



Title	Evaluation of virus reduction efficiency in wastewater treatment unit processes as a credit value in the multiple-barrier system for wastewater reclamation and reuse
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Supplemental materials for

Evaluation of virus reduction efficiency in wastewater treatment unit processes as a credit value in the multiple-barrier system for wastewater reclamation and reuse

Author names and affiliations:

Toshihiro Ito^a, Tsuyoshi Kato^b, Makoto Hasegawa^b, Hiroyuki Katayama^c, Satoshi Ishii^d, Satoshi Okabe^a, Daisuke Sano^{a*}

^aDivision of Environmental Engineering, Faculty of Engineering, Hokkaido University, North 13, West 8, Kita-ku, Sapporo, Hokkaido 060-8628, Japan

^bDepartment of Computer Science, Graduate School of Engineering, Gunma University, Tenjinmachi 1-5-1, Kiryu, Gunma 376-8515, Japan

^cDepartment of Urban Engineering, School of Engineering, University of Tokyo, Bunkyo-ku, Tokyo, 190-8518, Japan

^dDepartment of Soil, Water, and Climate, University of Minnesota, 258 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

***Corresponding Author Address:**

Division of Environmental Engineering, Faculty of Engineering, Hokkaido University, North 13, West 8, Kita-ku, Sapporo, Hokkaido 060-8628, Japan.

Telephone/Fax: +81-11-706-7597.

E-mail: dsano@eng.hokudai.ac.jp

26 Table S1. Basic information of wastewater treatment plants where the virus concentration in
 27 wastewater was analyzed.

Plant	Prefecture	Area of sewer coverage (km ²)	Number of resident in the covered area (individuals)	Daily volume of treated wastewater (m ³ /day)
A	Osaka	25	290,000	73,000
B	Kyoto	81	770,000	571,000
C	Saitama	44	297,000	121,000
D	Tokyo	35	63,000	28,000

Table S2. The statistics of Akaike information criterion (AIC) and Bayesian information criterion (BIC) for the datasets of norovirus genogroup I (NoV GI), norovirus genogroup II (NoV GII) and adenovirus (AdV).

Virus	Sample	Plant	AIC			BIC		
			Normal	Log-normal	Gamma	Normal	Log-normal	Gamma
NoV GI	Influent	A	148.2	32.8	125.4	146.2	30.9	123.5
		B	180.0	41.5	139.6	178.2	39.6	137.7
		C	179.0	31.0	146.8	177.2	29.1	145.0
		D	213.8	37.7	NaN ^a	212.0	35.9	NaN
	Secondary effluent	A	124.1	42.2	77.0	122.2	40.4	75.1
		B	104.3	31.9	74.5	102.5	30.1	72.6
		C	79.7	31.3	65.6	77.9	29.5	63.8
		D	82.3	27.7	52.0	80.4	25.7	50.1
	Chlorine-disinfected effluent	A	69.9	34.3	42.3	68.0	32.5	40.5
		B	89.1	30.0	63.5	87.3	28.1	61.7
		C	88.7	31.6	52.8	86.8	29.8	50.9
		D	83.6	32.4	57.4	81.7	30.5	55.4
NoV GII	Influent	A	143.0	30.5	121.2	141.1	28.6	119.4
		B	179.1	35.3	145.9	177.3	33.5	144.1
		C	178.8	25.3	145.7	177.0	23.4	143.9
		D	213.6	34.9	NaN	211.8	33.1	NaN
	Secondary effluent	A	60.2	28.6	39.4	58.2	26.6	37.6
		B	73.7	31.6	62.0	71.8	29.8	60.1
		C	88.5	34.6	53.5	86.7	32.8	51.6
		D	75.7	33.0	45.1	73.8	31.1	43.3
	Chlorine-disinfected effluent	A	46.9	25.2	33.1	44.9	23.2	30.4
		B	96.8	30.2	68.3	94.9	28.3	66.4
		C	88.9	35.6	39.7	87.1	33.8	37.9
		D	50.3	28.6	26.1	48.4	26.8	24.3
AdV	Influent	A	188.0	22.7	177.0	186.2	20.9	175.1
		B	182.2	22.2	156.8	180.3	20.4	155.0
		C	200.1	21.3	184.6	198.3	19.4	182.8
		D	226.0	37.3	NaN	224.2	35.5	NaN
	Secondary effluent	A	127.3	27.7	96.6	125.4	25.9	94.8
		B	115.0	29.7	105.0	113.2	27.9	103.2
		C	161.8	28.0	123.9	159.9	26.2	122.1
		D	118.0	25.5	100.5	116.0	23.6	98.6
	Chlorine-disinfected effluent	A	89.4	13.9	79.8	87.5	12.0	78.0
		B	145.7	36.6	113.5	143.9	34.8	111.6
		C	97.5	18.7	96.6	95.6	16.9	94.7
		D	96.0	26.5	87.8	94.2	24.7	85.9

a, not a number (non-finite value)

Table S3. Mean, standard deviation (SD) and 95% confidence interval of the virus concentration ($\log_{10}$ (PCR detection unit/mL)) in influent, secondary-effluent and chlorine-disinfected effluent.

Sample	Virus	Plant	Number of detect (positive rate)	Mean	SD	95% confidence interval (lower, upper)
Influent	NoV GI	A	11/12 (92%)	1.2	1.4	(0.4, 2.0)
		B	12/12 (100%)	1.4	1.3	(0.7, 2.2)
		C	12/12 (100%)	1.7	0.9	(1.2, 2.2)
		D	12/12 (100%)	1.7	1.1	(1.1, 2.4)
	NoV GII	A	12/12 (100%)	1.3	0.8	(0.8, 1.7)
		B	12/12 (100%)	1.6	1.0	(1.0, 2.2)
		C	12/12 (100%)	1.7	0.7	(1.3, 2.1)
		D	12/12 (100%)	2.0	1.0	(1.4, 2.6)
	AdV	A	12/12 (100%)	2.4	0.6	(2.1, 2.7)
		B	12/12 (100%)	2.0	0.6	(1.6, 2.3)
		C	12/12 (100%)	2.6	0.6	(2.2, 2.9)
		D	12/12 (100%)	2.8	1.1	(2.2, 3.5)
Secondary effluent	NoV GI	A	12/12 (100%)	0.2	1.4	(-0.5, 1.0)
		B	12/12 (100%)	0.4	0.9	(-0.1, 0.9)
		C	12/12 (100%)	0.3	0.9	(-0.2, 0.8)
		D	11/12 (92%)	-0.2	1.1	(-0.8, 0.5)
	NoV GII	A	10/12 (83%)	-0.6	1.5	(-1.4, 0.3)
		B	12/12 (100%)	0.2	0.9	(-0.3, 0.7)
		C	12/12 (100%)	-0.1	1.0	(-0.7, 0.5)
		D	12/12 (100%)	-0.2	0.9	(-0.7, 0.3)
	AdV	A	12/12 (100%)	0.8	0.8	(0.4, 1.2)
		B	12/12 (100%)	1.1	0.8	(0.6, 1.5)
		C	12/12 (100%)	1.2	0.8	(0.8, 1.7)
		D	11/12 (92%)	0.8	1.4	(0.0, 1.6)
Chlorine- disinfected effluent	NoV GI	A	12/12 (100%)	-0.2	1.0	(-0.8, 0.3)
		B	12/12 (100%)	0.2	0.8	(-0.3, 0.7)
		C	12/12 (100%)	-0.1	0.9	(-0.6, 0.4)
		D	11/12 (92%)	-0.1	1.3	(-0.9, 0.6)
	NoV GII	A	10/12 (83%)	-0.6	1.3	(-1.3, 0.2)
		B	11/12 (91%)	0.1	1.3	(-0.6, 0.8)
		C	12/12 (100%)	-0.4	1.0	(-1.0, 0.2)
		D	12/12 (100%)	— ^a	—	—
	AdV	A	12/12 (100%)	0.8	0.7	(0.4, 1.2)
		B	12/12 (100%)	1.1	1.1	(0.4, 1.7)
		C	12/12 (100%)	1.1	0.5	(0.8, 1.4)
		D	12/12 (100%)	0.8	0.7	(0.4, 1.2)

^a, the dataset of NoV GII density in chlorine-disinfected effluent of plant D were not fitted to log-normal distribution (tested by Akaike and Bayesian information criterion)

```

39
40 1. R code used in this study
41     The following R code was used for calculating Akaike and Bayesian information
42 criterion
43
44 #Virus concentration datasets in influent, secondary effluent and chlorine disinfected effluent
45 conc <- c() #Input of virus concentration datasets
46 logconc <- log10(conc)
47 mean <- mean (conc)
48 logmean <- mean(logconc)
49 sd <- sd(conc)
50 logsd<- sd(logconc)
51 count.data <- length(conc)
52
53 # Estimation of logarithmic maximum likelihood estimator in normal distribution
54 kn <- 2 #the number of parameters in normal distribution
55 Ln <- function(arg){
56 likelihoodn <- 1/sqrt(2*pi*arg[2]^2)*exp(-(conc-arg[1])^2/(2*arg[2]^2))
57 return(sum(log(likelihoodn)))
58 }
59 data.optn <- optim(par=c(mean, sd), Ln, control=list(fnscale=-1))
60 LMLEN <- data.optn$value #logarithmic maximum likelihood estimator for normal
61 distribution
62
63 # Calculation of Akaike and Bayesian information criterion (AIC and BIC) for normal
64 distribution

```

```

65  AICn <- -2*(LMLEn-kn) # Akaike information criterion for normal distribution
66  print(AICn)
67  BICn <- -2*LMLEn+kn*log10(count.data) # Bayesian information criterion for normal
68  distribution
69  print(BICn)
70
71  # Estimation of logarithmic maximum likelihood estimator in log-normal distribution
72  kln <- 2 #the number of parameters in log-normal distribution
73  Lln <- function(arg){
74    likelihoodln <- 1/sqrt(2*pi*arg[2]^2)*exp(-(logconc-arg[1])^2/(2*arg[2]^2))
75    return(sum(log(likelihoodln)))
76  }
77  data.optln <- optim(par=c(logmean, logsd), Lln, control=list(fnscale=-1))
78  LMLEln <- data.optln$value #logarithmic maximum likelihood estimator for log-normal
79  distribution
80
81  # Calculation of Akaike and Bayesian information criterion (AIC and BIC) for log-normal
82  distribution
83  AICln <- -2*(LMLEln-kln) # Akaike information criterion for log-normal distribution
84  print(AICln)
85  BICln <- -2*LMLEln+kln*log10(count.data) # Bayesian information criterion for log-normal
86  distribution
87  print(BICln)
88
89  # Estimation of logarithmic maximum likelihood estimator in gamma distribution
90  library(MASS)

```

```
91  kg <- 2  #the number of parameters in gamma distribution
92  parameter <- fitdistr(conc,"gamma")
93  parameterlist <- matrix(unlist(parameter), ncol=1)
94  shape <- parameterlist[1]
95  rate <- parameterlist[2]
96  LMLEg <- sum(dgamma(conc, shape, rate, log=TRUE))  #logarithmic maximum likelihood
97  estimator for gamma distribution
98
99  # Calculation of Akaike and Bayesian information criterion (AIC and BIC) for gamma
100 distribution
101  AICg <- -2*(LMLEg-kg)  # Akaike information criterion for gamma distribution
102  print(AICg)
103  BICg <- -2*LMLEg+kg*log10(count.data)  # Bayesian information criterion for gamma
104 distribution
105  print(BICg)
```