

TRAIN COMPARTMENT AIR ADJUSTMENT AND CONTROL METHOD AND APPARATUS, AND STORAGE MEDIUM, AND PROGRAM PRODUCT

FIELD OF THE INVENTION

The present invention relates to the field of train environment monitoring, in particular to a train compartment air adjustment and control method and apparatus, a storage medium, and a program product.

BACKGROUND OF THE INVENTION

With continuous development of China's rail transit industry, comfort requirements of passenger trains have gradually been concerned by the public. As affected by the air pressure wave, proper pressure difference between inside and outside of a train compartment is required during high-speed running, so a high-speed train usually has a sealed body structure, and all windows cannot be opened. In this case, treatment of air pollutants inside the compartment entirely depends on a ventilation system. Therefore, quality and adjustment strategies of the ventilation system will directly affect passenger comfort. Thus, how to monitor a train environment and correspondingly adjust the ventilation system has become an urgent problem to be solved.

The prior art for environment control of train compartments mainly involves the following two aspects:

1. Installation of a novel air quality detection apparatus and a purification apparatus is proposed. For example, patent application with Publication No. CN101885338A provides an intelligent sampling, detecting and air purification apparatus for a train air conditioning and ventilation system, including a variable frequency cyclone dust catcher, a high efficiency filter, and the like. Patent application with Publication No. CN105172818A provides a special air purifier for a train, including an upper box body and a lower box body matched with the upper box body.
2. A compartment environment adjustment method based on air pollutant detection is proposed. Patent application with Publication No. CN110239577A provides a system and method for protecting train crew members' health in an internal contamination

environment, the system including a basic data acquisition module, a train external air quality prediction module, a train internal air quality prediction module, and a ventilation strategy formulation module. Patent application with Publication No. CN104608785A provides an intelligent management and control method for an air conditioning system of a high-speed train.

The above methods mainly use the concentration of air pollutants such as $PM_{2.5}$ inside a train as the basis for air quality evaluation. However, the prior art does not concern harm of biological contamination in an air environment to human health. At present, no relevant research focuses on biological pollutants in a closed environment of a train compartment. Moreover, because a measurement mechanism for microorganisms is different from that for pollutants such as $PM_{2.5}$, microbial measurement requires long-term colony culture, while direct detection and real-time adjustment and control of microbial are difficult.

SUMMARY OF THE INVENTION

The technical problem to be solved by the present invention is, aiming at the deficiencies of the prior art, to provide a train compartment air adjustment and control method and apparatus, a storage medium, and a program product, where optimal-level protection measures are implemented for passenger health according to microbial distribution in a compartment.

In order to solve the foregoing technical problem, the technical solution employed by the present invention is as follows: a train compartment air adjustment and control method, wherein the method including the following steps:

- 1) detecting $PM_{2.5}$ concentration, PM_{10} concentration, CO concentration, NO_2 concentration, SO_2 concentration, O_3 concentration, and the total number of bacterial colonies at an air supply port, an air exhaust port and a seat of a train;
- 2) establishing, according to the $PM_{2.5}$ concentration, PM_{10} concentration, CO concentration, NO_2 concentration, SO_2 concentration, O_3 concentration, and the total number of bacterial colonies at each detection point in a compartment, a mapping relationship between the total number of bacterial colonies D and the concentration of

air pollutants d in each micro environmental unit, where the micro environmental unit is the detection point;

3) selecting a measured air pollutant concentration data set with a time length of N minutes, calculating the total number of bacterial colonies according to the mapping relationship, denoting a time series of the total number of bacterial colonies at the i^{th} seat as X_N^i , denoting a time series of the total number of bacterial colonies at the j^{th} air supply port or air exhaust port as Y_N^j , performing hypothesis test by using Granger causality test to determine whether there is causality between X_N^i and Y_N^j , and then obtaining a test result set of m air supply ports and n air exhaust ports at each seat detection point;

4) obtaining a nonlinear description model base of all seat detection points according to the mapping relationship and the test result set; and

5) inputting ventilation rates of all air supply ports and all air exhaust ports of the train to a grey wolf optimizer, calculating fitting results of the total number of bacterial colonies at the air supply ports/air exhaust ports under different ventilation rates, inputting the fitting results to the nonlinear description model base to obtain a fitting result of the total number of bacterial colonies at each seat, and determining the ventilation rates of all the air supply ports and all the air exhaust ports by using the fitting result of the total number of bacterial colonies at each seat.

According to the present invention, the mapping relationship between microbial contamination and air pollutant concentration in the compartment is studied, and optimal protective measures for passenger health are implemented in real time according to microbial distribution in the compartment. Microorganisms in the train compartment are detected, analyzed and treated, and the ventilation system is adjusted according to the microbial distribution among the detection points, thereby reducing microbial contamination in a passenger area. The method has a guide effect on air quality adjustment and control of a railway train.

In step 2), a specific implementation process of establishing a mapping relationship between the total number of bacterial colonies D and the concentration of air pollutants

d in each micro environmental unit includes:

A, reading an index data set of air pollutant concentration and total number of bacterial colonies of the current micro environmental unit at M consecutive historical moments, and dividing the index data set into a training set and a test set;

B, constructing a microorganism-air pollutant model by using a deep belief network, and training the deep belief network by using the air pollutant concentration and the total number of bacterial colonies at the same moment respectively as input and output of the deep belief network;

C, using the test set as input of the trained deep belief network, and selecting a group of parameters with highest description accuracy on the test set as a microorganism-air pollutant mapping model of the micro environmental unit; and

D, repeating steps A-C for all the micro environmental units to obtain mapping relationships between the total number of bacterial colonies and the air pollutants of $m + n + p$ detection points, where m , n , and p are numbers of detection points at the air supply ports, the air exhaust ports, and the seats respectively.

The present invention studies the mapping relationship between microbial contamination and air pollutant concentration, which can effectively solve a real-time problem of microbial detection and ensure real-time adjustment and control on microbial contamination in train compartments.

In step 3), the test result set is $\varphi_i = \{T_{i,1}^{in}, T_{i,2}^{in}, \dots, T_{i,m}^{in}, T_{i,1}^{out}, T_{i,2}^{out}, \dots, T_{i,n}^{out}\}$, where $T_{i,j}^{in}$ is a test result of the air supply port, $T_{i,j}^{in} = GCT(X_N^i, Y_N^j)$, $T_{i,j}^{out}$ is a test result of the air exhaust port, and $T_{i,j}^{out} = GCT(X_N^i, Y_N^j)$; and value of the test result $T_{i,j}^{in/out}$ (i.e., $T_{i,j}^{in}$ and $T_{i,j}^{out}$) is 0 or 1.

According to the method of the present invention, by performing causality test on microbial time series data between different detection points, detection points closely related to passenger seats are further selected for subsequent modeling, and spatial dimensions of the detection points are compressed, making the provided data features have strong representation ability.

A specific implementation process of step 4) includes:

I) reading $PM_{2.5}$ concentration, PM_{10} concentration, CO concentration, NO_2 concentration, SO_2 concentration, and O_3 concentration at the seats, the air supply ports, and the air exhaust ports at P consecutive historical moments, and calculating the total number of bacterial colonies at each detection point at the P consecutive historical moments according to the mapping relationship;

II) reading the total number of bacterial colonies at the i^{th} seat detection point $O_i = [S_i^{seat}]_t$ and the total number of bacterial colonies at the air supply port and the air exhaust port which have causality with the i^{th} seat detection point $I_i = [S_j^{in/out}, \text{ s.t. } T_{i,j}^{in/out} = 1]_t$, where S_j^{in} is the total number of bacterial colonies at the air supply port, S_j^{out} is the total number of bacterial colonies at the air exhaust port, $S_j^{in/out}$ represents S_j^{in} or S_j^{out} , and $T_{i,j}^{in/out}$ represents $T_{i,j}^{in}$ or $T_{i,j}^{out}$;

III) using I_i as input of a deep echo state network and O_i as output of the deep echo state network, and learning the corresponding relationship between the total number of bacterial colonies at the seat and the total number of bacterial colonies at the air supply port/air exhaust port at different historical moments; and

IV) repeating steps I) to III) for all the seat detection points to obtain the nonlinear description model base of all the seat detection points, where the nonlinear description model base is a set of corresponding relationships of the total number of bacterial colonies at all the seat detection points and the total number of bacterial colonies at the air supply ports/air exhaust ports.

The present invention uses a deep neural network to describe the nonlinear mapping relationship between microorganism and air pollutant concentrations and between microorganism at seat and microorganism at air support port/air exhaust port, thereby ensuring description accuracy.

In step 5), a specific implementation process of calculating fitting results of the total number of bacterial colonies at the air supply ports/air exhaust ports under different ventilation rates includes:

i) increasing the ventilation rate by a fixed value and measuring the total number of bacterial colonies under the corresponding ventilation rate;

ii) performing least square fitting on the total number of bacterial colonies at the k^{th} air supply port/air exhaust port to obtain a polynomial expression of the total number of bacterial colonies $\hat{S}_k$ with respect to the ventilation rate v_k ; and

iii) repeating steps i) and ii) for all the air supply ports and all the air exhaust ports, to obtain a polynomial fitting result $\{\hat{S}_k | k=1,2,3,\dots,m+n\}$ of the total number of bacterial colonies at all the air supply ports and all the air exhaust ports varying with the ventilation rate, where m and n are numbers of detection points at the air supply ports and the air exhaust ports respectively.

In step 5), an optimization objective is set to simultaneously minimize the fitting result of the total number of bacterial colonies at each seat, and an optimization function is

$$\begin{aligned} \min \quad & \{\hat{S}_1, \hat{S}_2, \dots, \hat{S}_k, \dots, \hat{S}_{m+n}\} \\ \text{s.t.} \quad & \hat{S}_k = g(v_k), l_k \leq v_k \leq u_k \end{aligned}$$

The present invention uses a multi-objective optimization method to minimize the total number of bacterial colonies at each seat, so that the degree of microbial contamination in the passenger area reaches overall optimum, and secondary contamination in some areas caused during the adjustment process of the ventilation system is avoided.

In step 5), a non-dominated solution $NS^* = \arg \min E$, which minimizes an evaluation

$$\text{index } E = \sum_{k=1}^{m+n} \hat{S}_k + \text{Var}(\hat{S}),$$

is selected for determining the ventilation rates NS^* of all

the air supply ports and all the air exhaust ports, wherein $\text{Var}(\hat{S})$ is a variance of the total number of bacterial colonies at all the seats in the test set, and u_k and l_k are an upper limit and a lower limit of the ventilation rate v_k at the k^{th} air supply port/air exhaust port respectively.

The evaluation index is a combination of a cumulative fitting result and the variance of the total number of bacterial colonies at all the seats, where the cumulative fitting result of the total number of bacterial colonies at all the seats represents a degree of microbial contamination after ventilation adjustment and control, and the variance represents a

degree of dispersion of microbial contamination among the seats. Selecting the non-dominated solution that minimizes the evaluation index may ensure: (1) the overall degree of microbial contamination in the compartment is minimal; and (2) the difference of microbial contamination among the seats is minimal, so as to avoid extreme contamination in some area/areas.

The present invention further provides a computer apparatus, including a memory, a processor, and a computer program stored on the memory, wherein the processor executes the computer program to implement the steps of the train compartment air adjustment and control method of the present invention.

As an inventive concept, the present invention further provides a computer-readable storage medium, storing a computer program/instruction. When the computer program/instruction is executed by a processor, the steps of the train compartment air adjustment and control method of the present invention are implemented.

As an inventive concept, the present invention further provides a computer program product, including a computer program/instruction. When the computer program/instruction is executed by a processor, the steps of the train compartment air adjustment and control method of the present invention are implemented.

Compared with the prior art, the present invention has the following beneficial effects:

- 1) According to the present invention, microorganisms in a train compartment are tested, analyzed and treated, and a ventilation system adjustment is carried out according to microbial diffusion among detection points, thereby reducing the microbial contamination index in a passenger area. The method has a guide effect on railway train air quality adjustment and control.
- 2) The present invention studies a mapping relationship between microbial contamination and air pollutant concentration, which can effectively solve a real-time problem of microbial detection and ensure a implementation of real-time adjustment and control on microbial contamination in train compartments .
- 3) The present invention uses a comprehensive detection manner of multiple detection points at air supply ports, air exhaust ports and seats, which can effectively describe diffusion of air pollutants and microorganisms in the internal environment of

compartments and ensure authenticity of depiction of actual spatial distribution by the test results.

4) According to the method of the present invention, causality test is performed on microbial time series data among different detection points, detection points closely related to passenger seats are further selected for subsequent modeling, and spatial dimensions of the detection points are compressed, making the provided data features have strong representation ability.

5) The present invention uses a deep neural network to describe a nonlinear mapping relationship between microorganism and air pollutant concentrations and between microorganisms at seat and microorganisms at air supply port/air exhaust port, thereby ensuring description accuracy.

6) The present invention uses a multi-objective optimization method to minimize the total number of bacterial colonies at each seat, so that the degree of microbial contamination in the passenger area reaches overall optimum, and secondary contamination in some areas caused during the adjustment process of the ventilation system is avoided.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a flowchart of a method of the present invention.

DETAILED DESCRIPTION OF THE EMBODIMENTS

As shown in FIG. 1, a specific implementation process of an embodiment of the present invention is as follows:

Step 1: collection of contamination data at multiple detection points

The interior contamination of a train compartment includes six air pollutants which are PM_{2.5}, PM₁₀, CO, NO₂, SO₂, and O₃, as well as microbial contamination such as bacteria, fungi, and viruses. Microorganisms are closely related to air quality. Generally, the total number of bacterial colonies in air is positively correlated with probability of existence of pathogenic microorganisms (bacteria, fungi and viruses). Therefore, this patent application measures the pathogenicity of microorganisms by the total number of

bacterial colonies as an index. TS WES-C air pollutant detectors (for measuring PM_{2.5} concentration, PM₁₀ concentration, CO concentration, NO₂ concentration, SO₂ concentration, and O₃ concentration in real time) and Anderson impaction air microbial samplers (for measuring the total number of bacterial colonies, which requires 48h microbial culture) are arranged at multiple air supply ports, air exhaust ports, and seats of the train compartment.

Obtained data includes PM_{2.5} concentration, PM₁₀ concentration, CO concentration, NO₂ concentration, SO₂ concentration, O₃ concentration, and the total number of bacterial colonies at the air supply ports, the air exhaust ports, and the seats, which may be expressed as

$$d(i) = [C(i)_1^{in}, C(i)_2^{in}, \dots, C(i)_m^{in}, C(i)_1^{out}, C(i)_2^{out}, \dots, C(i)_n^{out}, C(i)_1^{seat}, C(i)_2^{seat}, \dots, C(i)_p^{seat}]_T$$

$$\text{and } D = [S_1^{in}, S_2^{in}, \dots, S_m^{in}, S_1^{out}, S_2^{out}, \dots, S_n^{out}, S_1^{seat}, S_2^{seat}, \dots, S_p^{seat}]_T, \text{ where } C(i)_m^{in}$$

represents the concentration of air pollutants at the m^{th} air supply port, $C(i)_n^{out}$ represents the concentration of air pollutants at the n^{th} air exhaust port, $C(i)_p^{seat}$ represents the concentration of air pollutants at the p^{th} seat, S_m^{in} represents the total number of bacterial colonies at the m^{th} air supply port, S_n^{out} represents the total number of bacterial colonies at the n^{th} air exhaust port, S_p^{seat} represents the total number of bacterial colonies at the p^{th} seat, i represents six air pollutants PM_{2.5}, PM₁₀, CO, NO₂, SO₂, and O₃, and m , n and p are numbers of detection points at the air supply port, the air exhaust port and the seat respectively. Each detection point is regarded as a micro environmental unit, detection data correspond to compartment numbers, time stamps of the detection data are recorded, and an interval between adjacent data is 5 minutes. The collected data is transmitted to a data storage platform in a 4G manner.

Step 2: learning of microorganism-air pollutant mapping relationship

According to historical contamination data of compartment detection points, a model is built to learn a mapping relationship between the total number of bacterial colonies D and the concentration of air pollutants d in each micro environmental unit. A specific modeling process is as follows:

A1: a micro environmental unit is selected, and a data set of air pollutant concentration

and total number of bacterial colony indexes of the micro environmental unit in 200 consecutive historical moments is read.

A2: the data set is divided. The foregoing data set includes 200 consecutive historical moments, data of 1-160 moments are used as a training set, and data of 161-200 moments are used as a test set.

A3: a microorganism-air pollutant model is constructed by using a deep belief network, the air pollutant concentration and the total number of bacterial colonies at the same moment are respectively used as input and output of the deep belief network. Layers of the deep belief network are determined by 5-fold cross-validation, and are selected in a range of [1, 2, 3, 4, 5].

A4: the trained deep belief network is tested with the test set, and a group of parameters with highest description accuracy on the test set is selected as a microorganism-air pollutant mapping model of the micro environmental unit.

A5: Steps A1 to A4 are carried out for all micro environmental units (i.e., detection points), to obtain mapping relationships $\{D=f(d)|i=1,2,3,\dots,m+n+p\}$ between the total number of bacterial colonies and the air pollutants of $m+n+p$ detection points, where f represents the mapping relationship.

Step 3: testing on causality among detection points based on microbial diffusion mechanism

Spatial distribution and diffusion of microorganisms in compartments are affected by air movement, and there is causality among the total number of bacterial colonies at the detection points. For each compartment, causality between time series of the total number of bacterial colonies at each seat and each air supply port or air exhaust port is analyzed.

A measured air pollutant concentration data set with a time length of N minutes is selected, the total number of bacterial colonies is calculated according to the mapping relationship obtained in step 2. A time series of the total number of bacterial colonies at the i^{th} seat is denoted as X_N^i , a time series of the total number of bacterial colonies at the j^{th} air supply port or air exhaust port is denoted as Y_N^j , and hypothesis test is performed

by using Granger causality test (GCT) to determine whether there is causality between X_N^i and Y_N^j . Test result $T_{i,j}^{in/out}$ is output as 0 or 1, wherein 0 represents that there is no causality between the time series X_N^i of the total number of bacterial colonies at the seat and the time series Y_N^j of the total number of bacterial colonies at the air supply port/air exhaust port, while 1 represents that there is causality:

$$T_{i,j}^{in/out} = GCT(X_N^i, Y_N^j)$$

$GCT()$ represents Granger causality test. A test result set of m air supply ports and n air exhaust ports at each seat detection point is obtained:

$$\varphi_i = \{T_{i,1}^{in}, T_{i,2}^{in}, \dots, T_{i,m}^{in}, T_{i,1}^{out}, T_{i,2}^{out}, \dots, T_{i,n}^{out}\}$$

Step 4: nonlinear description of causality among detection points modeling

For each seat detection point, a nonlinear description model for an air supply port/air exhaust port related to the seat detection point is built. A specific modeling process is as follows:

B1: $PM_{2.5}$ concentration, PM_{10} concentration, CO concentration, NO_2 concentration, SO_2 concentration, and O_3 concentration at the seats, the air supply ports, and the air exhaust ports at 100 consecutive historical moments are read, and the total number of bacterial colonies at each detection point at the 100 consecutive historical moments is calculated according to the mapping relationship obtained in step 2.

B2: a data set is divided. The data set includes data at 100 consecutive historical moments, data of 1-60 moments are used as a training set, data of 61-80 moments are used as a validation set, and data of 81-100 moments are used as a test set.

B3: the total number of bacterial colonies at the i^{th} seat detection point $O_i = [S_i^{seat}]_t$ and the total number of bacterial colonies at the air supply port and the air exhaust port which have causality with the i^{th} seat detection point $I_i = [S_j^{in/out}, \text{ s.t. } T_{i,j}^{in/out} = 1]_t$ are read, where S_j^{in} is the total number of bacterial colonies at the air supply port, S_j^{out} is the total number of bacterial colonies at the air exhaust port, $S_j^{in/out}$ represents S_j^{in} or S_j^{out} , and $T_{i,j}^{in/out}$ represents $T_{i,j}^{in}$ or $T_{i,j}^{out}$.

B4: a nonlinear description model is constructed by using a deep echo state network, with model input I_i and model output O_i , so as to learn a corresponding relationship between the total numbers of bacterial colonies at the seat and the total numbers of bacterial colonies at the air supply port/air exhaust port at different historical moments. The number of reservoir nodes in the deep echo state network is set to 10. The number of reservoir layers and a spectral radius of a reservoir matrix at each layer are determined by 5-fold cross-validation, where the two parameters are selected in ranges of $[1, 2, 3, \dots, 10]$ and $[0.1, 0.3, 0.5, 0.7, 0.9]$ respectively. A trained nonlinear description model $h(I_i)$ is obtained by selecting a group of parameters with highest description accuracy on the validation set.

B5: steps A1 to A4 are carried out for all seat detection points, to obtain a nonlinear description model base $\{h(I_i)|i=1,2,3,\dots,p\}$ of all the seat detection points.

Step 5: compartment ventilation adjustment strategies based on multi-objective optimization

C1: a total number of bacterial colonies at all the air supply ports/air exhaust ports changing with ventilation rate is measured according to the following steps:

1) The ventilation rate is increased by a fixed value, the total number of bacterial colonies under the corresponding ventilation rate is measured, and data are recorded in a data storage platform in a format of time stamp-ventilation rate-total number of bacterial colonies.

2) Least square fitting is performed for the k^{th} air supply port/air exhaust port to obtain a polynomial expression of the total number of bacterial colonies $\hat{S}_k$ with respect to the ventilation rate v_k :

$$\hat{S}_k = g(v_k)$$

3) The above steps are repeated for all the air supply ports and all the air exhaust ports to obtain a polynomial fitting result $\{\hat{S}_k|k=1,2,3,\dots,m+n\}$ of the total number of bacterial colonies at all the air supply ports and all the air exhaust ports changing with the ventilation rate.

C2: A multi-objective optimization model is built. Specific implementation details are

as follows:

1) An optimizer is selected and initial super parameters are set: multi-objective grey wolf optimizer is used, and a leader selection mechanism and an archive storage mechanism are embedded to improve convergence ability (MIRJALILI S, SAREMI S, MIRJALILI S M, et al. Multi-objective grey wolf optimizer [J]. Expert Systems With Applications, 2016, 47: 106-19.). A number of search populations, a maximum number of iterations, and an archive size of the multi-objective grey wolf optimizer are set to 200, 100, and 50 respectively.

2) An optimization variable is the ventilation rate v at all the air supply ports and all the air exhaust ports, and the search range of the variable satisfies the following formula:

$$l_k \leq v_k \leq u_k$$

u_k and l_k are an upper limit and a lower limit of the ventilation rate at the k^{th} air supply port/air exhaust port respectively.

3) According to the polynomial fitting method of the total number of bacterial colonies at the air supply ports and the air exhaust ports changing with the ventilation rate obtained in C1, fitting results of the total number of bacterial colonies at the air supply ports/the air exhaust ports under different ventilation rates are calculated. The total number of bacterial colonies is input to the non-linear description model base of the seat detection points obtained in B5, to output a fitting result of the total number of bacterial colonies at each seat. An optimization objective is set to simultaneously minimize the fitting result of the total number of bacterial colonies at each seat, and an optimization function is:

$$\begin{aligned} \min \quad & \{\hat{S}_1, \hat{S}_2, \dots, \hat{S}_k, \dots, \hat{S}_{m+n}\} \\ \text{s.t.} \quad & \hat{S}_k = g(v_k), l_k \leq v_k \leq u_k \end{aligned}$$

4) Multi-objective optimization (MIRJALILI S, SAREMI S, MIRJALILI S M, et al. Multi-objective grey wolf optimizer [J]. Expert Systems With Applications, 2016, 47: 106-19.) is performed, and the number of iterations $Iter = 1$ is recorded. Optimization function values of all search results are calculated, and non-dominated solutions are archived.

- 5) Search paths are updated to generate new ventilation rate search results.
- 6) The number of searches is $It = It + 1$. If the updated It is less than the maximum number of iterations, return to step4); otherwise, the multi-objective optimization algorithm ends, and a non-dominated solution set NS in the final archive is output.
- 7) Performance of the non-dominated solutions on the test set is evaluated, where the evaluation index is a combination of a cumulative fitting result of the total number of bacterial colonies at all the seats and a variance (Var):

$$E = \sum_{k=1}^{m+n} \hat{S}_k + Var(\hat{S})$$

A non-dominated solution $NS^* = \arg \min E$, which minimizes the evaluation index, is selected for determining the ventilation rates of all the air supply ports and all the air exhaust ports

Step 6: after ventilation adjustment of the train compartments according to the obtained ventilation rate is completed, the total number of bacterial colonies at each detection point is continuously detected, and data are transmitted to the data storage platform.

Step 7: the model does not need to be trained again within a period of time after the first ventilation adjustment is completed, and only calculation is required to be carried out according to the subsequent detection data to output an optimal ventilation adjustment strategy. Because the distribution of microbes in air changes with different crowd behaviors, the causality test, nonlinear description and multi-objective optimization model all require regular training and parameter update to ensure the effectiveness of the model. The retraining time interval may be set to 3 hours.

Claims

1. A train compartment air adjustment and control method based on microorganism, comprising the following steps:

1) testing $PM_{2.5}$ concentration, PM_{10} concentration, CO concentration, NO_2 concentration, SO_2 concentration, O_3 concentration, and the total number of bacterial colonies at an air supply port, an air exhaust port and a seat of a train;

2) establishing, according to the $PM_{2.5}$ concentration, PM_{10} concentration, CO concentration, NO_2 concentration, SO_2 concentration, O_3 concentration, and the total number of bacterial colonies at each test point in a compartment, a mapping relationship between the total number of bacterial colonies D and the concentration d of air pollutants in each micro environmental unit, wherein the micro environmental unit is the test point;

3) selecting a measured air pollutant concentration data set with a time length of N minutes, calculating the total number of bacterial colonies according to the mapping relationship, denoting a time series of the total number of bacterial colonies at the i^{th} seat as X_N^i , denoting a time series of the total number of bacterial colonies at the j^{th} air supply port or air exhaust port as Y_N^j , performing hypothesis test by using Granger causality test to determine whether there is causality between X_N^i and Y_N^j , performing hypothesis test by using Granger causality test and then obtaining a test result set of each seat test point, m air supply ports and n air exhaust ports;

4) obtaining a nonlinear description model base of all seat test points according to the mapping relationship and the test result set; and

5) inputting ventilation rates of all air supply ports and air exhaust ports of the train to a grey wolf optimizer, calculating fitting results of the total number of bacterial colonies at the air supply ports/air exhaust ports under different ventilation rates, inputting the fitting results to the nonlinear description model base to obtain a fitting result of the total number of bacterial colonies at each seat, and determining the ventilation rates of all the air supply ports and air exhaust ports by using the fitting result of the total number of bacterial colonies at each seat.

2. The train compartment air adjustment and control method based on microorganism

according to claim 1, wherein in step 2), a specific implementation process of establishing a mapping relationship between the total number of bacterial colonies D and the concentration d of air pollutants in each micro environmental unit comprises:

A, reading a data set of air pollutant concentration and total bacterial colony indexes of the current micro environmental unit in M consecutive historical moments, and dividing the index data set into a training set and a test set;

B, constructing a microorganism-air pollutant model by using a deep belief network, and training the deep belief network by using the air pollutant concentration as input of the deep belief network and the total number of bacterial colonies at the same moment as output of the deep belief network;

C, using the test set as input of the trained deep belief network, and selecting a group of parameters with highest description accuracy on the test set as a microorganism-air pollutant mapping model of the micro environmental unit; and

D, repeating steps A-C until all the micro environmental units are traversed to obtain the mapping relationship between the total number of bacterial colonies and the air pollutants in the total $m + n + p$ test points, where m , n , and p are numbers of test points at the air supply ports, the air exhaust ports, and the seats respectively.

3. The train compartment air adjustment and control method based on microorganism according to claim 1, wherein in step 3), the test result set is $\phi_i = \{T_{i,1}^{in}, T_{i,2}^{in}, \dots, T_{i,m}^{in}, T_{i,1}^{out}, T_{i,2}^{out}, \dots, T_{i,n}^{out}\}$, where $T_{i,j}^{in/out} = GCT(X_N^i, Y_N^j)$, and values of the test results $T_{i,j}^{in/out}$ are 0 or 1; and $GCT()$ represents Granger causality test.

4. The train compartment air adjustment and control method based on microorganism according to claim 1, wherein a specific implementation process of step 4) comprises:

I) reading $PM_{2.5}$ concentration, PM_{10} concentration, CO concentration, NO_2 concentration, SO_2 concentration, and O_3 concentration at the seats, the air supply ports, and the air exhaust ports at P consecutive historical moments, and calculating the total number of bacterial colonies at each test point in the P consecutive historical moments according to the mapping relationship;

II) reading the total number of bacterial colonies $O_i = [S_i^{seat}]_t$ at the i^{th} seat test point and the total number of bacterial colonies $I_i = [S_j^{in/out}, \text{ s.t. } T_{i,j}^{in/out} = 1]_t$;

III) using I_i as input of a deep echo state network and O_i as output of the deep echo state network, and learning the corresponding relationship between the total number of bacterial colonies at the seat and the air supply port/air exhaust port at different historical moments; and

IV) repeating steps I) to III) until all the seat test points are traversed to obtain the nonlinear description model base of all the seat test points.

5. The train compartment air adjustment and control method based on microorganism according to one of claims 1-4, wherein in step 5), a specific implementation process of calculating fitting results of the total number of bacterial colonies at the air supply ports/air exhaust ports under different ventilation rates comprises:

i) increasing a ventilation rate at equal intervals and measuring the total number of bacterial colonies under the corresponding ventilation rate;

ii) performing least square fitting on the total number of bacterial colonies at the k^{th} air supply port/air exhaust port to obtain a polynomial expression method of the total number of bacterial colonies $\hat{S}_k$ with respect to the ventilation rate v_k ; and

iii) repeating steps i) and ii), and traversing all the air supply ports and the air exhaust ports, to obtain a polynomial fitting result $\{\hat{S}_k | k = 1, 2, 3, \dots, m+n\}$ of the total number of bacterial colonies at all the air supply ports and the air exhaust ports changing with the ventilation rate, where m and n are numbers of test points at the air supply ports and the air exhaust ports respectively.

6. The train compartment air adjustment and control method based on microorganism according to claim 5, wherein in step 5), an optimization objective is set to simultaneously minimize the fitting result of the total number of bacterial colonies at each seat, and an

$$\min \quad \{\hat{S}_1, \hat{S}_2, \dots, \hat{S}_k, \dots, \hat{S}_{m+n}\}$$

optimization function is s.t. $\hat{S}_k = g(v_k), l_k \leq v_k \leq u_k$, where u_k and l_k are an upper limit and a lower limit of the ventilation rate at the k^{th} air supply port/air exhaust port respectively.

7. The train compartment air adjustment and control method based on microorganism according to claim 2, wherein in step 5), a non-dominated solution $NS^* = \arg \min E$, which

minimizes an evaluation index $E = \sum_{k=1}^{m+n} \hat{S}_k + Var(\hat{S})$, is selected for determining the ventilation rates NS^* of all the air supply ports and the air exhaust ports, where $\hat{S}_k = g(v_k)$, $l_k \leq v_k \leq u_k$; $Var(\hat{S})$ is a variance of the total number of bacterial colonies at all the seats in the test set and u_k and l_k are an upper limit and a lower limit of the ventilation rate v_k at the k^{th} air supply port/air exhaust port respectively.

8. A train compartment air adjustment and control system based on microorganism comprising a computer equipment, wherein the computer equipment is programmed to execute the steps of the method according to one of claims 1 to 7.