A computational fluid dynamics analysis of placing UV reactors in series
Patrick C. Young and Yuri A. Lawryshyn

ABSTRACT

Ultraviolet (UV) light water treatment reactors are commonly used in both wastewater and drinking water disinfection. UV technology can effectively inactivate a large number of pathogens at low UV doses, however adenovirus requires a substantially higher dose than most pathogens of interest. In order to meet adenovirus inactivation requirements, UV reactors are often placed in series and the total inactivation is calculated as the sum of the reactors’ individual UV doses. In this paper, it is shown that this simple summation treatment of UV dose may be acceptable. A parameter called the reactor additivity factor is introduced to properly characterize the interaction between UV reactors in series. Three types of UV reactors are modelled using computational fluid dynamics, and their RAFs are computed. The validity of reactor additivity in practice in wastewater and drinking water systems is discussed.

Key words | computational fluid dynamics, UV disinfection, UV reactor modelling, UV reactors in series

INTRODUCTION

Ultraviolet (UV) light disinfection is a proven technology for wastewater and drinking water disinfection. In order to meet UV dosing requirements, several UV reactors, or banks, are often placed in series. However, few studies have addressed how putting UV reactors in series impacts their validation protocols. Health Canada and the United States Environmental Protection Agency recommend an inactivation/removal of at least 4-log for enteric viruses, i.e. adenovirus, for groundwater and surface water sources (Health Canada 2012; United States Environmental Protection Agency 1989). There is some regulatory concern that UV disinfection alone is not enough to effectively disinfect adenovirus in drinking water in the absence of chlorine and filtration processes.

Although adenovirus is extremely resistant to UV disinfection, it is not immune. The Ultraviolet Disinfection Guidance Manual (UVDGM) by Schmelling et al. (2006) specifies a reactor equivalent dose (RED) of 186 mJ/cm² to achieve 4-log ‘virus’ inactivation credit. Since few validated UV disinfection reactors exist that are able to deliver such a high UV dose, the National Water Research Institute (NWRI) guidelines allow for UV drinking water and wastewater reactors to be installed in series and the UV dose delivered is calculated as the cumulative dose of the individual reactors (National Water Research Institute 2012). The reactors in series must be shown to be hydraulically independent or the reactors in series must be validated in such a way that the installed system is identical to the validated one. Therefore, the guidelines allow for a drinking water system to meet the requirement of 4-log adenovirus inactivation by installing multiple UV disinfection units in series. The UVDGM specifies that ‘good mixing should be confirmed’ when placing UV reactors in series. However, the underlying assumption that UV doses are additive is inconsistent in the literature and has not been thoroughly investigated.
LITERATURE REVIEW

To date, there exist a few papers that consider the impact of placing UV reactors in series on overall UV system performance. Tang et al. (2006) investigated the interaction between multiple UV banks in series for an open channel configuration using MS2 as a test organism. The delivered UV doses from multiple reactors were shown to be not exactly additive, with the overall dose being greater than additive. However, no explanation for the result was given. Ferran & Scheible (2007) found that for two low pressure high output (LPHO) UV reactors in series in an open channel, the RED was twice the RED of a single LPHO reactor. Ducoste & Alpert (2011) numerically evaluated the RED of UV reactors in series for both open channels and closed conduits. It was shown that additivity may only be assumed provided that there is sufficient mixing between reactor banks. They also commented that the UV response kinetics of the target microorganism will impact the degree of additivity. However, their results only looked at what happens for the two cases of perfect mixing and no mixing between reactors.

Recently, Lawryshyn & Hofmann (2015) looked at UV reactor additivity from a completely theoretical perspective. A reactor additivity factor (RAF) was introduced to quantify the degree of additivity. RAF was defined as the RED of two reactors in series divided by twice the RED of a single reactor. Thus, an RAF of 1 means exact additivity, whereas an RAF > 1 means better than exact additivity and RAF < 1 means less than exact additivity – i.e. an RAF greater than 1 implies that the RED of the system is greater than the sum of the RED of the original reactors, and vice-versa for an RAF less than one. For two reactors in series with perfect mixing between the reactors, it was shown that the RAF will necessarily be one. Furthermore, it was shown that for systems with a negative correlation among the dose paths between the two reactors, the RAF will be greater than or equal to one, whereas for a positive correlation, the RAF will be less than or equal to one. Additionally, it was shown that in the extreme case of perfect positive correlation, which is considered to be a worst case scenario, if the test organism is two or more times more sensitive than the target organism, then the RAF will necessarily be greater than 1 from the perspective of the target organism. The author’s corollary is that if two identical reactors, each of which can deliver a RED of 93 mJ/cm² with MS2, are put in series, the resulting system will necessarily achieve a RED of at least 186 mJ/cm² based on adenovirus.

It has been well established that computational fluid dynamics (CFD) analysis coupled with fluence rate modelling is a reliable method for evaluating UV reactor performance. Furthermore, it is very difficult to perform experiments to gain significant technical insights into the effects of reactor additivity. Specifically, there is no simple way to measure the dose received for each particle path per reactor for two reactors in series, in an effort to determine the overall dose correlation between two reactors. Therefore, in this paper, the topic of reactor additivity will be explored from a numerical and CFD perspective. Two simple reactor configurations will be considered to investigate both positive and negative dose correlation (and will henceforth be referred to as the ‘correlated systems’). Additionally, two real-world reactor configurations will be investigated to demonstrate the phenomenon of reactor additivity in practice.

As mentioned previously, the use of CFD for evaluating UV reactor performance is an established practice. Unluturk et al. (2004) coupled CFD velocity fields with fluence rate models to compute the UV dose delivered to apple cider, and found reasonable agreement between simulated and experimental values. Lawryshyn & Cairns (2005) showed that CFD UV reactor models can be carefully used in place of the bioassay testing of prototype reactors in order to speed up development and reduce associated prototyping costs. Sozzi & Taghipour (2006) further demonstrated that CFD flow fields were in agreement with particle image velocimetry measurements and that the resulting microbial inactivation was consistent with experimentally obtained biodosimetry results. Other studies also support the use of CFD to predict reactor performance (Chiu et al. 1999; Lyn et al. 1999; Pareek et al. 2005).

METHODOLOGY

In this section, theory is introduced that will allow us to discuss the performance of UV reactors placed in
series. Additionally, the reactor models used will be introduced.

Theory

It has been well established that UV reactors deliver a distribution of doses to the microbes traversing the reactor (Wright & Lawryshyn 2000). The entry point as well as the path that a microbe takes as it flows through the reactor in relation to the lamps results in its obtained UV dose. Consider the two correlated systems depicted in Figures 1 and 2. Suppose that there exist two identical UV reactors, R1 and R2, in series and that the dose distribution through each is identical. A microbe that receives a certain dose from R1 will not necessarily receive the same dose from R2 due to mixing between reactors. The amount of mixing between R1 and R2 may be characterized by a correlation (represented mathematically by $\rho$) of the doses delivered by R1 and subsequently R2 for a given microbial path. For the theoretical case of absolutely no mixing between reactors, one would expect perfect positive correlation in dose paths between R1 and R2, i.e. a given microbe would receive exactly the same dose from each of the two reactors. For positively correlated reactors, a microbe that receives a high dose from R1 would be expected to receive a high dose from R2. Similarly, particles that receive a low dose from R1 would be expected to receive a low dose from R2. Perfect mixing between reactors implies zero correlation between dose paths. With zero correlation, it is not possible to estimate the dose that a microbe receives from R2 given the dose that it receives from R1. There also exists an opportunity for the dose paths through R1 and R2 to be negatively correlated. In this case, a microbe that receives a high dose in R1 is expected to receive a low dose in R2 and vice versa. While this may be difficult to achieve in practice, it is possible to construct such a reactor for demonstration purposes. Figures 1 and 2 depict two very simple cross flow reactor configurations where one would expect positive and negative dose path correlations, respectively. In the positively correlated case, the lamps in both R1 and R2 are positioned to be near the lower wall so that particles receiving a high dose in R1 will also receive a high dose in R2. In the negatively correlated case, the lamp in R1 is positioned near the bottom wall and the lamp in R2 is positioned near the top wall so that particles that receive a high dose in R1 will receive a low dose in R2.

The performance of a UV reactor is characterized by a distribution of doses that microbes are expected to receive as they traverse through the reactor. Therefore, it is generally not useful to characterize a reactor’s inactivation potential by an average dose. UV reactor performance is often characterized by the RED or ‘reactor equivalent dose’. For first order microbial inactivation kinetics, RED is given by:

$$\text{RED} = -\frac{1}{k} \ln \left( \int_0^{\infty} f(D) e^{-kD} dD \right)$$

(1)

where $f(D)$ is the probability density function, i.e. the dose distribution for a given reactor, and $k$ is the microbe specific inactivation constant (see Wright & Lawryshyn (2000) or Lawryshyn & Hofmann (2015) for more details).

In the negatively correlated reactor case, although the reactors are effectively reversed in their alignment, the water layers on each side of the lamps of R1 and R2 are the same. On an individual basis, it is expected that the RED for R1 and R2 will be very similar. However, across the entire system, the RED for the two reactors in series will be different. Thus, the two reactor configurations, i.e. the positively and negatively correlated configurations, will have different additivities. Let us define a dimensionless
additivity factor (RAF) given by:

\[
RAF = \frac{RED_{12}}{2RED_1}
\]  

(2(a))

or,

\[
RAF = \frac{RED_{12}}{RED_1 + RED_2}
\]

(2(b))

where RED_{12} is the RED calculated across the entire system, RED_1 is the RED of the first reactor, and RED_2 is the RED of the second reactor. Equation (2(a)) is an idealization that assumes that the dose distributions for R1 and R2 are identical. In practice, R1 will influence R2 and the dose distributions are not the same. Thus, Equation (2(b)) should generally be used. It should be noted that in the case of different test versus target organisms, the RED of the system, i.e. RED_{12}, should be calculated based on the target organism, whereas RED_1 and RED_2 should be based on the test organism as is the case with a bioassay validation. As will be shown in the results, we will also present a RAF calculated with RED_{12} based on adenovirus and RED_1 and RED_2 based on MS2.

Although the proof has been omitted, it is intuitive that the negatively correlated reactor configuration will have a higher RED and superior inactivation performance to that of the positively correlated reactor configuration. In the positively correlated reactor configuration, there is extreme short circuiting along the top of the reactor. Microbes flowing along the bottom of the reactor will receive high UV doses from both R1 and R2, whereas particles flowing along the top will receive very low doses through each of the two reactors. In the negatively correlated reactor configuration, the microbes flowing along the bottom of the reactor will first receive high doses from R1 and then low doses from R2 with the reverse happening along the bottom of the reactor. As corollary, it is clear that the RAF will be greater for the case of negative correlation than that of positive correlation. In fact, for any given value of k, the RAF is greater than 1 for negative correlation, less than 1 for positive correlation, and equal to 1 for zero correlation.

The interactions with the inactivation constant are not as simple, however. In the case of a UV resistant organism \((k \to 0)\) the RAF will approach 1. For a sensitive organism \((k \to \infty)\) the RAF will also approach 1 except for the case of \(\rho = -1\), in which case the RAF will necessarily be greater than 1. The effects of correlation and the inactivation constant on the RAF are summarized in Table 1.

### Numerical model

CFD work was carried out using Workbench 14.5 (ANSYS 2011). All CFD models used the velocity-inlet boundary condition on the inlet, pressure-outlet on the outlet, and the no-slip boundary condition (wall) was used on all wall and lamp surfaces. A pressure-based solver was used in Fluent, and turbulence was modelled with the realizable k–\(\varepsilon\) model. Particle tracking was done by Fluent and dose calculation code was developed and executed using MATLAB R2008a. The process is summarized in Table 2 below.

The radial model (Blatchley 1997) was used for all fluence rate calculations for its simplicity and low computational cost. Despite the fact that it is not as accurate as other fluence rate models, the objective of this study was to show the relative trends in dose, and this is easily achievable with the radial model. It is defined by:

\[
I(r) = \frac{\tau_s \eta LILT \alpha (r/C0 - R) 2\pi r}{2\pi r}
\]  

(3)

where I is the UV light intensity, \(r\) is the radial distance from the centre of the lamp, \(R\) is the radius of the lamp sleeve, \(\tau_s\) is

### Table 1 | Trends in \(\rho\) and \(k\) on RAF

<table>
<thead>
<tr>
<th>(\rho)</th>
<th>(k)</th>
<th>(AF)</th>
</tr>
</thead>
<tbody>
<tr>
<td>-1</td>
<td>(0)</td>
<td>(1)</td>
</tr>
<tr>
<td>(\rho)</td>
<td>(k)</td>
<td>(AF)</td>
</tr>
<tr>
<td>0</td>
<td>(\infty)</td>
<td>(1)</td>
</tr>
</tbody>
</table>

### Table 2 | Software used in workflow

<table>
<thead>
<tr>
<th>Operation</th>
<th>Vendor</th>
<th>Software</th>
</tr>
</thead>
<tbody>
<tr>
<td>Geometry</td>
<td>ANSYS</td>
<td>DesignModeler</td>
</tr>
<tr>
<td>Meshing</td>
<td>ANSYS</td>
<td>Meshing</td>
</tr>
<tr>
<td>Physics and particle tracking</td>
<td>ANSYS</td>
<td>Fluent</td>
</tr>
<tr>
<td>Fluence rate modelling and dose calculations</td>
<td>Mathworks</td>
<td>MATLAB</td>
</tr>
</tbody>
</table>
the lamp sleeve transmittance, \( \eta_L \) is the lamp efficiency, \( I_L \) is the power intensity per unit length of the lamp, \( \tau \) is the UV transmittance (UVT) of the water, and \( \alpha \) is a non-dimensionalizing coefficient dependent on the UVT unit of measurement. For a discrete dose distribution, RED is calculated as:

\[
\text{RED} = \frac{1}{k} \ln \left( \frac{1}{N} \sum_{i=1}^{N} e^{-kD_i} \right)
\]

where \( N \) is the total number of particles, and \( D_i \) is the dose of the \( i \)th particle (Wright & Lawryshyn 2000). In this paper, \( D_{10} \) (dose required for a 1-log reduction of microbes) will primarily be used in place of \( k \). \( D_{10} \) is defined as follows:

\[
D_{10} = \frac{\ln (10)}{k}
\]

**Correlated systems**

The two correlated systems were modelled as described in Table 3. The reactors were modelled in three dimensions, with the lamps and lamp sleeves extending from wall to wall. A length of 10 hydraulic diameters (\( D_H \)) was given for flow to develop before the lamps, and 5 \( D_H \) was given after the lamps and before the outlet. A mesh was created of \( 7.0 \times 10^5 \) hex elements. The minimum orthogonal quality was greater than 0.50 and grid convergence was achieved. Turbulent flow was achieved with a Reynolds number (Re) greater than \( 10^5 \) based on \( D_H \). A sufficient number of massless particles were injected uniformly across the inlet surface to achieve convergence. The number of particles used for the positively correlated and negatively correlated systems were 4158 and 3846 respectively. The number of particles was roughly doubled until the resultant RED between iterations differed by less than 1%.

### Wastewater reactor system

The wastewater reactor was modelled to mimic a UV system used in practice. Lamps were arranged in virtual (using a symmetry plane) \( 4 \times 4 \) banks, and included lamp supports. The flow direction was parallel to the lamps. The lamps were 1.5 m in length, had a diameter of 0.10 m, and formed a square grid with a spacing of 0.20 m between lamp centres. Lamps were spaced such that there was a 0.05 m water layer between the sides, top and bottom, as can be seen in Figure 3 (dashed lines represent symmetry.

**Table 3** | Positively and negatively correlated reactor geometry

<table>
<thead>
<tr>
<th>Feature</th>
<th>Correlation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reactor width</td>
<td>1.5 m</td>
</tr>
<tr>
<td>Lamp diameter</td>
<td>0.10 m</td>
</tr>
<tr>
<td>Inlet length</td>
<td>10 ( D_H )</td>
</tr>
<tr>
<td>Inter lamp length</td>
<td>10 ( D_H )</td>
</tr>
<tr>
<td>Lamp 1 top water layer</td>
<td>0.15 m</td>
</tr>
<tr>
<td>Lamp 1 bottom water layer</td>
<td>0.05 m</td>
</tr>
<tr>
<td>Lamp 2 top water layer</td>
<td>0.15 m</td>
</tr>
<tr>
<td>Lamp 2 bottom water layer</td>
<td>0.05 m</td>
</tr>
</tbody>
</table>
planes). The spacing between banks was left as a variable between 0.5 and 6 m, the effect of which will be discussed later. The meshing algorithm used adaptive refinement in order to give detail to the more complicated geometry features such as lamp supports (see Figure 4). Grid convergence was achieved with $3.9 \times 10^6$ tetra cells, and the minimum orthogonal quality was 0.18. Symmetry planes were used to model the open channel’s free surface and to create the virtual $4 \times 4$ lamp arrangement from a $2 \times 4$ lamp arrangement. The flow was turbulent such that the Reynolds number based on hydraulic diameter was greater than $10^5$. Convergence was achieved by injecting 9900 massless particles using the same criteria as the correlated systems.

**Drinking water reactor**

A drinking water reactor was modelled after a generic residential system with two units placed in series. Each unit had an annular configuration, with the lamp placed in the centre and parallel to flow. The lamp length was 0.4 m, the sleeve radius was 0.01 m and the wall radius was 0.04 m, as can be seen in Figure 5. Meshing was done using adaptive refinement on proximity and curvature, and inflation was used to give more detail near the walls and lamps; as shown in Figure 6. Grid convergence was achieved with $5.3 \times 10^5$ mixed tetra and hex cells, and the
minimum orthogonal quality was 0.14. The flow was turbulent with a Reynolds number greater than \(1.7 \times 10^4\) based on the reactor’s diameter. Convergence was achieved by injecting 2066 massless particles using the same criteria as the correlated systems.

**RESULTS AND DISCUSSION**

CFD models were created for the correlated systems, the wastewater reactor, and the drinking water reactor. In all cases, the RAF was calculated by computing the individual RED for one reactor (or bank), followed by the individual RED of the subsequent reactor, and then the RED of the total system and using Equation (2(b)). Additionally, the correlation between the two dose distributions was calculated. In this section, the results obtained are compared to the theoretical results presented by Lawryshyn & Hofmann (2015) with the intent of verifying them through numerical experiments.

**Correlated systems**

As discussed, two systems were modelled with configurations such that it was expected that one model would exhibit a positive correlation of dose paths between reactors, and the other model, negative. The predicted trends in correlation were observed, and the resultant REDs and RAFs are summarized in Table 4. RED\(_1\) and RED\(_2\) refer to the REDs of the individual reactors 1 and 2 respectively, and RED\(_{12}\) refers to the total RED of the system. Lamp power was adjusted in each system such that the first reactor in series would have a RED of 20 mJ/cm\(^2\) for a D\(_{10}\) of 10 mJ/cm\(^2\). It is important to note that in each case the dose histogram for the individual reactors is practically identical and it is difficult to distinguish between the superimposed histograms, as can be seen in Figure 7. Thus, one would expect the numerical results to match the theory of

![Figure 7](https://iwaponline.com/wqrj/article-pdf/52/2/79/378662/wqrjc0520079.pdf)
Lawryshyn & Hofmann (2015). With the exception of where the $D_{10}$ is 1 mJ/cm² (due to numerical instabilities), the RAF tends towards 1 as the $D_{10}$ increases, as is expected. For the positively and negatively correlated UV systems tested with MS2 ($D_{10} = 20$ mJ/cm²), the RAF when targeting adenovirus ($D_{10} = 46.5$ mJ/cm²) was calculated to be 1.16 and 1.57 respectively. This result is consistent with the theory presented by Lawryshyn & Hofmann (2015).

### Wastewater reactor system

An open channel reactor was modelled with a virtual 4×4 parallel flow lamp configuration. Two banks of lamps were placed in series as was discussed previously, and the distance between the two banks was adjusted to be between 0.5 and 6 m. Lamp power was adjusted such that the first bank in series would have a RED of 20 mJ/cm² for a $D_{10}$ of 10 mJ/cm². It was observed that the correlation between dose paths was positive and decreased almost to zero as the inter-bank length increased. The results of the RED and RAF analysis are summarized in Table 5. The dose distributions for reactor banks are virtually identical, as can be seen in Figure 8. Particle tracks coloured by velocity magnitude can be seen in Figure 9. The RAF tends towards 1 as $\rho$ approaches 0. When the reactor is validated for 1-log MS2, the RAFs on the 0.5, 3, and 6 m reactors are 1.08, 1.11, and 1.12 respectively, when adenovirus is assumed to be the target.

### Drinking water reactor system

Two single-lamp drinking water reactors were placed in series, and the effect was analysed. Lamp power was adjusted such that the first reactor in series would have a RED of 20 mJ/cm² for a $D_{10}$ of 10 mJ/cm². The results of the RED and RAF computation can be seen below in

<table>
<thead>
<tr>
<th>Inter-lamp length (m)</th>
<th>$D_{10}$ (mJ/cm²)</th>
<th>$\text{RED}_1$ (mJ/cm²)</th>
<th>$\text{RED}_2$ (mJ/cm²)</th>
<th>$\text{RED}_{12}$ (mJ/cm²)</th>
<th>RAF (mJ/cm²)</th>
<th>$\rho$</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.50</td>
<td>1.00</td>
<td>9.54</td>
<td>9.19</td>
<td>17.58</td>
<td>0.92</td>
<td>0.39</td>
</tr>
<tr>
<td>10.00</td>
<td>20.00</td>
<td>19.69</td>
<td>34.79</td>
<td>0.87</td>
<td>0.50</td>
<td></td>
</tr>
<tr>
<td>20.00</td>
<td>23.09</td>
<td>22.83</td>
<td>42.25</td>
<td>0.91</td>
<td>0.60</td>
<td></td>
</tr>
<tr>
<td>30.00</td>
<td>24.60</td>
<td>24.38</td>
<td>46.11</td>
<td>0.94</td>
<td>0.70</td>
<td></td>
</tr>
<tr>
<td>40.00</td>
<td>25.51</td>
<td>25.32</td>
<td>48.50</td>
<td>0.95</td>
<td>0.80</td>
<td></td>
</tr>
<tr>
<td>3.00</td>
<td>1.00</td>
<td>9.77</td>
<td>9.52</td>
<td>17.59</td>
<td>0.91</td>
<td>0.17</td>
</tr>
<tr>
<td>10.00</td>
<td>20.00</td>
<td>19.56</td>
<td>35.94</td>
<td>0.91</td>
<td>0.50</td>
<td></td>
</tr>
<tr>
<td>20.00</td>
<td>23.48</td>
<td>22.99</td>
<td>43.87</td>
<td>0.94</td>
<td>0.60</td>
<td></td>
</tr>
<tr>
<td>30.00</td>
<td>25.20</td>
<td>24.69</td>
<td>48.03</td>
<td>0.96</td>
<td>0.70</td>
<td></td>
</tr>
<tr>
<td>40.00</td>
<td>26.26</td>
<td>25.72</td>
<td>50.57</td>
<td>0.97</td>
<td>0.80</td>
<td></td>
</tr>
<tr>
<td>6.00</td>
<td>1.00</td>
<td>9.80</td>
<td>9.64</td>
<td>18.11</td>
<td>0.92</td>
<td>0.07</td>
</tr>
<tr>
<td>10.00</td>
<td>20.00</td>
<td>19.84</td>
<td>37.75</td>
<td>0.94</td>
<td>0.50</td>
<td></td>
</tr>
<tr>
<td>20.00</td>
<td>23.11</td>
<td>22.88</td>
<td>44.80</td>
<td>0.97</td>
<td>0.60</td>
<td></td>
</tr>
<tr>
<td>30.00</td>
<td>24.62</td>
<td>24.38</td>
<td>48.26</td>
<td>0.98</td>
<td>0.70</td>
<td></td>
</tr>
<tr>
<td>40.00</td>
<td>25.54</td>
<td>25.29</td>
<td>50.33</td>
<td>0.99</td>
<td>0.80</td>
<td></td>
</tr>
</tbody>
</table>

**Figure 8** | Wastewater reactor normalized dose histograms.

Downloaded from https://iwaponline.com/wqrj/article-pdf/52/2/79/378662/wqrj0520079.pdf
Table 6. The resultant dose distributions for the two reactors are unimodal and positively skewed, and can be seen in Figure 10. Particle tracks of the microbes traversing the reactor are shown in Figure 11. As would be expected for a near zero correlation, the RAF very rapidly approaches 1 as the $D_{10}$ increases. For the drinking water UV system tested with MS2, the RAF, when targeting adenovirus was calculated to be 1.07.

**CONCLUSIONS**

Three fundamentally different UV reactor configurations were analysed: the correlated systems, a wastewater reactor, and a drinking water reactor. For the correlated systems, it was shown through the numerical experiments that a strong positive correlation leads to a RAF less than one and that a strong negative correlation leads to a RAF greater than one. For both positively and negatively correlated systems, the RAF was shown to converge to unity as the $D_{10}$ increases. With the open-channel wastewater reactor it was shown that the correlation between dose paths is...
positive, and significant with respect to the RAF. The correlation decreased as the second bank was placed further downstream. The implication of this is that the proximity between banks should be considered when placing reactors in series and assuming additivity. Reactor banks should be placed as far apart as reasonably possible. A residential scale drinking water reactor was also modelled, and the correlation between dose paths was found to be near zero. The very low correlation justifies the additivity assumption for this reactor geometry. Finally, it was shown for all systems that additivity could be achieved when sizing was done based on MS2 validation and targeting adenovirus.

ACKNOWLEDGEMENTS

The authors are very grateful for the generous support of Ontario Centres of Excellence, Trojan Technologies, and the University of Toronto.

REFERENCES


United States Environmental Protection Agency 1989 National Primary Drinking Water Regulations; Giardia Lamblia, Viruses, and Legionella, Maximum Contaminant Levels, and Turbidity and Heterotrophic Bacteria (Surface Water...