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Bioaerosol Emissions: A Stochastic Approach

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1. Introduction

Several studies have shown that one of the main and uncontrollable mechanisms of bioaerosols dispersion is atmospheric transport (Casal et al., 1995; Daggupaty & Sellers, 1990; Donaldson et al., 2001; Lighthart & Frish, 1976; Lighthart & Kirilenko, 1998; Pillai & Ricke, 2002). This phenomenon can cause serious social and economic consequences, so the prediction of affected zones is very important for controlling epidemics and for avoiding economic losses.

Atmospheric micro-organism dispersion can come from natural origin as well as agricultural and industrial activities. Activities associated to waste treatment plants (liquid or solid), waste processing sites, compost plants, landfill, etc., can produce aerosols containing bacteria, viruses, fungi and odours (Buttner & Stetzenbach, 1991; Crawford & Jones, 1979; Pascual et al., 2003; Ranalli et al., 2000). They can cause serious health upsets on workers and people neighbouring these sites. As several studies about biologic risk evaluation have shown, the exposure to low levels of fine particles over an extended period of time greatly affects human health (Ackermann-Liebrich et al., 1999; Ebelt et al., 2000; Lippmann, 2007; U.S. EPA, 2004). Particles with diameter between 2.5 and 10 μm can enter the lungs, however, those with diameter less than or equal to 2.5 can reach the alveolus and enter directly into the bloodstream, causing consequences like light discomfort, allergic reactions, sinusitis, pulmonary infection and aggravate asthma.

Bioaerosol size particles can vary from 0.1 μm or less for viruses, to approximately 1 μm for simple bacteria; even though, in some cases, can be formed conglomeration of about 50 μm in diameter (Eduard, 2003; Wickman, 1994).

In other hand, several authors have remarked the importance of studying the propagation mechanism of animal epidemics like foot-and-mouth disease (FMD), one of the most important animal diseases (Casal et al., 1995-1997; Donaldson & Alexandersen, 2002; Donaldson et al., 2001; Thompson et al., 2002).

It is well known that bioaerosol multiplication and survival as well as downwind levels concentrations strongly depend on meteorological conditions like wind intensity, wind direction, temperature, humidity, and atmospheric stability, which are uncertain and specific of the place under study.

Airborne virus concentrations in FMD epidemic cases (Hampshire & Worcestershire - 1997) as well as micro-organism dispersion in rubbish dump, transference sites and municipal wastewater treatment plants, have been estimated using Gaussian models (Garner &

Beckett, 2005a; Gloster et al., 2010; Karra & Katsivela, 2007; Mikkelsen et al., 2003; Pascual et al., 2003; Sorensen et al., 2000). In many works algorithms developed for consequences analysis (gas diffusion) have been modified and used for bioaerosols diffusion simulations (Casal et al., 1995; Garner et al., 2005b; Holmes & Morawska, 2006; Sorensen et al., 2000).

Consequently, it is very important for managers to provide useful information about those activities that can potentially generate bioaerosols, considering the meteorological influence in the prediction of impacted areas.

So, in this chapter a methodology that takes into account the stochastic behaviour of atmospheric variables, which was successfully used for toxic gas release risk assessment, is adapted for the analysis of micro-organism spread.

Bacteria and fungi concentration distribution from a waste water treatment plant and the foot-and-mouth disease spread from an infected farm, are presented as study cases from this point of view, in a specific region of Argentine.

2. Dispersion models

2.1 Virus

The Gaussian model is recognized to be appropriate to estimate aerosols concentration consisting of particles of less than about 20 μm in diameter, released from a continuous point source (Sellers & Parker, 1969). In this size ranges, particles have the same behaviour as the gas which drags it, and the effect of atmospheric turbulence is more important than the gravitational deposition.

Also, considering the low virus concentration emitted from the source, it is accepted that the exhaled air has the same density as air does.

So, the basic equation of the Gaussian plume for a continuous emission placed at a height (h), following a two-dimension dispersion model is used. Reflection and thermal inversion are not considered. On the other hand, the chemical formation or aerosol dynamics (nucleation, coagulation, condensation, etc.) to evaluate particle processes occurring within the plumes are not modelled. Also, it is supposed that emission takes place on open plain areas not including the effect of obstacles such as mountains, trees or buildings which can cause a plume deviation, turbulence and dilution of the particle concentration.

So, according to these assumptions, the more important input parameters affecting pollutants dispersion are temperature, wind velocity, stability class, mixing height, horizontal and vertical dispersion parameters as well as seasonal variation. Frequency distributions of wind velocity, wind direction and stability class are included in the input files. Mixing height is computed as a function of the other meteorological parameters. The average concentration (given as ID_{50}[1]$/m^3$) at each point is given by means of the following equation:

$$\overline{C} = \frac{Q}{2\pi u \sigma_y \sigma_z} \exp\left[-\left(\frac{y^2}{2\sigma_y^2} + \frac{(z-h)^2}{2\sigma_z^2}\right)\right] \tag{1}$$

Where

$\overline{C}$ = Average infection dose at point x, y, z (ID_{50}/m^3)

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[1] ID_{50} (Infectious Dose 50%): the dose of a pathogen that will infect 50% of the population.

Q = Emission rate (ID_{50}/s)

h = Emission source height (m)

σ_y, σ_z = Dispersion coefficients (m)

x = Downwind distance from the source (m).

u = Wind speed (m/s).

The FMD emission rate is calculated considering a certain flow rate of exhaled air containing a given concentration of virus which depends on the different virus strain, species and the date and period of time of the infection (Casal et al., 1995; Donaldson et al., 2002; Kitching et al., 2005).

2.2 Bacteria

It is accepted that simple bacteria size range vary between 0.2 μm y 10 μm (Wickman, 1994) and for fungi spore between 4 μm y 20 μm. It is accepted that under this conditions, downwind concentration can be modelled through a Gaussian model, introducing a lethality factor or micro-organism death rate, to consider the bacteria viability.

Some works present experimental measurement of this factor (Lighthart & Frisch, 1976; Pascual et al., 2003; Santos Burgoa et al., 1992). Although the environmental conditions under micro-organism which are exposed in the "real world" are different from lab conditions (due to the atmospheric dynamic), these values are a good approximation of the lethality factors. So, atmospheric bacteria and fungi dispersion, for a point source and fixed meteorological conditions can be evaluated by means of the following equation:

$$\overline{C} = \frac{Q}{2\pi u \sigma_y \sigma_z} \exp\left(-\frac{fx}{u}\right) \exp\left[-\left(\frac{y^2}{2\sigma_y^2} + \frac{(z-h)^2}{2\sigma_z^2}\right)\right] \qquad (2)$$

$\overline{C}$ = Average concentration at point x, y, z (CFU^2/m^3)

Q = Emission rate (CFU/s)

h, σ_y, σ_z, u and x have the same meaning as in equation (1)

f = Lethality or death rate factor (s^{-1}).

For fungi particles, due to their major size, it must be considered particle deposition effects introducing the Stokes settling velocity (W_p), according to the following expression:

$$\overline{C} = \frac{Q}{2\pi u \sigma_y \sigma_z} \exp\left(-\frac{fx}{u}\right) \exp\left[-\left(\frac{y^2}{2\sigma_y^2} + \frac{\left(z-h-\frac{w_p x}{u}\right)^2}{2\sigma_z^2}\right)\right] \qquad (3)$$

When considering a background bioaerosol concentration, C_b, the total bioaerosol concentration C_B can be obtained as:

$$C_B = \overline{C} + C_b \qquad (4)$$

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[2] CFU (Colony-forming unit): the number of viable bacterial cells in a sample per ml.

3. Stochastic concentration levels and impact distances calculation methodology

3.1 Concentration distribution calculation

As previously stated, a Gaussian-type dispersion model is used to carry out simulations considering bioaerosol emission rate, release concentration and ground roughness as deterministic inputs. In addition, some atmospheric parameters within the model are considered by frequency distributions using a Monte Carlo strategy. In this way, a number of random scenarios are generated.

For fungi dispersion, the settling velocity is calculated as function of the scenario characteristics (particle diameter ranges, Reynolds number, spreading coefficients, etc.)

The proposed methodology is based on a simple representation of emitters and receptors (a squared grid) according to Godoy et al., 2007, 2010 and Scenna & Santa Cruz, 2005.

Every potential receptor is supposed to be placed in the geometrical centre of each grid square represented by the (X_j, Y_k) coordinates. Considering random scenarios, the expected micro-organism concentration at ground-level is calculated at every grid point (or receptor) applying the appropriate dispersion model (Eq. (1) to (3)). As a result, the approximation to the output concentration distribution or the critical concentrations levels (those exceeding the lethal/infectious threshold), are computed at each given grid point according to the input data distributions and the assumed specified (seasonal, annual, or other) time horizon. According to Eq. (4), a background concentration level (given by either a distribution or a single value) can be used if it is available.

Then, a map concentration identifying bioaerosol levels and critical areas (with potential health problems) can be plotted. Representative concentration values at each receptor $R_{jk}(X_j, Y_k)$ can be computed by taking the 90-percentile value of the concentration distribution.

Finally, using the same strategy, area sources are modelled as multiple point sources.

Summarizing, Fig. 1 shows the general implemented computational strategy which can be concise in the flowchart and presents the three basic modules the computational package STRRAP (Godoy et al., 2007, 2010; Scenna & Santa Cruz, 2005) has:

1. The pre-processor
2. The processor
3. The post-processor

The pre-processor module is in charge of the input file generation for the dispersion model. It reads the emission data included within a pattern file (micro-organism characteristics, emission rates, meteorological data, etc.) and then generates the random variable values. That is, it writes a file to be used by the processor or calculus module. After the time horizon (a season or the whole year) and the day or night condition are fixed, the values of the random variables (wind direction, wind velocity and atmospheric stability) are determined. Then, the processor module (using the appropriate dispersion model) computes the downwind bioaerosol concentration according to each trial previously defined by the pre-processor module.

The post-processor module stores and manages all trial results in the database and displays graphic results (for example, bioaerosol concentration and frequency maps, as well as affected zones).
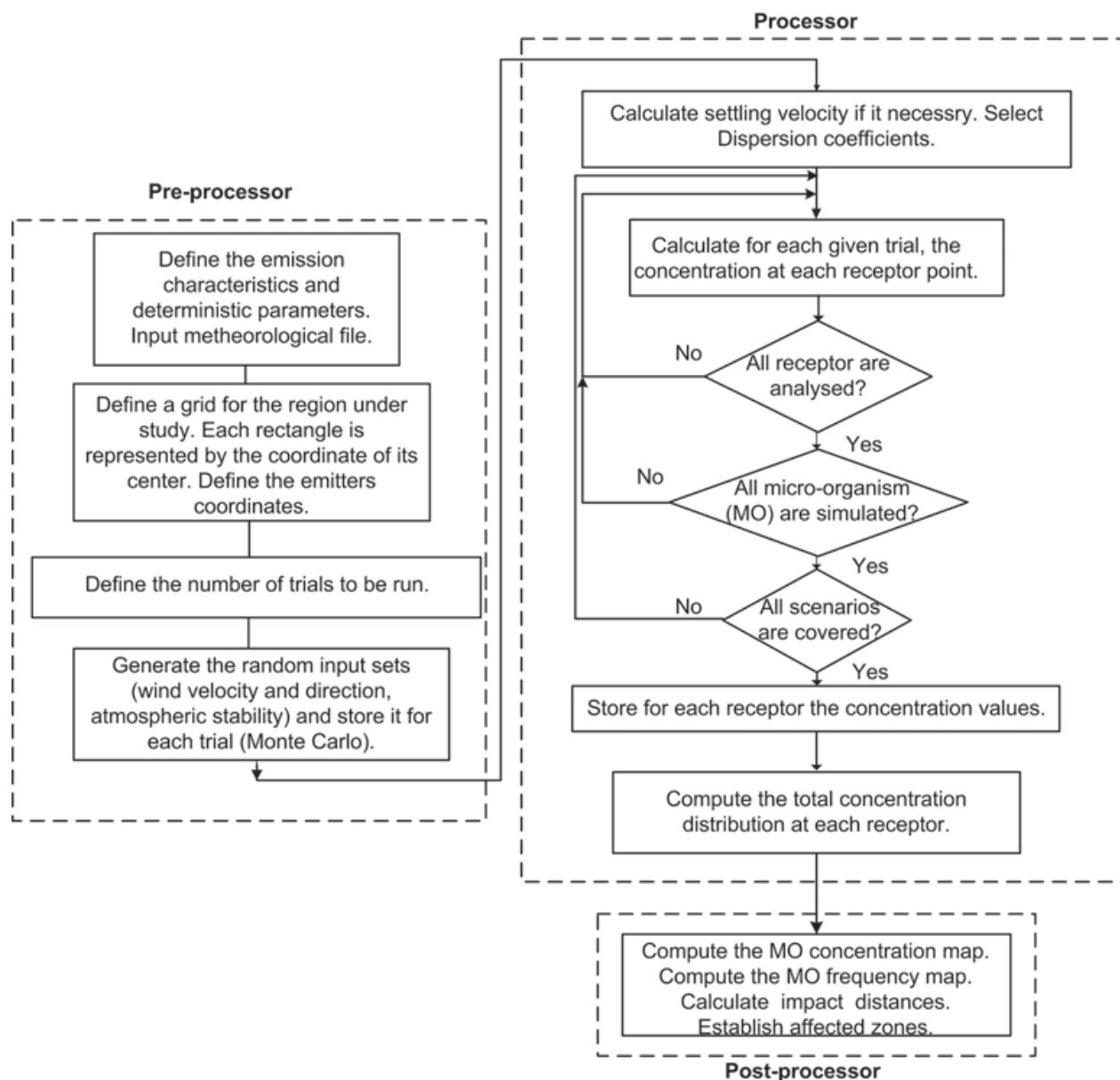
Fig. 1. System Calculus Steps

3.2 Statistically weighted impact distance definition

Considering the concentration distributions at each defined receptor point as explained in Section 3.1, and the micro-organism unhealthy concentration levels, we can determine the zones around the source where these critical concentrations levels are exceeded. For receptors where the limit concentration is exceeded, the distance between each affected receptor and the emission point/s can be computed. As a result, a distance frequency distribution is achieved.

In this way, we can calculate a statistically weighted impact distance (RI) by taking, for example, the maximum, or the 90 percentile as representative impact distance values. The unhealthy or critical area is defined here as a circle of radius RI (see Fig. 2). In fact, every receptor placed at a distance longer than RI can practically be considered as not affected.
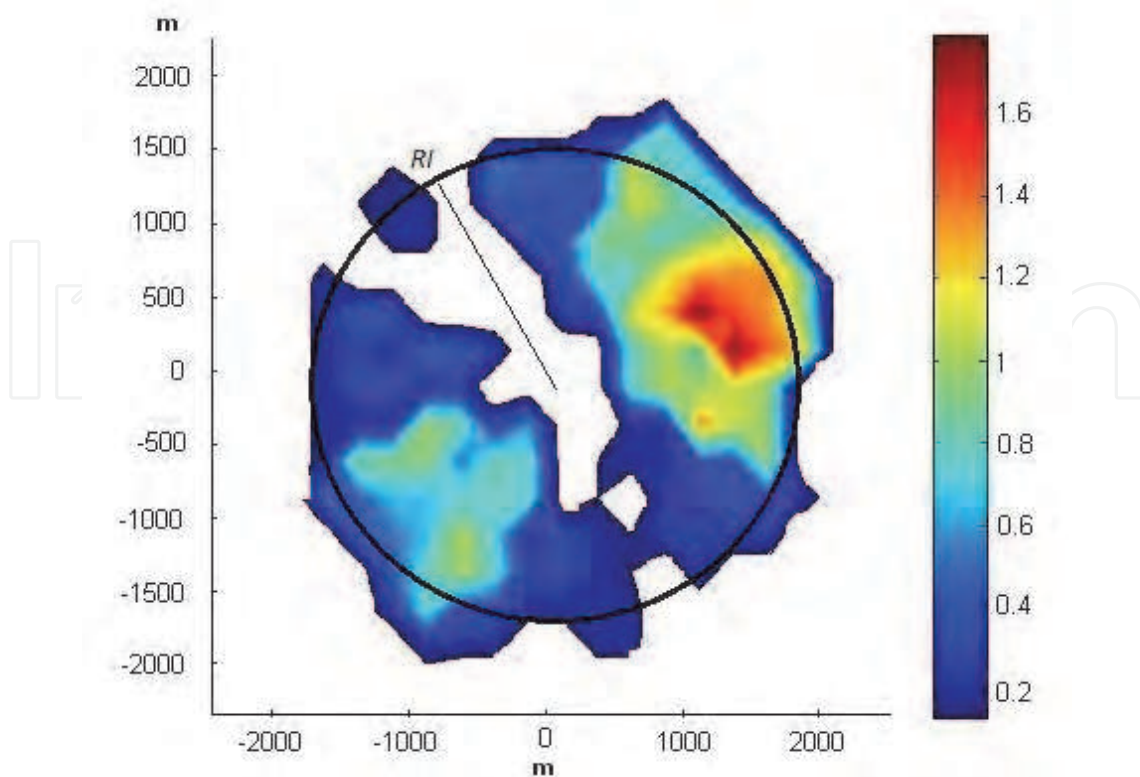
Fig. 2. Impact distance definition

4. Study cases

4.1 Bacteria, coliform and fungi dispersion

Different stages in effluent treatment plants are important bioaerosols sources (Cannon, 1983; Kenline & Scarpino 1972; Napolitano & Rowe, 1966); particularly, the aeration chambers at municipal waste water treatment plants (Brandi et al., 2000). So, bioaerosol emission from a sewage treatment plant near the city of Rosario is presented as a study case. The major potential pathogen micro-organism to study here are bacteria, total fungi, total coliforms, enterococcus and staphylococcus. Sometimes, gram-negative bacteria are studied. It is known that bioaerosols are subjected to certain conditions which can inhibit their biological activity (solar radiation, humidity, etc.), but some of them can survive in the unfavourable environmental conditions (Jones & Harrison, 2007; Karra & Katsivela, 2007, Korzeniewska et al., 2009). Mean temperature, pressure and humidity for the region under study are included in the input files. Indeed, wind velocity; wind direction and stability class distributions must be provided for this zone. Data collected over the last ten years are used in this work to obtain the histograms for each stochastic parameter. So, probability density functions which take into account the variability of the local meteorological conditions are used. As the local relative humidity is always higher than 75% in the selected time horizon, it is assumed a high bacteria survival. Also it is accepted that fungi are resistant to very low relative humidity. So, it is adopted a mean death rate factor of 5×10^{-5} micro-organism/s for all species (Barth, E., 2006; Brandi et al., 2000; Karra & Katsivela, 2007; Santos Burgoa et al., 1992). Although this is a very important factor in the downwind bioaerosol level concentration determination, there is a great uncertainty on experimental

data due to the lack of exhaustive studies considering different species and environmental parameters (Lighthart & Frisch, 1976; Lighthart et al. 1995).

Emission flowrates are taken from literature (Karra & Katsivela, 2007). Currently there are some uncertainties in this parameter but it is important to note that some expressions were exposed to reduce it (Swan et al., 2003). Background concentration for Salmonella, Coliforms and Aspergillus fumigatus are taken from Barth, 2006. The adopted density (Kg/m³) and particle diameter (μm) (Deacon et al., 2009) for fungi settling velocity calculation are shown in figure 5.

Here the health criteria values suggested by NIOSH, 1994 are adopted as shown in Table 1.

Micro-organism	Flowrate (CFU /s)	Background Conc. (CFU /m³)	Health criteria (CFU /m³)
Total Bacteria	$1.9 \; 10^6$	10	10^3
Total Coliforms	$2.0 \; 10^6$	5	10^3
Fungi	$2,5 \; 10^6$	2,1	10^3

Table 1. Simulation Parameters

Figures 3 to 5 summarize all input parameters to the model, according to the software input windows.
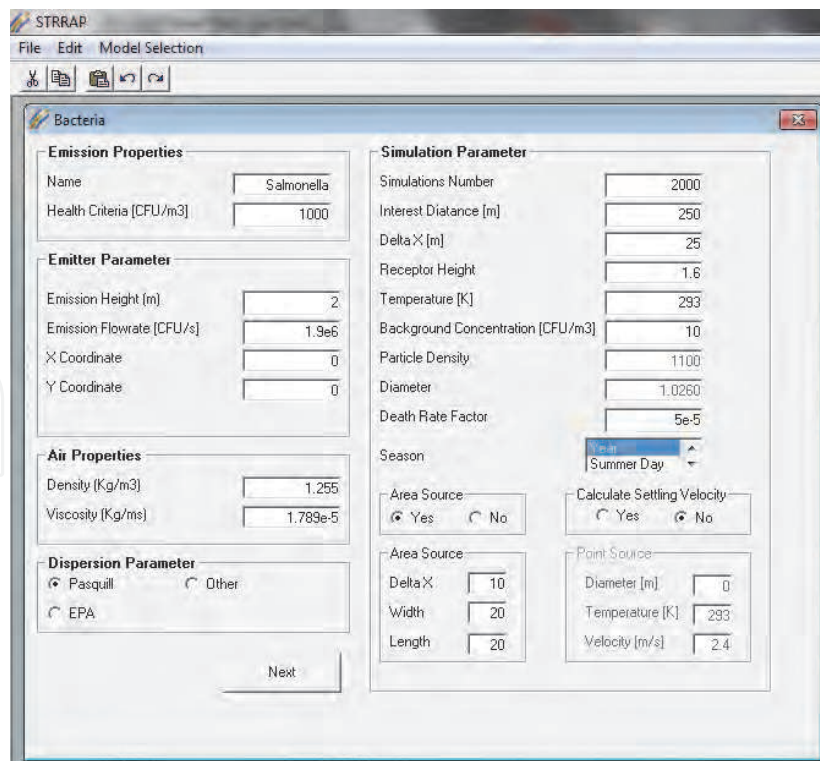

Fig. 3. Simulation parameters (Bacteria)

Fig. 4. Simulation parameters (Total Coliforms)

Fig. 5. Simulation parameters (Fungi)

After all simulations are performed (Monte Carlo method), assuming open plain areas, bioaerosol concentration distributions are obtained. Figures 6 to 8 show the estimated

colony-forming unit (CFU) maps of the evaluated species and their corresponding impact distances (*RI*). These were computed taking the 90 percentile of distance distributions as was explained in Section 3.2.
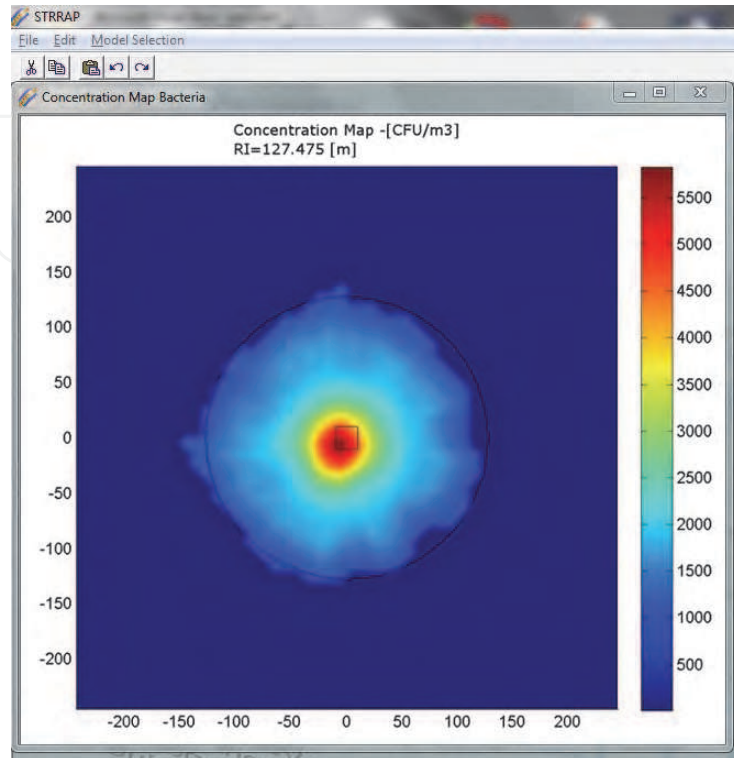

Fig. 6. Concentration map and impact distance (*RI*) for Bacteria
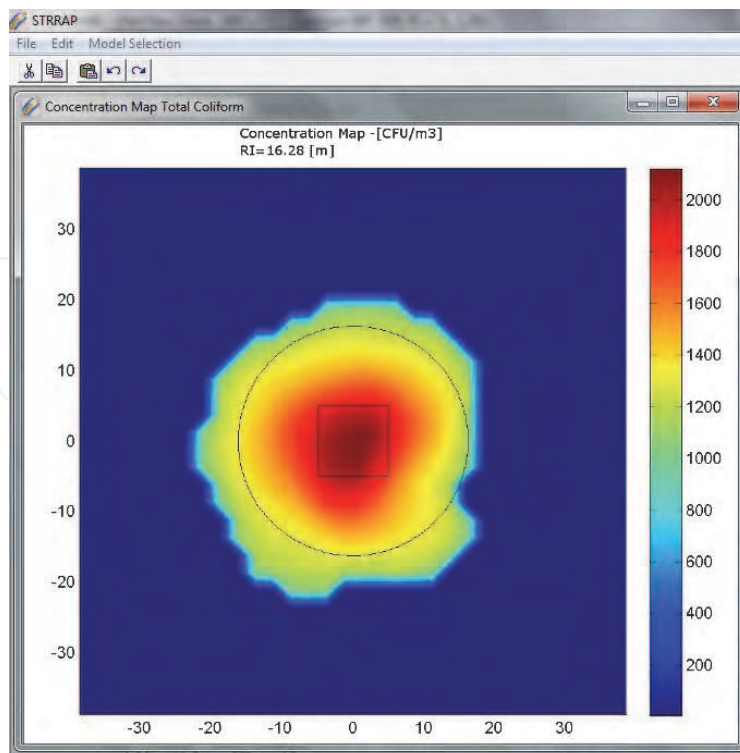
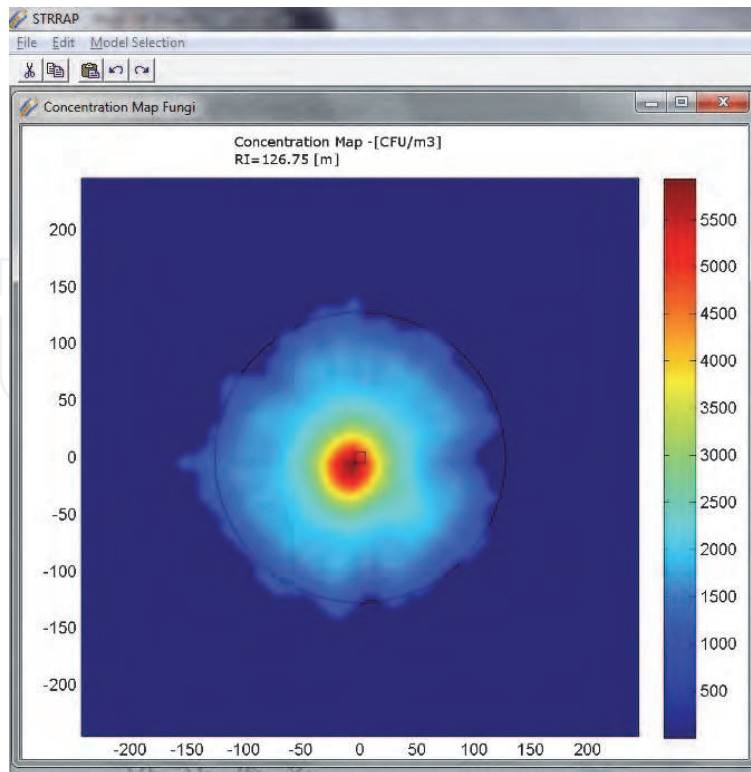Fig. 7. Concentration map and impact distance (*RI*) for Total Coliforms

Fig. 8. Concentration map and impact distance (*RI*) for Fungi

For bacteria, every receptor placed at a distance longer than 127.475 m can practically be considered as not affected. For coliforms and fungi, the receptors in a radius of 16.28 m and 126.75 m, respectively, could be seriously affected.

4.2 Virus dispersion

In this section we consider a hypothetical infected farm placed near Rosario city. The number of animals at the source, the virus strain and species affected have significant effect on the distance that virus can travel and still be infectious. Here it is supposed that there are 50 infected pigs with the FMD C Noville strain (Sorensen et al., 2000). The emission flowrate of FMD is calculated considering certain exhaled air flow by each infected animal with a given virus concentration while infection occurs. The adopted infectious units and respiratory rates for common farm animal are taken from literature as summarized in Table 2.

Here we define the impact zones considering the critical infection dose, which is capable to cause the infection on half of the sheep population of a neighbouring farm, because it is well known that sheep are the more vulnerable species (Kitching, 2005; Donaldson, 2002).

Source	Flow of infectious units (ID_{50}/min)	Respiratory rate (lt/min)
Pig	4×10^3	25
Cattle	85	100
Sheep	66	10

Table 2. Emission rate of FMD virus for common farm animals (Taken from Casal et al., 1995)

Table 3 shows the rest of simulation parameters required to define the model input files completely

Emission flowrate (ID_{50}/s)	3,333
Min. Concentration required to cause infection in sheep (ID_{50}/m^3)	6×10^{-2}
Number of simulation	2,000

Table 3. Simulation Parameters

After all simulations are performed (Monte Carlo method), virus concentration distributions around the infection source are computed as explained in previous Sections, considering critical concentration. So, the calculated impact distance value (90-percentile) is 3,005.2 m.
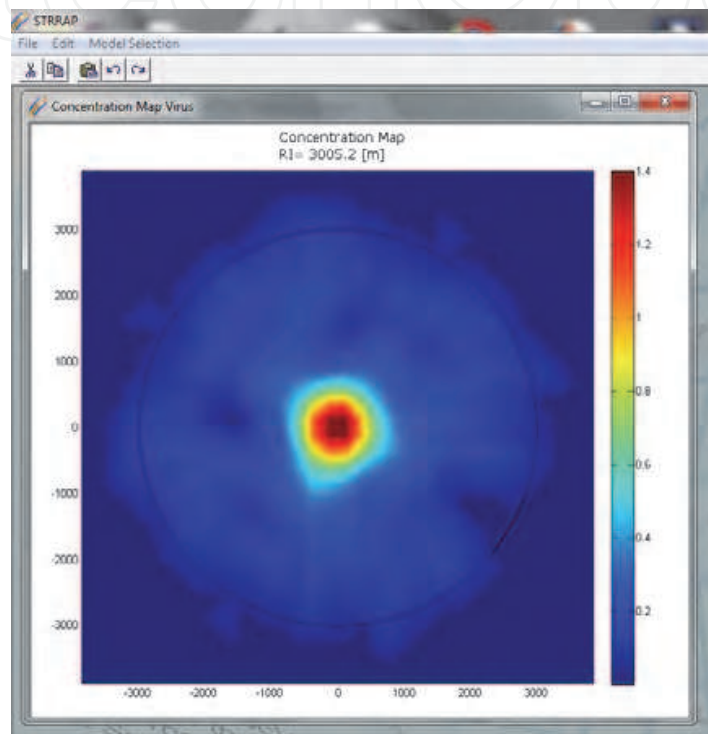

Fig. 9. Concentration map and impact distance (RI) for FMD

5. Conclusion

A methodology to compute stochastic air micro-organism concentration and impact distances due to bioaerosols emission from different sources is presented. The emission of bacteria and fungi at a sewage treatment plant, and an outbreak of FMD virus at a hypothetical infected farm are studied. The model considers variability of meteorological conditions. If micro-organism death rate factor as a function of temperature and relative humidity were available, it would be included in the different scenarios generation. In both cases map concentration and impact distances are obtained.

It is important to note that uncertainty was found in some data reported in the literature, such as the excretion rate, the infectious dose of different species and death rate factor, critical for an accurate prediction.

Furthermore, it must be remarked that only atmospheric transport mechanism were considered. Other complex physicochemical mechanism involved can affect the estimations significantly. Also, in FMD virus spread the movement of animals, people and articles may increase the infected area determined by this methodology.

Despite of the fact that bioaerosols threshold levels are a complex topic and nowadays is under discussion, it is very important to develop tools capable of predicting stochastic bioaerosol level dispersion and to determine the affected zones, with the aim of avoiding environmental and health population risks.

6. Acknowledgment

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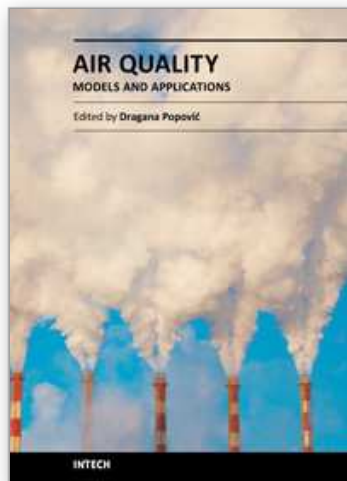
Air Quality-Models and Applications

Edited by Prof. Dragana Popovic

Air pollution has been a major transboundary problem and a matter of global concern for decades. High concentrations of different air pollutants are particularly harmful to large cities residents, where numerous anthropogenic activities strongly influence the quality of air. Although there are many books on the subject, the one in front of you will hopefully fulfill some of the gaps in the area of air quality monitoring and modeling, and be of help to graduate students, professionals and researchers. The book is divided in five sections, dealing with mathematical models and computing techniques used in air pollution monitoring and forecasting; air pollution models and application; measuring methodologies in air pollution monitoring and control; experimental data on urban air pollution in China, Egypt, Northeastern U.S, Brazil and Romania; and finally, the health effects due to exposure to benzene, and on the influence of air pollutants on the acute respiratory diseases in children in Mexico.

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