The user did
not enter a valid option
  dlg_message("You did not enter a valid option.\nClick OK to assume both water and hands have some
pathogens.", "ok")$res
  handsorwater <- 1
} else {
  if (handsorwater==1) {
    dlg_message("You selected option 1 (assume both water and hands have some pathogens).", "ok")$res
  } else {
    if (handsorwater==2){
      dlg_message("You selected option 2 (assume water has no pathogens).", "ok")$res
    } else {
      dlg_message("You selected option 3 (assume hands have no pathogens).", "ok")$res
    }
  }
}

############### - Choose assumptions about pathogens on hands before handwashing - ###################
if (handsorwater == 3) {
  MinConcHands <- -10
  MaxConcHands <- -9
  #these values don't matter because of the equation in the JAGS code that sets the concentration on
hands to zero under this scenario
```

```
} else {
  MinConcHands <- as.numeric(dlgInput(message="Enter the MINIMUM assumed number of log10(pathogens) per
square centimeter of a person's hands prior to handwashing", default = -10,
                                      Sys.info()["user"])$res)
  if (!is.numeric(MinConcHands) || !length(MinConcHands)) { # The user did not enter a valid option
    dlg_message("You did not enter a valid option.\nClick OK to assume a minimum log10-transformed
concentration of -10.", "ok")$res
    MinConcHands <- -10
  }
  MaxConcHands <- as.numeric(dlgInput(message="Enter the MAXIMUM assumed number of log10(pathogens) per
square centimeter of a person's hands prior to handwashing", default = 10,
                                      Sys.info()["user"])$res)
  if (!is.numeric(MaxConcHands) || !length(MaxConcHands)) { # The user did not enter a valid option
    dlg_message("You did not enter a valid option.\nClick OK to assume a maximum log10-transformed
concentration of 10.", "ok")$res
    MaxConcHands <- 10
  } else {
    dlg_message(c("You assume that the concentration of pathogens per square centimeter of a person's
hands prior to handwashing ranges uniformly (on a log10 scale) from ",10^MinConcHands," to
",10^MaxConcHands), "ok")$res
  }
}

############### - Choose assumptions about pathogens in handwashing water - ###################
if (handsorwater == 2) {
  MinConcWater=-10
  MaxConcWater=-9
  #these values don't matter because of the equation in the JAGS code that sets the concentration in
water to zero under this scenario
} else {
  MinConcWater <- as.numeric(dlgInput(message="Enter the MINIMUM assumed number of log10(pathogens) per
mL of handwashing water", default = -10,
                                      Sys.info()["user"])$res)
  if (!is.numeric(MinConcWater) || !length(MinConcWater)) { # The user did not enter a valid option
    dlg_message("You did not enter a valid option.\nClick OK to assume a minimum log10-transformed
concentration of -10.", "ok")$res
    MinConcWater <- -10
  }
  MaxConcWater <- as.numeric(dlgInput(message="Enter the MAXIMUM assumed number of log10(pathogens) per
mL of handwashing water", default = 6,
                                      Sys.info()["user"])$res)
  if (!is.numeric(MaxConcWater) || !length(MaxConcWater)) { # The user did not enter a valid option
    dlg_message("You did not enter a valid option.\nClick OK to assume a maximum log10-transformed
concentration of 6.", "ok")$res
    MaxConcWater <- 6
  } else {
    dlg_message(c("Assume that the concentration of pathogens per mL of handwashing water ranges
uniformly (on a log10 scale) from ",10^MinConcWater," to ",10^MaxConcWater), "ok")$res
  }
}

############### - Set Conditions of MCMC - ###############
n.adapt=1000
n.update=1000 #burn-in
n.iter=20000

############### - custom functions - ###############
getCoda=function(coda,var) return(c(coda[[1]][,var],coda[[2]][,var],coda[[3]][,var]))

############### - HANDWASHING MODEL (to get priors on shape and rate) - ###############
#---Data set: Compilation of Data on the Efficacy of Handwashing for Different Waterborne Pathogens
  # authors     The full reference for the study from which the data were reported
  # agent         The microbial agent used in the study
  # type          The type of microorganism (acceptable values: virus, bacteria, protozoa, helminth
egg)
  # soap          Yes/No variable based on whether or not soap was used during handwashing
  # time          The number of seconds spent handwashing
  # N         The number of replicate measurements reported in the study
  # LRV     The log10 reduction of the microorganism from hands based on data presented in the study
  # SE      The standard error of the mean log10 reduction value
d1=read.csv(url("http://hydro.sdsu.edu/~verbyla/wordpress/wp-
content/uploads/2018/10/hw_data.csv"),sep=",",header=T);head(d1) #all handwashing data (reviewed)

data=list(
  n=length(d1$LRV),
  lrv=d1$LRV #expressed as the log removal achieved by handwashing
```

```
); data

washing.model="
      model{
  #prior distributions
      shape ~ dunif(.000001,1000) #alpha
      rate ~ dunif(.000001,1000)  #beta

  #likelihood function
      for(i in 1:n){lrv[i] ~ dgamma(shape,rate)} # the LRV of pathogens removed (cannot be negative)

  #derived quantities
      lrw ~ dgamma(shape,rate) #log10 of microbes removed by handwashing
      }
"

inits=list(
  list(shape=3.1,rate=20),
  list(shape=3.5,rate=50),
  list(shape=3.9,rate=40)
)

jm.wash=jags.model(textConnection(washing.model),data=data,n.adapt=n.adapt,inits=inits,n.chains=length(
inits)) #Compile the model
update(jm.wash,n.iter=n.update) #Execute the MCMC
zc.wash=coda.samples(jm.wash,variable.names=c("shape","rate","lrw"),n.iter=n.iter) #Analyze the
posterior distributions
gelman.diag(zc.wash) #this indicates if the model has converged (general guideline is that if
multivariate psrf <1.05, the model has converged sufficiently)

mean.shape=mean(getCoda(zc.wash,"shape"))
mean.rate=mean(getCoda(zc.wash,"rate"))
mean.lrv=mean(getCoda(zc.wash,"lrw"))
sd.shape=sd(getCoda(zc.wash,"shape"))
sd.rate=sd(getCoda(zc.wash,"rate"))
sd.lrv=sd(getCoda(zc.wash,"lrw"))

WASHING.priors=data.frame(mean.shape,mean.rate,sd.shape,sd.rate,mean.lrv,sd.lrv)
WASHING.priors

par(mfrow=c(1,2))
plot(density(getCoda(zc.wash,"shape")),col="blue",main=expression(paste("Density Plot of Shape
Parameter '",alpha,"'")),ylim=c(0,0.6))
curve(dnorm(x,mean=mean.shape,sd=sd.shape),from=0,to=20,n=1000,add=T,lty=2,col="red")
legend(2,0.6,c("Posterior from Washing Model","Prior used in Microbial Transfer
Model"),col=c("blue","red"),lty=c(1,2))
plot(density(getCoda(zc.wash,"rate")),col="blue",main=expression(paste("Density Plot of Rate Parameter
'",beta,"'")),ylim=c(0,1))
curve(dnorm(x,mean=mean.rate,sd=sd.rate),from=0,to=10,n=1000,add=T,lty=2,col="red")
legend(1.1,1,c("Posterior from Washing Model","Prior used in Microbial Transfer
Model"),col=c("blue","red"),lty=c(1,2))

############### - RINSING MODEL (to get priors on slope and intercept) - ###############
d2=read.csv(url("https://zenodo.org/record/1454505/files/phagetransferwatertohand.csv"),sep=",",header=
T);head(d2) # Transfer of bacteriophages between the fingers of volunteers and water or saliva;
https://doi.org/10.25678/000099; data have the units pfu/mL for Cw and pfu/cm2 for Ch.un and Ch.ad

data=list(
  n=length(d2$Cw),
  y=log10(d2$Ch.un+d2$Ch.ad),
  x=log10(d2$Cw)
); data

rinsing.model="
      model{

  #prior distributions
      m ~ dgamma(.0001,.0001)
      b ~ dunif(-1000,1000)
      sigma ~ dgamma(.001,.001)
      tau <- 1/(sigma)^2

  #likelihood functions
      for(j in 1:n){
        z[j] <- m*x[j]+b
        y[j] ~ dnorm(z[j],tau)
```

```
      }
    }
"

inits=list(
  list(m=1,b=0,sigma=1),
  list(m=2,b=0.1,sigma=2),
  list(m=3,b=0.2,sigma=3)
)

jm.hr=jags.model(textConnection(rinsing.model),data=data,n.adapt=n.adapt,inits=inits,n.chains=length(in
its)) #Compile the model
update(jm.hr,n.iter=n.update) #Execute the MCMC
zc.hr=coda.samples(jm.hr,variable.names=c("m","b","Xd","zd","sigma"),n.iter=n.iter) #Analyze the
posterior distributions
zj.hr=jags.samples(jm.hr,variable.names=c("zdt"),n.iter=n.iter)
gelman.diag(zc.hr)

mean.m=mean(getCoda(zc.hr,"m"))
mean.b=mean(getCoda(zc.hr,"b"))
mean.sigma=mean(getCoda(zc.hr,"sigma"))
sig.m=sd(getCoda(zc.hr,"m"))
sig.b=sd(getCoda(zc.hr,"b"))
sd.sigma=sd(getCoda(zc.hr,"sigma"))

par(mfrow=c(1,2))
plot(density(getCoda(zc.hr,"m")),col="blue",main=expression("Density Plot of Slope 'm'"),ylim=c(0,30))
curve(dnorm(x,mean=mean.m,sd=sig.m),from=0,to=2,n=1000,add=T,lty=2,col="red")
legend(0.878,29,c("Posterior from Rinsing Model","Prior used in Microbial Transfer
Model"),col=c("blue","red"),lty=c(1,2))
plot(density(getCoda(zc.hr,"b")),col="blue",main=expression("Density Plot of Intercept
'b'"),ylim=c(0,4))
curve(dnorm(x,mean=mean.b,sd=sig.b),from=-3,to=0,n=1000,add=T,lty=2,col="red")
legend(-2.5,3.9,c("Posterior from Rinsing Model","Prior used in Microbial Transfer
Model"),col=c("blue","red"),lty=c(1,2))

RINSING.priors=data.frame(mean.m,mean.b,sig.m,sig.b)
RINSING.priors

#--------------------------------------

washPriors=WASHING.priors
rinsePriors=RINSING.priors

#---Data set: Concentration of E. coli in the handwashing water source and on the hands of volunteers
(before and after handwashing) from Harare, Zimbabwe
  # id  Household ID
  # Ns  Number of CFU of E. coli per hand of the volunteer prior to handwashing
  # Nr  Number of CFU of E. coli per hand of the volunteer after handwashing
  # Cw  Concentration of E. coli (CFU/100 mL) in the handwashing water used by the volunteer at the
household
df=read.csv(url("https://zenodo.org/record/1453407/files/ecolihandswater.csv"),sep=";",header=T);head(d
f) # E. coli in handwashing water and hands (Harare, Zimbabwe) dataset; https://doi.org/10.25678/000088

#---Data set: Transfer of bacteriophages from the fingers of volunteers to saliva under wet and dry
conditions
  # pt_wet      Percentage transferred (hand-to-saliva) for wet hands. This refers to the percentage of
phage transferred to saliva five seconds after the inoculum was added to the skin.
  # pt_dry      Percentage transferred (hand-to-saliva) for dry hands. This refers to the percentage of
phage transferred to saliva after the inoculum in the hand was visibly dry.
  # phage         Type of bacteriophage used in the study
d.hm=read.csv(url("https://zenodo.org/record/1454505/files/phagetransferhandtosaliva.csv"),header=T,sep
=",");head(d.hm) # Transfer of bacteriophages between the fingers of volunteers and water or saliva;
https://doi.org/10.25678/000099

#---Data set: Hand and palm surface areas measured (cm2); Table 1 from Joo-Young Lee, Jeong-Wha Choi,
Ho Kim, Determination of Hand Surface Area by Sex and Body Shape using Alginate, Journal of
PHYSIOLOGICAL ANTHROPOLOGY, 2007, Volume 26, Issue 4, Pages 475-483, Released August 15, 2007, Online
ISSN 1880-6805, Print ISSN 1880-6791, https://doi.org/10.2114/jpa2.26.475
d.hsa=data.frame(gender=c(rep('M',34),rep('F',31)),

weight=c('SL','N','O','N','SO','SL','L','O','O','N','N','N','L','O','L','N','N','O','SL','SL','SO','N',
'SO','SL','SL','L','SL','O','SL','N','SO','L','N','O','O','N','N','L','O','SO','SO','SO','O','L','N','N
','N','O','SO','SL','SO','N','L','O','N','SL','SO','SO','SL','O','N','O','L','L','SL'),

hsa_cm2=c(415,428,447,494,432,409,443,448,371,389,434,430,390,436,437,430,448,515,458,386,497,429,476,4
```

```
10,442,443,443,526,495,444,477,469,516,540,355,333,363,297,379,356,435,350,451,364,379,382,379,406,373,
360,433,398,359,457,381,377,429,389,461,401,426,482,403,374,410),

bsa_cm2=c(15416,16875,17844,16986,17630,15800,15628,18261,18770,17153,17733,16784,16016,22106,15885,179
18,18307,22753,17969,16538,20324,18733,19820,17386,17879,17617,18018,20661,19082,19127,20394,18610,2081
3,22675,15411,14034,13642,12825,17337,15540,16173,15978,18455,14598,15334,15294,15867,20683,16233,14980
,16951,15922,14603,18468,16416,15916,17414,16194,17179,19639,17798,22025,15811,15777,17504)
                );head(d.hsa) # hand surface area and body surface area relationship study of Koreans
(Lee et al. 2007)

#---Data set: Dose-response data for select pathogens
d.dr=read.csv(url("http://hydro.sdsu.edu/~verbyla/wordpress/wp-
content/uploads/2018/09/dose_response_data.csv"),header=T,sep=",");head(d.dr)

#---Data set: Body-mass index data for adults
    # source of data: Worldwide trends in body-mass index, underweight, overweight, and obesity from
1975 to 2016: a pooled analysis of 2416 population-based measurement studies in 128.9 million children,
adolescents, and adults. Lancet 2017, 390:2627-2642
d.bmi=read.csv(url("http://www.ncdrisc.org/downloads/bmi/NCD_RisC_Lancet_2017_BMI_age_standardised_coun
try.csv"),colClasses=c("factor","factor","factor","character","numeric","numeric","numeric",rep("NULL",
27)),header=F,skip=1);colnames(d.bmi)=c("country","iso","sex","year","mean_bmi","mean_bmi_lower95","mea
n_bmi_upper95");head(d.bmi)

#---Data set: Mean height at age 18
    # source of data: A century of trends in adult human height. eLife 2016, 5:e13410
d.bsa=read.csv(url("http://www.ncdrisc.org/downloads/height/NCD_RisC_eLife_2016_height_age18_countries.
csv"),header=F,skip=1);colnames(d.bsa)=c("country","iso","sex","year_of_birth","mean_height_cm","lower_
95_interval","upper_95_interval");head(d.bsa)

#---Data transformation: only use most recent available BMI data (from 2014), and only use the height
data of 18-year-olds born in 1996 (to align with the BMI data from 2014)
d.bmi=d.bmi[d.bmi$year==2014,]
d.bsa=d.bsa[d.bsa$year_of_birth==1996,]

#---Data transformation: estimate the weight in kg based on the BMI and the height
d.bsa$weight_kg=d.bmi$mean_bmi*(d.bsa$mean_height_cm/100)^2
d.bsa$weight_upper95=d.bmi$mean_bmi_upper95*(d.bsa$upper_95_interval/100)^2;head(d.bsa)
d.bsa$weight_lower95=d.bmi$mean_bmi_lower95*(d.bsa$lower_95_interval/100)^2;head(d.bsa)

#---Data transformation: estimate the mean body surface area using height and weight data with the
Gehan and George (1970) model
d.bsa$BSAmean_cm2=d.bsa$weight_kg^0.51456*d.bsa$mean_height_cm^0.42246*0.0235*10000 #based on the Gehan
and George model
d.bsa$BSAlower=d.bsa$weight_lower95^0.51456*d.bsa$lower_95_interval^0.42246*0.0235*10000 #based on the
Gehan and George model
d.bsa$BSAupper=d.bsa$weight_upper95^0.51456*d.bsa$upper_95_interval^0.42246*0.0235*10000 #based on the
Gehan and George model
d.bsa$BSAsd=((d.bsa$BSAlower-d.bsa$BSAmean_cm2)/qnorm(0.05)+(d.bsa$BSAupper-
d.bsa$BSAmean_cm2)/qnorm(0.95))/2

#---Data set: Population figures for countries, regions (e.g. Asia) and the world; from
https://datahub.io/core/population
    # Data comes originally from World Bank and has been converted into standard CSV. Original source:
https://data.worldbank.org/indicator/SP.POP.TOTL
d.pop=read.csv(url("https://datahub.io/core/population/r/population.csv"),header=T,sep=",");head(d.pop)

#---Data set: Population, female (% of total); from https://datahub.io/world-bank/sp.pop.totl.fe.zs/
    # Data comes originally from World Bank and has been converted into standard CSV. Original source:
https://data.worldbank.org/indicator/SP.POP.TOTL
d.fm=read.csv(url("https://datahub.io/world-
bank/sp.pop.totl.fe.zs/r/data.csv"),header=T,sep=",");head(d.fm)

#---Data transformation: only use most recent available population data (from 2016) and merge
population data with BSA estimates by ISO country code
d.pop2016=d.pop[d.pop$Year==2016,]
d.fm2016=d.fm[d.fm$Year==2016,]
d.pop=merge(d.pop2016,d.fm2016,by.x=c("Country.Code","Country.Name","Year"),by.y=c("Country.Code","Coun
try.Name","Year"))
d.pop$Women=round(d.pop$Value.x*(d.pop$Value.y/100),0)
d.pop$Men=round(d.pop$Value.x*(1-d.pop$Value.y/100),0)
d.pop=d.pop[,c(1,6,7)]
d.pop=melt(d.pop,id="Country.Code")
colnames(d.pop)[3]="population"
head(d.pop)
head(d.bsa)
d.bsa=merge(d.bsa,d.pop,by.x=c("iso","sex"),by.y=c("Country.Code","variable"));head(d.bsa)
```

```
#---Data transformation: calculate a weighting factor for estimated BSA based on the relative
population
d.bsa$wtFactor=d.bsa$population/sum(d.bsa$population)
BSAdist=d.bsa$BSAmean_cm2*d.bsa$wtFactor

Matti=data.frame(NoV=c(rep(log10(24.3),88-
9),log10(124),log10(53),log10(60),log10(41),log10(13397),log10(154),log10(18884),log10(656),log10(371))
,
                 NoVcen=c(rep(TRUE,88-9),rep(FALSE,9)))

wlow=MinConcWater;whi=MaxConcWater
hlow=MinConcHands;hhi=MaxConcHands
jagslength=50    #this is the resolution of the BCIs

data=list(
# FULL AUTOMIZATION DUMMY VARIABLES
  IIPperDay=IIPperDay,
  handsorwater=handsorwater,
# HANDWASHING AND RINSING PRIORS
  m.sh=washPriors$mean.shape,
  s.sh=washPriors$sd.shape,
  m.ra=washPriors$mean.rate,
  s.ra=washPriors$sd.rate,
  mean.m=rinsePriors$mean.m,
  mean.b=rinsePriors$mean.b,
  sd.m=rinsePriors$sig.m,
  sd.b=rinsePriors$sig.b,
# DATA FOR E. COLI ON HANDS AND IN HANDWASHING WATER IN ZIMBABWE
  talaLD=log10(df$Nr/df$Ns),     #calculated log10 difference from handwashing
  Cw=df$Cw[df$Cw!=0]/100,        #converted the units to cfu/mL
# HSA, BSA, and HAND TO MOUTH TRANSFER
  hsa=d.hsa$hsa_cm2,
  bsa=d.hsa$bsa_cm2,
  BSAmean_global=d.bsa$BSAmean_cm2,
  BSAsd_global=d.bsa$BSAsd,
  BSAwtFactor=d.bsa$wtFactor,
  pw=d.hm$pt_wet/100,
  pd=d.hm$pt_dry/100,
# Ns and Cw assumptions for QMRA model
  jagslength=jagslength,
  logCw=seq(wlow,whi,by=(whi-wlow)/(jagslength-1)),
  logNs=seq(hlow,hhi,by=(hhi-hlow)/(jagslength-1)),
  Matti.mean=mean(ros(Matti$NoV,Matti$NoVcen,forwardT=NULL,reverseT=NULL)),
  Matti.sd=sd(ros(Matti$NoV,Matti$NoVcen,forwardT=NULL,reverseT=NULL)),
  wlow=wlow,
  whi=whi,
  hlow=hlow,
  hhi=hhi,
# DOSE-RESPONSE DATA
  RVdose=d.dr$dose[d.dr$pathogen=="rotavirus"],             #dose received in each group
  RVtotal=d.dr$total[d.dr$pathogen=="rotavirus"],           #total volunteers in each group
  RVinf=d.dr$infected[d.dr$pathogen=="rotavirus"],          #number of volunteers infected in each
group
  NVdose=d.dr$dose[d.dr$pathogen=="norovirus"],
  NVtotal=d.dr$total[d.dr$pathogen=="norovirus"],
  NVinf=d.dr$infected[d.dr$pathogen=="norovirus"],
  ETdose=d.dr$dose[d.dr$pathogen=="ETEC"],
  ETtotal=d.dr$total[d.dr$pathogen=="ETEC"],
  ETsymp=d.dr$symptoms[d.dr$pathogen=="ETEC"],
  EPdose=d.dr$dose[d.dr$pathogen=="EPEC"],
  EPtotal=d.dr$total[d.dr$pathogen=="EPEC"],
  EPsymp=d.dr$symptoms[d.dr$pathogen=="EPEC"],
  CRdose=d.dr$dose[d.dr$pathogen=="Cryptosporidium"],
  CRtotal=d.dr$total[d.dr$pathogen=="Cryptosporidium"],
  CRinf=d.dr$infected[d.dr$pathogen=="Cryptosporidium"],
  SAdose=d.dr$dose[d.dr$pathogen=="Salmonella"],
  SAtotal=d.dr$total[d.dr$pathogen=="Salmonella"],
  SAinf=d.dr$infected[d.dr$pathogen=="Salmonella"],
  VCdose=d.dr$dose[d.dr$pathogen=="Vibrio"],
  VCtotal=d.dr$total[d.dr$pathogen=="Vibrio"],
  VCinf=d.dr$infected[d.dr$pathogen=="Vibrio"],
  SHdose=d.dr$dose[d.dr$pathogen=="Shigella"],
  SHtotal=d.dr$total[d.dr$pathogen=="Shigella"],
  SHinf=d.dr$infected[d.dr$pathogen=="Shigella"],
  GIdose=d.dr$dose[d.dr$pathogen=="Giardia"],
```

```
  GItotal=d.dr$total[d.dr$pathogen=="Giardia"],
  GIinf=d.dr$infected[d.dr$pathogen=="Giardia"]
)

############### - Write the JAGS Model - ###############
qmra.model="
model{

###############################################################################
####################         PRIOR      DISTRIBUTIONS         ###################
###############################################################################

# INFORMATIVE - washing and rinsing
  shape ~ dnorm(m.sh,1/s.sh^2)
  rate ~ dnorm(m.ra,1/s.ra^2)
  lrv ~ dgamma(shape,rate)
  t.m <- 1/sd.m^2
  t.b <- 1/sd.b^2
  m ~ dnorm(mean.m,t.m)
  b ~ dnorm(mean.b,t.b)
  sigNd ~ dgamma(0.0001,0.0001)
  tNd <- 1/sigNd^2

# VAGUE - transfer efficiency
  alphaTEd ~ dgamma(.001,.001)
  betaTEd ~ dgamma(.001,.001)
  alphaTEw ~ dgamma(.001,.001)
  betaTEw ~ dgamma(.001,.001)

# VAGUE - HSA & BSA
  beta1 ~ dunif(0,2)
  beta0 ~ dunif(0,1000)
  sigHSA ~ dgamma(.001,.001)
  tHSA <- 1/(sigHSA)^2

# VAGUE DOSE-RESPONSE MODEL PARAMETERS
  RValpha ~ dgamma(.1,.01)
        RVbeta ~ dgamma(.001,.001)
  NVphi ~ dbeta(1,1)
  NVa ~ dbeta(1,1)
  ETalpha ~ dgamma(.01,.01)
  ETbeta ~ dgamma(.001,.001)
  EPalpha ~ dgamma(.01,.01)
  EPbeta ~ dgamma(.001,.001)
  CRalpha ~ dgamma(.001,.001)
  CRbeta ~ dgamma(.001,.001)
  SAalpha ~ dgamma(.001,.001)
  SAbeta ~ dgamma(.001,.001)
  VCalpha ~ dgamma(.001,.001)
  VCbeta ~ dgamma(.001,.001)
  SHalpha ~ dgamma(.001,.001)
  SHbeta ~ dgamma(.001,.001)
  GIr ~ dunif(0,1)

###############################################################################
####################         LIKELIHOOD       FUNCTIONS       ###################
###############################################################################
# HANDWASHING MODEL
  for(i in 1:length(Cw)){
    zLD[i] <- ifelse(Cw[i]==0,-lrv,m*(log(Cw[i])/log(10))+b - lrv)
    talaLD[i] ~ dnorm(zLD[i],tNd)
  }
  dlogcw <- (lrv-b)/m   #this is the log10 concentration (log10(cells)/mL) in water when LD=0

# TRANSFER EFFICIENCY
  for(j in 1:length(pw)){pw[j] ~ dbeta(alphaTEw,betaTEw)}
  for(i in 1:length(pd)){pd[i] ~ dbeta(alphaTEd,betaTEd)}

# HSA from BSA
  for(i in 1:length(bsa)){
    zHSA[i] <- beta1*bsa[i]+beta0
    hsa[i] ~ dnorm(zHSA[i],tHSA)
  }

# DOSE-RESPONSE MODELS
  for(i in 1:length(RVdose)){
```

```
    RVpinf[i] <- 1-exp(-RVr[i]*RVdose[i])             #Exact Beta Poisson model for Rotavirus
    RVr[i] ~ dbeta(RValpha,RVbeta)
    RVinf[i] ~ dbin(RVpinf[i],RVtotal[i])
  }
  for(i in 1:length(NVdose)){
    NVpinf[i] <- NVphi*(1-exp(-NVdose[i]/NVmu[i]))      #Fractional Poisson model for Norovirus
    NVmu[i] <- -NVa/((1-NVa)*log(1-NVa))
    NVinf[i] ~ dbin(NVpinf[i],NVtotal[i])
  }
  for(i in 1:length(ETdose)){
    ETpill[i] <- 1-exp(-ETr[i]*ETdose[i])             #Exact Beta Poisson model for ETEC
    ETr[i] ~ dbeta(ETalpha,ETbeta)
    ETsymp[i] ~ dbin(ETpill[i],ETtotal[i])
  }
  for(i in 1:length(EPdose)){
    EPpill[i] <- 1-exp(-EPr[i]*EPdose[i])             #Exact Beta Poisson model for EPEC
    EPr[i] ~ dbeta(EPalpha,EPbeta)
    EPsymp[i] ~ dbin(EPpill[i],EPtotal[i])
  }
  for(i in 1:length(SHdose)){
    SHpinf[i] <- 1-exp(-SHr[i]*SHdose[i])             #Exact Beta Poisson model for Shigella
    SHr[i] ~ dbeta(SHalpha,SHbeta)
    SHinf[i] ~ dbin(SHpinf[i],SHtotal[i])
  }
  for(i in 1:length(SAdose)){
    SApinf[i] <- 1-exp(-SAr[i]*SAdose[i])             #Exact Beta Poisson model for Salmonella
    SAr[i] ~ dbeta(SAalpha,SAbeta)
    SAinf[i] ~ dbin(SApinf[i],SAtotal[i])
  }
  for(i in 1:length(VCdose)){
    VCpinf[i] <- 1-exp(-VCr[i]*VCdose[i])             #Exact Beta Poisson model for Cholera
    VCr[i] ~ dbeta(VCalpha,VCbeta)
    VCinf[i] ~ dbin(VCpinf[i],VCtotal[i])
  }
  for(i in 1:length(CRdose)){
    CRpinf[i] <- 1-exp(-CRr[i]*CRdose[i])             #Exact Beta Poisson model for Crypto
    CRr[i] ~ dbeta(CRalpha,CRbeta)
    CRinf[i] ~ dbin(CRpinf[i],CRtotal[i])
  }
  for(i in 1:length(GIdose)){
    GIpinf[i] <- 1-exp(-GIr*GIdose[i])             #Exponential model for Giardia
    GIinf[i] ~ dbin(GIpinf[i],GItotal[i])
  }

##############################################################################
####################          DERIVED      QUANTITIES         ###################
##############################################################################
# HAND-TO-MOUTH TRANSFER
  TEw ~ dbeta(alphaTEw,betaTEw) #percent of pathogens transferred from wet hands
  TEd ~ dbeta(alphaTEd,betaTEd) #percent of pathogens transferred from dried hands
  moist ~ dunif(0,1)
  TE <- moist*TEw+(1-moist)*TEd

# SURFACE AREA CONTACT
  tauBSA <- 1/BSAsd_global^2
  for(i in 1:length(BSAmean_global)){BSAnw[i] ~ dnorm(BSAmean_global[i],tauBSA[i])}
  for(j in 1:length(BSAmean_global)){BSAwtd[j] <- BSAnw[j]*BSAwtFactor[j]}
  BSAwtdSUM <- sum(BSAwtd)
  HSAwtd <- beta1*BSAwtdSUM+beta0
  fc ~ dbeta(5,40)              # the fraction of hand area that comes in contact with the mouth (from
Auyeung 2007, assumed same for children as for adults)
  Sx <- fc*2*HSAwtd             # Sx is the surface area of contact between hands and mouth (Julian et
al. 2009)

##########################################################################
############# ASSUMPTIONS ABOUT HAND AND WATER CONCENTRATIONS #############
##########################################################################
##-- logNs = log10 pathogen concentration per cm2 of unwashed hands.   --##
##-- logNr = log10 pathogen concentration per cm2 of washed hands.     --##
##########################################################################

Xw ~ dunif(wlow,whi)                          # uniform distribution of water concentration values; this
is in logCFU/mL, so if I put -10 to 6 here, that means 10^-8 to 10^8 CFU/100 mL
logNs.MCMC ~ dunif(hlow,hhi)              # uniform distribution of hand concentrations, for
determination of the maximum number of allowable pathogens on hands for Table 3
```

```
logNs.Matti.dist ~ dnorm(Matti.mean,1/Matti.sd^2)  #this is based on cenros; LOD was 24.3 copies/2
hands
logNs.Matti <- log((10^logNs.Matti.dist)/HSAwtd*2)/log(10)

##-- to get MCMC points under scenario specified (via dummy variable handsorwater)
    ##-- handsorwater=1 --> water has some pathogens, hands have some pathogens
    ##-- handsorwater=2 --> water has no pathogens, hands have some pathogens
    ##-- handsorwater=3 --> water has some pathogens, hands have no pathogens
logNr.MCMC.G <- ifelse(handsorwater==1, log(10^logNs.MCMC + 10^(m*Xw+b))/log(10) - lrv,
ifelse(handsorwater==2, logNs.MCMC - lrv, m*Xw+b))
logNr.Matti <- ifelse(handsorwater==1, log(10^logNs.Matti + 10^(m*Xw+b))/log(10) - lrv,
ifelse(handsorwater==2, logNs.Matti - lrv, log(10^logNs.Matti + 10^(m*Xw+b))/log(10) - lrv))

##############################################################################
##-- Two scenarios have to be run here as well, to test the sensitivity of --##
##-- the model to the number of independent infection probabilities over   --##
##-- the course of a year. Approach A assumes that each day represents a   --##
##-- single probability of getting infected (i.e. periods = 365). Approach --##
##-- B assumes that a person has more than one opportunity of acquiring an --##
##-- an infection in a single day. The maximum number of opportunities of  --##
##-- acquiring an infection in a single day (from handwashing) is assumed  --##
##-- to be equal to the number of times that a person washes hands on that --##
##-- particular day (i.e., periods = 365 * timesPerDay). One hypothesis is --##
##-- that this might correspond to the number of small intestine residence --##
##-- times per day. For example, it takes ~4.8 h for ingested material to  --##
##-- reach the small intestine (which is the site of infection). If people --##
##-- spend on average 14 - 15 h awake per day, this would correspond to    --##
##-- approx. 3 small intestine residence times (15 / 4.8 = ~3). However,   --##
##-- there is not enough literature on this topic to be certain which is   --##
##-- best approach, so we run multiple scenarios to test the sensitivity   --##
##-- of the model to these assumptions.                                    --##
##                                                                          ##
##-- APPROACH A: 365 opportunities per year of getting infected           --##
##-- APPROACH B: 365*timesPerDay opportunities per year of getting infected--##
##                                                                          ##
##############################################################################

lambda ~ dunif(3,12)        # the average number of times per day that Zimbabwean women wash their
hands is between 8 and 12 (Pickering et al. 2011)
timesPerDay ~ dpois(lambda)   # Poisson dist. used to discretize/randomize the number of handwashing
events per day
periods <- ifelse(IIPperDay==1,365,365*timesPerDay)       # IF periods = 365, THEN dose =
dose*timesPerDay. So kappa=timesPerDay.   IF periods = 365*timesPerDay, THEN dose=dose. So kappa=1
kappa <- ifelse(periods==365,timesPerDay,1)   ##--kappa is the number of hand-to-mouth transfer events
that contributes to a single independent dose

##--use the posterior distributions for beta distribution parameters (alpha and beta)
##--of each pathogen based on the Beta Poisson Exact model; here are those distributions:
rVC ~ dbeta(VCalpha,VCbeta)
rSH ~ dbeta(SHalpha,SHbeta)
rSA ~ dbeta(SAalpha,SAbeta)
rET ~ dbeta(ETalpha,ETbeta)
rEP ~ dbeta(EPalpha,EPbeta)
rCR ~ dbeta(CRalpha,CRbeta)
rRV ~ dbeta(RValpha,RVbeta)

############# CODA ############# CODA ############# CODA ############# CODA #############
########## This code is to get the individual MCMC points using coda.samples ############
############# CODA ############# CODA ############# CODA ############# CODA #############

dose.MCMC.G <- Sx*TE*(10^logNr.MCMC.G)*kappa   # average dose if hands are washed
dose.Matti <- Sx*TE*(10^logNr.Matti)*kappa
pinfVC.MCMC.G <- 1-exp(-rVC*dose.MCMC.G)
pinfSH.MCMC.G <- 1-exp(-rSH*dose.MCMC.G)
pinfSA.MCMC.G <- 1-exp(-rSA*dose.MCMC.G)
pinfET.MCMC.G <- 1-exp(-rET*dose.MCMC.G)
pinfEP.MCMC.G <- 1-exp(-rEP*dose.MCMC.G)
pinfCR.MCMC.G <- 1-exp(-rCR*dose.MCMC.G)
pinfGI.MCMC.G <- 1-exp(-GIr*dose.MCMC.G)
pinfNV.MCMC.G <- NVphi*(1-exp(-dose.MCMC.G/NVmu[1]))
pinfRV.MCMC.G <- 1-exp(-rRV*dose.MCMC.G)

pinfNV.Matti <- NVphi*(1-exp(-dose.Matti/NVmu[1]))

dose.MCMC.G.n <- Sx*TE*(10^logNs.MCMC)*kappa   # average dose if hands are not washed
dose.Matti.n <- Sx*TE*(10^logNs.Matti)*kappa
```

```
pinfVC.MCMC.G.n <- 1-exp(-rVC*dose.MCMC.G.n)
pinfSH.MCMC.G.n <- 1-exp(-rSH*dose.MCMC.G.n)
pinfSA.MCMC.G.n <- 1-exp(-rSA*dose.MCMC.G.n)
pinfET.MCMC.G.n <- 1-exp(-rET*dose.MCMC.G.n)
pinfEP.MCMC.G.n <- 1-exp(-rEP*dose.MCMC.G.n)
pinfCR.MCMC.G.n <- 1-exp(-rCR*dose.MCMC.G.n)
pinfGI.MCMC.G.n <- 1-exp(-GIr*dose.MCMC.G.n)
pinfNV.MCMC.G.n <- NVphi*(1-exp(-dose.MCMC.G.n/NVmu[1]))
pinfRV.MCMC.G.n <- 1-exp(-rRV*dose.MCMC.G.n)

pinfNV.Matti.n <- NVphi*(1-exp(-dose.Matti.n/NVmu[1]))

pinfVCanG <- 1-(1-pinfVC.MCMC.G)^periods
pinfVCanG.n <- 1-(1-pinfVC.MCMC.G.n)^periods
pinfSHanG <- 1-(1-pinfSH.MCMC.G)^periods
pinfSHanG.n <- 1-(1-pinfSH.MCMC.G.n)^periods
pinfSAanG <- 1-(1-pinfSA.MCMC.G)^periods
pinfSAanG.n <- 1-(1-pinfSA.MCMC.G.n)^periods
pinfETanG <- 1-(1-pinfET.MCMC.G)^periods
pinfETanG.n <- 1-(1-pinfET.MCMC.G.n)^periods
pinfEPanG <- 1-(1-pinfEP.MCMC.G)^periods
pinfEPanG.n <- 1-(1-pinfEP.MCMC.G.n)^periods
pinfCRanG <- 1-(1-pinfCR.MCMC.G)^periods
pinfCRanG.n <- 1-(1-pinfCR.MCMC.G.n)^periods
pinfGIanG <- 1-(1-pinfGI.MCMC.G)^periods
pinfGIanG.n <- 1-(1-pinfGI.MCMC.G.n)^periods
pinfNVanG <- 1-(1-pinfNV.MCMC.G)^periods
pinfNVanG.n <- 1-(1-pinfNV.MCMC.G.n)^periods
pinfRVanG <- 1-(1-pinfRV.MCMC.G)^periods
pinfRVanG.n <- 1-(1-pinfRV.MCMC.G.n)^periods

pinfNVanM <- 1-(1-pinfNV.Matti)^periods
pinfNVanM.n <- 1-(1-pinfNV.Matti.n)^periods

############# JAGS ############# JAGS ############# JAGS ############# JAGS #############
###### This code is to get the BCIs using jags.samples, not needed for coda.samples #####
############# JAGS ############# JAGS ############# JAGS ############# JAGS #############

# to get BCIs under scenario specified (via dummy variable handsorwater)
    ##-- handsorwater=1 --> water has some pathogens, hands have some pathogens
    ##-- handsorwater=2 --> water has no pathogens, hands have some pathogens
    ##-- handsorwater=3 --> water has some pathogens, hands have no pathogens
  for(k in 1:jagslength){
    logNr[k] <- ifelse(handsorwater==1, log(10^logNs[k] + 10^(m*logCw[k]+b))/log(10) - lrv,
ifelse(handsorwater==2, logNs[k] - lrv, m*logCw[k]+b))
    logNr.M[k] <- ifelse(handsorwater==1, log(10^logNs.Matti + 10^(m*logCw[k]+b))/log(10) - lrv,
ifelse(handsorwater==2, logNs.Matti - lrv, log(10^logNs.Matti + 10^(m*logCw[k]+b))/log(10) - lrv))
    dose.G[k] <- (Sx*TE*10^logNr[k])*kappa
    dose.M[k] <- (Sx*TE*10^logNr.M[k])*kappa
    pinfVC.G[k] <- 1-exp(-rVC*dose.G[k])
    pinfSH.G[k] <- 1-exp(-rSH*dose.G[k])
    pinfSA.G[k] <- 1-exp(-rSA*dose.G[k])
    pinfET.G[k] <- 1-exp(-rET*dose.G[k])
    pinfEP.G[k] <- 1-exp(-rEP*dose.G[k])
    pinfCR.G[k] <- 1-exp(-rCR*dose.G[k])
    pinfGI.G[k] <- 1-exp(-GIr*dose.G[k])
    pinfNV.G[k] <- NVphi*(1-exp(-dose.G[k]/NVmu[1]))
    pinfNV.M[k] <- NVphi*(1-exp(-dose.M[k]/NVmu[1]))
    pinfRV.G[k] <- 1-exp(-rRV*dose.G[k])

    pinfVCanG.bci[k] <- 1-(1-pinfVC.G[k])^periods
    pinfSHanG.bci[k] <- 1-(1-pinfSH.G[k])^periods
    pinfSAanG.bci[k] <- 1-(1-pinfSA.G[k])^periods
    pinfETanG.bci[k] <- 1-(1-pinfET.G[k])^periods
    pinfEPanG.bci[k] <- 1-(1-pinfEP.G[k])^periods
    pinfCRanG.bci[k] <- 1-(1-pinfCR.G[k])^periods
    pinfGIanG.bci[k] <- 1-(1-pinfGI.G[k])^periods
    pinfNVanG.bci[k] <- 1-(1-pinfNV.G[k])^periods
    pinfNVanM.bci[k] <- 1-(1-pinfNV.M[k])^periods
    pinfRVanG.bci[k] <- 1-(1-pinfRV.G[k])^periods
  }
}
"

inits=list(
```

```
list(lrv=1,m=1,b=0,sigNd=1,alphaTEd=1,alphaTEw=1,betaTEd=1,betaTEw=1,GIr=0.5,SHalpha=0.1,SHbeta=10,VCal
pha=0.1,VCbeta=10,SAalpha=0.1,SAbeta=10,CRalpha=0.5,CRbeta=50,ETalpha=0.08,ETbeta=2500,EPalpha=0.1,EPbe
ta=2500,NVa=0.9,NVphi=0.7,RValpha=0.3,RVbeta=5),
  list(lrv=2,m=0.5,b=-
1,sigNd=2,alphaTEd=2,alphaTEw=2,betaTEd=2,betaTEw=2,GIr=0.1,SHalpha=0.1,SHbeta=10,VCalpha=0.1,VCbeta=10
,SAalpha=0.1,SAbeta=10,CRalpha=0.1,CRbeta=10,ETalpha=0.1,ETbeta=5000,EPalpha=0.1,EPbeta=1500,NVa=0.99,N
Vphi=0.5,RValpha=0.5,RVbeta=10),

list(lrv=3,m=1.5,b=1,sigNd=3,alphaTEd=3,alphaTEw=3,betaTEd=3,betaTEw=3,GIr=0.9,SHalpha=0.1,SHbeta=10,VC
alpha=0.1,VCbeta=10,SAalpha=0.1,SAbeta=10,CRalpha=0.2,CRbeta=30,ETalpha=0.07,ETbeta=1000,EPalpha=0.1,EP
beta=1000,NVa=0.999,NVphi=0.6,RValpha=0.4,RVbeta=7)
)

jm.hw=jags.model(textConnection(qmra.model),data=data,n.adapt=n.adapt,inits=inits,n.chains=length(inits
))
update(jm.hw,n.iter=n.update)
zc.hw=coda.samples(jm.hw,variable.names=c("Xw","lrv","dlogcw","logNs.MCMC","logCw","logNs.Matti",
                                          "pinfVCanG","pinfSHanG","pinfSAanG","pinfETanG","pinfEPanG",

"pinfGIanG","pinfCRanG","pinfNVanG","pinfRVanG","pinfNVanM","pinfNVanM.n",

"pinfVCanG.n","pinfSHanG.n","pinfEPanG.n","pinfETanG.n","pinfSAanG.n",

"pinfGIanG.n","pinfCRanG.n","pinfNVanG.n","pinfRVanG.n","HSAwtd","BSAwtdSUM"),n.iter=n.iter)
zj.hw=jags.samples(jm.hw,variable.names=c("pinfVCanG.bci","pinfSHanG.bci","pinfSAanG.bci","pinfETanG.bc
i",

"pinfEPanG.bci","pinfGIanG.bci","pinfCRanG.bci","pinfNVanG.bci",

"pinfRVanG.bci","pinfNVanM.bci","HSAwtd"),n.iter=n.iter,n.thin=1)

################################################################################################
################################### PLOT FOR FIGURE 2 ##########################################
################################################################################################

par(mfrow=c(1,1))
logNs.MCMC=getCoda(zc.hw,"logNs.MCMC")
Xw=getCoda(zc.hw,"Xw")+2   ## this is the assumed concentration of pathogens in the water (uniform
distribution assumed to generate Fig. 3 plot); added 2 to get it to per 100 mL
logCw=data$logCw+2   # these are logCw=seq(low,hi,by=0.5) (used for the zj.hw jags.samples to get the
CIs of the plot for Fig. 3, and logNs=seq(-10,10,by=0.5), which is used when determining the max
concentration on hands for Table 2; added 2 to get it to per 100 mL
logNs=data$logNs
lrv=getCoda(zc.hw,"lrv") # this is the posterior distribution of the LRV provided by handwashing
summary(lrv)
LDzeroCw=getCoda(zc.hw,"dlogcw")  ## this is the posterior distribution of Xmax from Fig. 2
Xmax=(10^LDzeroCw)*100
plot(density(Xmax),log='x')
quantile(Xmax,c(0.001,0.025,0.05,0.25,0.5,0.75,0.95,0.975,0.999))
setwd("/Users/matthewverbyla/Dropbox/Non-Potable Water for Hygiene/")
if(IIPperDay==2) {
  write.csv(Xmax,file="Xmax20181027.csv")
} else {
  write.csv(Xmax,file="Xmax20181027_365.csv")
}
Xmax_o=read.csv("Xmax20181027.csv")
log10(quantile(Xmax_o$x,c(0.001,0.025,0.05,0.25,0.5,0.75,0.95,0.975,0.999))/quantile(Xmax,c(0.001,0.025
,0.05,0.25,0.5,0.75,0.95,0.975,0.999)))

require("fitdistrplus")
require("devtools")
#install_github("kassambara/easyGgplot2")
require("easyGgplot2")
require("RColorBrewer")
#allows formating of the x-axis labels to be scientific notation
fancy_scientific <- function(l) {
  # turn in to character string in scientific notation
  l <- format(l, scientific = TRUE)
  l <- gsub("e\\00","0",l)
  # quote the part before the exponent to keep all the digits
  l <- gsub("^(.*)e", "'\\1'e", l)
  # remove + after exponent, if exists. E.g.: (3x10^+2 -> 3x10^2)
  l <- gsub("e\\+","e",l)
  # turn the 'e+' into plotmath format
  l <- gsub("e", "%*%10^", l)
```

```
  # convert 1x10^ or 1.000x10^ -> 10^
  l <- gsub("\\'1[\\.0]*\\'\\%\\*\\%", "", l)
  # return this as an expression
  parse(text=l)
}

xmax_val <- log10(Xmax)  #XMAX Values inferred from the distribution
df.table_all = read.csv("data/DATA_Sara_WaterQuality_Nepal.csv",header=T)

#Amend XMAX simulation onto all data
df.table_xmax <- cbind.data.frame(10^xmax_val, xmax_val, "Stored", "Handwashing", "Xmax")
colnames(df.table_xmax) <- colnames(df.table_all)
df.table_all_new <- rbind.data.frame(df.table_all, df.table_xmax)
ggg <- "Site"
names(df.table_all_new)[5]<- ggg

#set color palette
all.cols <- brewer.pal(8, "Dark2")
my.cols <- c(all.cols[1], all.cols[2], all.cols[3], all.cols[5], all.cols[6], "#FF0000")

#create data frame without Xmax values
df.table_all_new_noxmax <- df.table_all_new[which(df.table_all_new$Site != "Xmax"),]

plot.Density <- ggplot2.density(data=df.table_all_new, xName = "value", groupName = ggg,
fillGroupDensity = TRUE, alpha = 0.4)+
  geom_segment(aes(x = 1, y = 0, xend = 1, yend = 1.85), linetype = 1, lwd = 1)+ #WHO guidelines
  annotate("text", x = 3.16, y = 2.05, label = "WHO Drinking")+
  annotate("text", x = 3.16, y = 1.95, label = "Water Guideline")+
  geom_segment(aes(x = 1000, y = 0, xend = 1000, yend = 1.85), linetype = 1, lwd = 1)+ #Recommended
  annotate("text", x = 4890, y = 2.05, label = "Probability~Handwashing~Reduces~italic('E. coli')",
parse = TRUE)+
  annotate("text", x = 900, y = 1.95, label = ">99.9%")+
  geom_segment(aes(x = quantile(Xmax,0.05), y = 0, xend = quantile(Xmax,0.05), yend = 1.85), linetype =
2, lwd = 1, col = "grey")+
  annotate("text", x = quantile(Xmax,0.05), y = 1.95, label = "95%")+
  geom_segment(aes(x = quantile(Xmax,0.5), y = 0, xend = quantile(Xmax,0.5), yend = 1.85), linetype =
1, lwd = 1, col = "grey")+
  annotate("text", x = quantile(Xmax,0.5), y = 1.95, label = "50%")+
  geom_segment(aes(x = quantile(Xmax,0.95), y = 0, xend = quantile(Xmax,0.95), yend = 1.85), linetype =
2, lwd = 1, col = "grey")+
  annotate("text", x = quantile(Xmax,0.95), y = 1.95, label = "5%")+
  annotate("text", x = 775, y = 1, label = "<1000 CFU / 100 ml", angle = 90)+
  #geom_segment(aes(x = 0.5, y = 0, xend = 0.5, yend = 1.85), linetype = 2, lwd = 1, col = "white")+
  annotate("text", x = 1.3, y = 1.3, label = "<1 CFU / 100 ml", angle = 90)+
  annotate("text", x = 5000, y = 0.5, label = "italic(X[MAX])", parse = TRUE)+
  xlab(expression(paste(italic("E. coli"),"(CFU per 100ml)")))+
  ylab("Density")+
  scale_x_log10(limits = c(0.1, 100000), breaks = c(0.1, 1, 10, 100, 1000, 10000, 100000), labels =
fancy_scientific)+
  #scale_fill_brewer(breaks = c("India - Source", "India - Stored", "Indonesia", "Kenya", "Nepal",
"Zimbabwe"), direction = -1, palette = "RdYlBu")+
  scale_fill_manual(breaks = c("India", "Indonesia", "Kenya", "Nepal", "Zimbabwe"), values = my.cols )+
  theme_bw()+
  theme(legend.position = "bottom")
plot.Density

#calculate probability over recommendation for each data set
recommend = 3 #1000 CFU/100ml

#upper limits are acting all weird, so empirical derivation of when an error is shown.
pOver_tanz = integrate(approxfun(dens_tanz), lower = recommend, upper = 5.5)
pOver_nep_source = integrate(approxfun(dens_nep_source), lower = recommend, upper = 3.5)
pOver_nep_stored = integrate(approxfun(dens_nep_stored), lower = recommend, upper = 3.5)
pOver_zim_handwash = integrate(approxfun(dens_zim_handwash), lower = recommend, upper = 4.8)
pOver_ind_source = integrate(approxfun(dens_ind_source), lower = recommend, upper = 5.65)

pOver_ken_ec = integrate(approxfun(dens_tanz), lower = recommend, upper = 4) #this is 0
pOver_ken_tc = integrate(approxfun(dens_ken_source_tc), lower = recommend, upper = 4.3)

#percent risk below recommended
pUnder_xmax = integrate(approxfun(density(xmax_val)), lower = 2.65,3)

################################################################################################
################################### PLOT FOR FIGURE 3 ##########################################
################################################################################################
```

```
## these are the probabilities of infection (individual points for Fig. 3 type plot) for washing hands
vs. not washing hands
pinfVC.MCMC=getCoda(zc.hw,"pinfVCanG")
pinfVC.MCMC.n=getCoda(zc.hw,"pinfVCanG.n")
pinfSH.MCMC=getCoda(zc.hw,"pinfSHanG")
pinfSH.MCMC.n=getCoda(zc.hw,"pinfSHanG.n")
pinfSA.MCMC=getCoda(zc.hw,"pinfSAanG")
pinfSA.MCMC.n=getCoda(zc.hw,"pinfSAanG.n")
pinfET.MCMC=getCoda(zc.hw,"pinfETanG")
pinfET.MCMC.n=getCoda(zc.hw,"pinfETanG.n")
pinfEP.MCMC=getCoda(zc.hw,"pinfEPanG")
pinfEP.MCMC.n=getCoda(zc.hw,"pinfEPanG.n")
pinfGI.MCMC=getCoda(zc.hw,"pinfGIanG")
pinfGI.MCMC.n=getCoda(zc.hw,"pinfGIanG.n")
pinfCR.MCMC=getCoda(zc.hw,"pinfCRanG")
pinfCR.MCMC.n=getCoda(zc.hw,"pinfCRanG.n")
pinfNV.MCMC=getCoda(zc.hw,"pinfNVanG")
pinfNV.MCMC.n=getCoda(zc.hw,"pinfNVanG.n")
pinfNV.Matti=getCoda(zc.hw,"pinfNVanM")
pinfNV.Matti.N=getCoda(zc.hw,"pinfNVanM.n")
pinfRV.MCMC=getCoda(zc.hw,"pinfRVanG")
pinfRV.MCMC.n=getCoda(zc.hw,"pinfRVanG.n")

pVCaGold=getCoda(zc.hw,'pinfVCanG')
pSHaGold=getCoda(zc.hw,'pinfSHanG')
pSAaGold=getCoda(zc.hw,'pinfSAanG')
pETaGold=getCoda(zc.hw,'pinfETanG')
pEPaGold=getCoda(zc.hw,'pinfEPanG')
pGIaGold=getCoda(zc.hw,'pinfGIanG')
pCRaGold=getCoda(zc.hw,'pinfCRanG')
pNVaGold=getCoda(zc.hw,'pinfNVanG')
pNVaGoldM=getCoda(zc.hw,'pinfNVanM')
pRVaGold=getCoda(zc.hw,'pinfRVanG')

if (handsorwater == 3 || handsorwater == 1) {   # plotting Fig. 2 only makes sense when handsorwater =
3
  par(mfrow=c(3,3),mai=c(0.5,0.7,0.3,0.2),family="serif")
  options(scipen=1, "digits"=3)
  xlab1=expression('log'[10]*'(CFU)/100 mL')
  xlab2a=expression('log'[10]*'(cysts)/100 mL')
  xlab2b=expression('log'[10]*'(oocysts)/100 mL')
  xlab3=expression('log'[10]*'(copies)/100 mL')
  xlab4=expression('log'[10]*'(FFU)/100 mL')
  ylim=c(1e-8,1)
  CL=c(0.025,0.5,0.975)
  lwd1=1
  lwd2=2
  plot(Xw,pVCaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("V. cholerae")),xlab=xlab1,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)
  lines(logCw,summary(zj.hw$pinfVCanG.bci,quantile,CL)$stat['2.5%',],col='black',lwd=lwd1,lty=2)
  lines(logCw,summary(zj.hw$pinfVCanG.bci,quantile,CL)$stat['50%',],col='black',lwd=lwd2)
  lines(logCw,summary(zj.hw$pinfVCanG.bci,quantile,CL)$stat['97.5%',],col='black',lwd=lwd1,lty=2)
  plot(Xw,pSHaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("Shigella")),xlab=xlab1,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)
  lines(logCw,summary(zj.hw$pinfSHanG.bci,quantile,CL)$stat['2.5%',],col='black',lwd=lwd1,lty=2)
  lines(logCw,summary(zj.hw$pinfSHanG.bci,quantile,CL)$stat['50%',],col='black',lwd=lwd2)
  lines(logCw,summary(zj.hw$pinfSHanG.bci,quantile,CL)$stat['97.5%',],col='black',lwd=lwd1,lty=2)
  plot(Xw,pSAaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("Salmonella")),xlab=xlab1,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)
  lines(logCw,summary(zj.hw$pinfSAanG.bci,quantile,CL)$stat['2.5%',],col='black',lwd=lwd1,lty=2)
  lines(logCw,summary(zj.hw$pinfSAanG.bci,quantile,CL)$stat['50%',],col='black',lwd=lwd2)
  lines(logCw,summary(zj.hw$pinfSAanG.bci,quantile,CL)$stat['97.5%',],col='black',lwd=lwd1,lty=2)
  plot(Xw,pETaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("ETEC")),xlab=xlab1,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)
  lines(logCw,summary(zj.hw$pinfETanG.bci,quantile,CL)$stat['2.5%',],col='black',lwd=lwd1,lty=2)
  lines(logCw,summary(zj.hw$pinfETanG.bci,quantile,CL)$stat['50%',],col='black',lwd=lwd2)
  lines(logCw,summary(zj.hw$pinfETanG.bci,quantile,CL)$stat['97.5%',],col='black',lwd=lwd1,lty=2)
  plot(Xw,pEPaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("EPEC")),xlab=xlab1,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)
  lines(logCw,summary(zj.hw$pinfEPanG.bci,quantile,CL)$stat['2.5%',],col='black',lwd=lwd1,lty=2)
  lines(logCw,summary(zj.hw$pinfEPanG.bci,quantile,CL)$stat['50%',],col='black',lwd=lwd2)
  lines(logCw,summary(zj.hw$pinfEPanG.bci,quantile,CL)$stat['97.5%',],col='black',lwd=lwd1,lty=2)
  plot(Xw,pGIaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("Giardia")),xlab=xlab2a,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)
  lines(logCw,summary(zj.hw$pinfGIanG.bci,quantile,CL)$stat['2.5%',],col='black',lwd=lwd1,lty=2)
  lines(logCw,summary(zj.hw$pinfGIanG.bci,quantile,CL)$stat['50%',],col='black',lwd=lwd2)
```

```
  lines(logCw,summary(zj.hw$pinfGIanG.bci,quantile,CL)$stat['97.5%',],col='black',lwd=lwd1,lty=2)
  plot(Xw,pCRaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("Cryptosporidium")),xlab=xlab2b,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)
  lines(logCw,summary(zj.hw$pinfCRanG.bci,quantile,CL)$stat['2.5%',],col='black',lwd=lwd1,lty=2)
  lines(logCw,summary(zj.hw$pinfCRanG.bci,quantile,CL)$stat['50%',],col='black',lwd=lwd2)
  lines(logCw,summary(zj.hw$pinfCRanG.bci,quantile,CL)$stat['97.5%',],col='black',lwd=lwd1,lty=2)
  plot(Xw,pNVaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("Norovirus")),xlab=xlab3,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)

polygon(c(logCw,rev(logCw)),c(summary(zj.hw$pinfNVanM.bci,quantile,CL)$stat['2.5%',],rev(summary(zj.hw$
pinfNVanM.bci,quantile,CL)$stat['97.5%',])),col="cornflowerblue",border=NA)
  points(Xw,pNVaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("Norovirus")),xlab=xlab3,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)
  lines(logCw,summary(zj.hw$pinfNVanG.bci,quantile,CL)$stat['2.5%',],col='black',lwd=lwd1,lty=2)
  lines(logCw,summary(zj.hw$pinfNVanG.bci,quantile,CL)$stat['50%',],col='black',lwd=lwd2)
  lines(logCw,summary(zj.hw$pinfNVanG.bci,quantile,CL)$stat['97.5%',],col='black',lwd=lwd1,lty=2)
  lines(logCw,summary(zj.hw$pinfNVanM.bci,quantile,CL)$stat['97.5%',],col='blue',lwd=lwd1,lty=2)
#Mattioli data assumption
  lines(logCw,summary(zj.hw$pinfNVanM.bci,quantile,CL)$stat['50%',],col='blue',lwd=lwd2)  #Mattioli
data assumption
  plot(Xw,pRVaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("Rotavirus")),xlab=xlab4,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)
  lines(logCw,summary(zj.hw$pinfRVanG.bci,quantile,CL)$stat['2.5%',],col='black',lwd=lwd1,lty=2)
  lines(logCw,summary(zj.hw$pinfRVanG.bci,quantile,CL)$stat['50%',],col='black',lwd=lwd2)
  lines(logCw,summary(zj.hw$pinfRVanG.bci,quantile,CL)$stat['97.5%',],col='black',lwd=lwd1,lty=2)
}
#par(mfrow=c(1,1))
#plot(Xw,pNVaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("Norovirus")),xlab=xlab3,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)
#polygon(c(logCw,rev(logCw)),c(summary(zj.hw$pinfNVanM.bci,quantile,CL)$stat['2.5%',],rev(summary(zj.hw
$pinfNVanM.bci,quantile,CL)$stat['97.5%',])),col="cornflowerblue",border=NA)
#points(Xw,pNVaGold,log='y',pch=".",col="grey",cex.lab=1.5,cex.axis=1.5,ylab=expression("P"[inf]*" for
"*italic("Norovirus")),xlab=xlab3,ylim=ylim)#;abline(h=1e-4,col='red',lty=2,lwd=4)
#lines(logCw,summary(zj.hw$pinfNVanM.bci,quantile,CL)$stat['2.5%',],col='blue',lwd=lwd1,lty=2)
#Mattioli data assumption
#lines(logCw,summary(zj.hw$pinfNVanM.bci,quantile,CL)$stat['50%',],col='blue',lwd=lwd2)  #Mattioli data
assumption
#lines(logCw,summary(zj.hw$pinfNVanM.bci,quantile,CL)$stat['97.5%',],col='blue',lwd=lwd1,lty=2)
#Mattioli data assumption

##############################################################################################
######################################## TABLE 1 ############################################
##############################################################################################

if (handsorwater == 3) {  # generating Table 1 only makes sense when handsorwater=3 --> water has some
pathogens, hands have no pathogens
  riskTol=0.001
  options(scipen=-1)
  n3=t(data.frame(

VC=10^approx(x=summary(zj.hw$pinfVCanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

SH=10^approx(x=summary(zj.hw$pinfSHanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

SA=10^approx(x=summary(zj.hw$pinfSAanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

ET=10^approx(x=summary(zj.hw$pinfETanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

EP=10^approx(x=summary(zj.hw$pinfEPanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

GI=10^approx(x=summary(zj.hw$pinfGIanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

CR=10^approx(x=summary(zj.hw$pinfCRanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

NV=10^approx(x=summary(zj.hw$pinfNVanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

RV=10^approx(x=summary(zj.hw$pinfRVanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y
  ))
  riskTol=0.0001
  options(scipen=-1)
  n4=t(data.frame(

VC=10^approx(x=summary(zj.hw$pinfVCanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

SH=10^approx(x=summary(zj.hw$pinfSHanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,
```

```
SA=10^approx(x=summary(zj.hw$pinfSAanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

ET=10^approx(x=summary(zj.hw$pinfETanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

EP=10^approx(x=summary(zj.hw$pinfEPanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

GI=10^approx(x=summary(zj.hw$pinfGIanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

CR=10^approx(x=summary(zj.hw$pinfCRanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

NV=10^approx(x=summary(zj.hw$pinfNVanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

RV=10^approx(x=summary(zj.hw$pinfRVanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y
  ))
  riskTol=0.00001
  options(scipen=-1)
  n5=t(data.frame(

VC=10^approx(x=summary(zj.hw$pinfVCanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

SH=10^approx(x=summary(zj.hw$pinfSHanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

SA=10^approx(x=summary(zj.hw$pinfSAanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

ET=10^approx(x=summary(zj.hw$pinfETanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

EP=10^approx(x=summary(zj.hw$pinfEPanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

GI=10^approx(x=summary(zj.hw$pinfGIanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

CR=10^approx(x=summary(zj.hw$pinfCRanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

NV=10^approx(x=summary(zj.hw$pinfNVanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y,

RV=10^approx(x=summary(zj.hw$pinfRVanG.bci,quantile,0.95)$stat,y=logCw,xout=riskTol,method="linear")$y
  ))
  thresh=cbind(n3,n4,n5);colnames(thresh)=c('P<0.001','P<0.0001','P<0.00001');thresh
  ###### NOTE! If NA values appear in this table, rerun the model with a broader range of
concentrations of pathogens in water ###
}
(thresh[,c(2)])
round(thresh[,2]/c(NA,NA,1e-4,2e-2,NA,1e-6,1e-6,5e-6,5e-6),1)

##############################################################################################
######################################## TABLE 2 ############################################
##############################################################################################

if (handsorwater == 2) {  # generating Table 2 only makes sense when handsorwater=2 --> water has no
pathogens, hands have some pathogens
  HSAwtd=getCoda(zc.hw,"HSAwtd")
  options(scipen=-1)
  logNs.MCMC=getCoda(zc.hw,"logNs.MCMC")
  n=10000000
  nHAND=t(data.frame(

VC=10^max(approx(logNs,summary(zj.hw$pinfVCanG.bci,quantile,0.95)$stat,n=n)$x[approx(logNs,summary(zj.h
w$pinfVCanG.bci,quantile,0.95)$stat,n=n)$y!=1]),

SH=10^max(approx(logNs,summary(zj.hw$pinfSHanG.bci,quantile,0.95)$stat,n=n)$x[approx(logNs,summary(zj.h
w$pinfSHanG.bci,quantile,0.95)$stat,n=n)$y!=1]),

SA=10^max(approx(logNs,summary(zj.hw$pinfSAanG.bci,quantile,0.95)$stat,n=n)$x[approx(logNs,summary(zj.h
w$pinfSAanG.bci,quantile,0.95)$stat,n=n)$y!=1]),

ET=10^max(approx(logNs,summary(zj.hw$pinfETanG.bci,quantile,0.95)$stat,n=n)$x[approx(logNs,summary(zj.h
w$pinfETanG.bci,quantile,0.95)$stat,n=n)$y!=1]),

EP=10^max(approx(logNs,summary(zj.hw$pinfEPanG.bci,quantile,0.95)$stat,n=n)$x[approx(logNs,summary(zj.h
w$pinfEPanG.bci,quantile,0.95)$stat,n=n)$y!=1]),

GI=10^max(approx(logNs,summary(zj.hw$pinfGIanG.bci,quantile,0.95)$stat,n=n)$x[approx(logNs,summary(zj.h
w$pinfGIanG.bci,quantile,0.95)$stat,n=n)$y!=1]),

CR=10^max(approx(logNs,summary(zj.hw$pinfCRanG.bci,quantile,0.95)$stat,n=n)$x[approx(logNs,summary(zj.h
w$pinfCRanG.bci,quantile,0.95)$stat,n=n)$y!=1]),
```

```
NV=10^max(approx(logNs,summary(zj.hw$pinfNVanG.bci,quantile,0.95)$stat,n=n)$x[approx(logNs,summary(zj.h
w$pinfNVanG.bci,quantile,0.95)$stat,n=n)$y!=1]),

RV=10^max(approx(logNs,summary(zj.hw$pinfRVanG.bci,quantile,0.95)$stat,n=n)$x[approx(logNs,summary(zj.h
w$pinfRVanG.bci,quantile,0.95)$stat,n=n)$y!=1])
  ))
  perHANDL=NA;perHANDU=NA;perHANDa=NA
  for(i in 1:length(nHAND[,1])){
    perHANDL[i]=quantile(nHAND[i,1]*HSAwtd,c(0.025))
  };perHANDL
  for(i in 1:length(nHAND[,1])){
    perHANDU[i]=quantile(nHAND[i,1]*HSAwtd,c(0.975))
  };perHANDU
  for(i in 1:length(nHAND[,1])){
    perHANDa[i]=mean(nHAND[i,1]*HSAwtd)
  };perHANDa
  perHAND=data.frame(nHAND,round(cbind(perHANDa,perHANDL,perHANDU),3));colnames(perHAND)=c("per sq.
cm.","per hand (mean)","per hand (lower 95%)","per hand (upper 95%)");perHAND
}

## RR defined as relative risk of not washing hands to risk of washing hands (if RR<1, you're better
off not washing hands)
RR.VC=pinfVC.MCMC.n/pinfVC.MCMC
RR.SH=pinfSH.MCMC.n/pinfSH.MCMC
RR.SA=pinfSA.MCMC.n/pinfSA.MCMC
RR.ET=pinfET.MCMC.n/pinfET.MCMC
RR.EP=pinfEP.MCMC.n/pinfEP.MCMC
RR.GI=pinfGI.MCMC.n/pinfGI.MCMC
RR.CR=pinfCR.MCMC.n/pinfCR.MCMC
RR.NV=pinfNV.MCMC.n/pinfNV.MCMC
RR.RV=pinfRV.MCMC.n/pinfRV.MCMC

RR=data.frame(RR.VC=RR.VC,RR.SH=RR.SH,RR.SA=RR.SA,RR.ET=RR.ET,RR.EP=RR.EP,RR.GI=RR.GI,RR.CR=RR.CR,RR.NV
=RR.NV,RR.RV=RR.RV,Xw=Xw,logNs.MCMC)
head(RR)
par(mfrow=c(1,1))
boxplot(RR)

# if RR<1, you're better off not washing hands
a = ggplot(RR,aes(Xw,RR.VC)) + geom_jitter(aes(color = logNs.MCMC)) + theme_minimal() + ylim(0,3)
b = ggplot(RR,aes(Xw,RR.SH)) + geom_jitter(aes(color = logNs.MCMC)) + theme_minimal() + ylim(0,3)
c = ggplot(RR,aes(Xw,RR.SA)) + geom_jitter(aes(color = logNs.MCMC)) + theme_minimal() + ylim(0,3)
d = ggplot(RR,aes(Xw,RR.ET)) + geom_jitter(aes(color = logNs.MCMC)) + theme_minimal() + ylim(0,3)
e = ggplot(RR,aes(Xw,RR.EP)) + geom_jitter(aes(color = logNs.MCMC)) + theme_minimal() + ylim(0,3)
f = ggplot(RR,aes(Xw,RR.GI)) + geom_jitter(aes(color = logNs.MCMC)) + theme_minimal() + ylim(0,3)
g = ggplot(RR,aes(Xw,RR.CR)) + geom_jitter(aes(color = logNs.MCMC)) + theme_minimal() + ylim(0,3)
h = ggplot(RR,aes(Xw,RR.NV)) + geom_jitter(aes(color = logNs.MCMC)) + theme_minimal() + ylim(0,3)
i = ggplot(RR,aes(Xw,RR.RV)) + geom_jitter(aes(color = logNs.MCMC)) + theme_minimal() + ylim(0,3)
grid.arrange(a,b,c,d,e,f,g,h,i,nrow=3)

RR$RR.NV[RR$Xw==8,]

##############################################################################################
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################################### SENSITIVITY ANALYSIS #####################################
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zc.sen=coda.samples(jm.hw,variable.names=c("m","b","lrv","tNd","beta1","beta0","tHSA","lambda","timesPe
rDay",
                                           "RValpha","RVbeta","NVphi","NVa","ETalpha","ETbeta",
                                           "EPalpha","EPbeta","SHalpha","SHbeta","SAalpha","SAbeta",

"VCalpha","VCbeta","CRalpha","CRbeta","GIr","TE","TEw","TEd",
                                           "alphaTEd","alphaTEw","betaTEd","betaTEw","fc","logNs.MCMC",
                                           "pinfVCanG","pinfSHanG","pinfSAanG","pinfETanG","pinfEPanG",

"pinfGIanG","pinfCRanG","pinfNVanG","pinfRVanG"),n.iter=n.iter)
gelman.diag(zc.sen)
gelman.plot(zc.sen)
n.iter

m=getCoda(zc.sen,'m')
```

```
b=getCoda(zc.sen,'b')
lrv=getCoda(zc.sen,'lrv')
tNd=getCoda(zc.sen,'tNd')
beta1=getCoda(zc.sen,'beta1')
beta0=getCoda(zc.sen,'beta0')
tHSA=getCoda(zc.sen,'tHSA')
lambda=getCoda(zc.sen,'lambda')
timesPerDay=getCoda(zc.sen,'timesPerDay')

RValpha=getCoda(zc.sen,'RValpha')
RVbeta=getCoda(zc.sen,'RVbeta')
NVphi=getCoda(zc.sen,'NVphi')
NVa=getCoda(zc.sen,'NVa')
ETalpha=getCoda(zc.sen,'ETalpha')
ETbeta=getCoda(zc.sen,'ETbeta')

EPalpha=getCoda(zc.sen,'EPalpha')
EPbeta=getCoda(zc.sen,'EPbeta')
SHalpha=getCoda(zc.sen,'SHalpha')
SHbeta=getCoda(zc.sen,'SHbeta')
SAalpha=getCoda(zc.sen,'SAalpha')
SAbeta=getCoda(zc.sen,'SAbeta')

VCalpha=getCoda(zc.sen,'VCalpha')
VCbeta=getCoda(zc.sen,'VCbeta')
CRalpha=getCoda(zc.sen,'CRalpha')
CRbeta=getCoda(zc.sen,'CRbeta')
GIr=getCoda(zc.sen,'GIr')

TE=getCoda(zc.sen,'TE')
TEw=getCoda(zc.sen,'TEw')
TEd=getCoda(zc.sen,'TEd')
alphaTEd=getCoda(zc.sen,'alphaTEd')
alphaTEw=getCoda(zc.sen,'alphaTEw')
betaTEd=getCoda(zc.sen,'betaTEd')
betaTEw=getCoda(zc.sen,'betaTEw')
fc=getCoda(zc.sen,'fc')
logNs.MCMC=getCoda(zc.sen,'logNs.MCMC')

pVCaGold=getCoda(zc.sen,'pinfVCanG')
pSHaGold=getCoda(zc.sen,'pinfSHanG')
pSAaGold=getCoda(zc.sen,'pinfSAanG')
pETaGold=getCoda(zc.sen,'pinfETanG')
pEPaGold=getCoda(zc.sen,'pinfEPanG')
pGIaGold=getCoda(zc.sen,'pinfGIanG')
pCRaGold=getCoda(zc.sen,'pinfCRanG')
pNVaGold=getCoda(zc.sen,'pinfNVanG')
pRVaGold=getCoda(zc.sen,'pinfRVanG')

require(corrplot)

options(scipen=9)
corMatrix=data.frame(m,b,lrv,tNd,beta1,beta0,tHSA,lambda,timesPerDay,TE,fc,RValpha,RVbeta,NVphi,NVa,ETa
lpha,ETbeta,
                     EPalpha,EPbeta,SHalpha,SHbeta,SAalpha,SAbeta,VCalpha,VCbeta,CRalpha,CRbeta,GIr,
                     pVCaGold,pSHaGold,pSAaGold,pETaGold,pEPaGold,pGIaGold,pCRaGold,pNVaGold,pRVaGold)

corCoef=round(cor(corMatrix,method="spearman"),3)
#vars=c("Pathogen transfer from water to skin, slope (m)","Pathogen transfer from water to skin,
intercept (b)","Log reduction value from handwashing",
#       "Precision of Model 1 (tau1)","Estimation of HSA from TSA, slope (beta1)","Estimation of HSA
from TSA, intercept (beta0)","Precision of HSA to TSA model (tauHSA)",
#       "Average number of times a person washes hands per day (lambda)","Number of times a person
washes hands per day (lambda)","Percent of pathogens transferred from hands to mouth (TE)","Fraction of
the hand that contacts the mouth (fc)",
#       "Rotavirus dose-response model (alpha)","Rotavirus dose-response model (beta)","Norovirus dose-
response model (phi)","Norovirus dose-response model (a)",
#       "ETEC dose-response model (alpha)","ETEC dose-response model (beta)","EPEC dose-response model
(alpha)","EPEC dose-response model (beta)",
#       "Shigella dose-response model (alpha)","Shigella dose-response model (beta)","Salmonella dose-
response model (alpha)","Salmonella dose-response model (beta)",
#       "Vibrio cholerae dose-response model (alpha)","Vibrio cholerae dose-response model
(beta)","Cryptosporidium dose-response model (alpha)","Cryptosporidium dose-response model
(beta)","Giardia dose-response model (r)",
#       "Annual probability of infection from Vibrio cholerae","Annual probability of infection from
Shigella","Annual probability of infection from Salmonella",
```

```
#       "Annual probability of infection from ETEC","Annual probability of infection from EPEC","Annual
probability of infection from Giardia",
#       "Annual probability of infection from Cryptosporidium","Annual probability of infection from
norovirus","Annual probability of infection from rotavirus")
#rownames(corCoef)=vars
#colnames(corCoef)=vars
corCoef
write.csv(corCoef,file="correlationTable3.csv")
```