DETERMINATION OF FLOWS AND VOLUMES IN MULTIPLE CELL SYSTEMS

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DETERMINATION OF FLOWS AND VOLUMES IN MULTIPLE CELL SYSTEMS

by Lars Jensen

1. INTRODUCTION

A new method to determine flows and volumes in multiple cell systems with a single tracer gas in one experiment is described. The tracer gas concentration is measured in each cell. The same tracer gas is released in each cell in a certain pattern in time. The pattern is such that the influence of different tracer gas inputs can be separated.

Ideal mixing is assumed in each cell. The interconnecting flows between the cells are constant and without time delays. The multiple cell model is described in Section 2.

The time derivatives of the tracer gas concentrations are calculated. A large equation system can be formulated based on the multiple cell model structure and its parameters, the measured tracer gas concentrations and their time derivatives, and the tracer gas inputs. The equation system is linear in the model parameters which are flows and volumes.

The linear equation system has normally more equations than model parameters. The linear programming method is used to determine the model parameters. All model parameters can be restricted to a given interval or even be given a fixed value. The model parameter identification is given in Section 3.

A three cell system is used as a test example. Four experiments are used to test four time derivative calculation methods based on simple interpolation and a fifth method using the previous model parameters iteratively. The results are given in Section 4.

2. MODEL FOR MULTIPLE CELL SYSTEM

This model is well known and it is based on the following assumptions:

1. The model consists of several cells with constant volumes interconnected with constant flows.
2. The concentration of any matter in a cell is the same (ideal mixing).
3. The flows between the cells have no time delays.

The following notations are made:

n	number of cells
V_i	volume of cell number i
q_{ij}	flow from cell number j to cell number i
q_{iu}	flow from outside to cell number i
q_{ui}	flow from cell number i to outside

q_{it} total inflow to cell number i

q_{ti} total outflow from cell number i

$c_i(t)$ tracer gas concentration in cell number i

$p_i(t)$ tracer gas inlet in cell number i

The total inflow and outflow for cell number i can be written:

$$q_{it} = \sum_{j \neq i}^{n} q_{ij} + q_{iu} \qquad (i=1,n) \qquad (2.1)$$

respectively

$$q_{ti} = \sum_{j \neq i}^{n} q_{ji} + q_{ui} \qquad (i=1,n) \qquad (2.2)$$

The total inflow is equal to the total outflow due to mass balance reasons for the flows. This means that

$$q_{it} = q_{ti} \qquad (i=1,n) \qquad (2.3)$$

or

$$\sum_{j \neq i}^{n} q_{ij} + q_{iu} = \sum_{j \neq i}^{n} q_{ji} + q_{ui} \qquad (i=1,n) \qquad (2.4)$$

A mass balance equation for the tracer gas in cell number i can be stated:

$$V_i \dot{c}(t) = \sum_{j \neq i}^{n} q_{ij} c_j(t) - q_{ti} c_i(t) + p_i(t) \qquad (2.5)$$

accumulation — inflow — outflow — production

The tracer gas concentration outside the model is assumed to be zero. The time derivative is denoted with a $\dot{}$. The whole multiple cell model can be stated using the following matrix notation.

$$V\dot{c}(t) = Qc(t) + p(t) \qquad (2.6)$$

where $c(t)$ tracer gas concentration vector
$p(t)$ tracer gas inlet vector
V diagonal volume matrix
Q flow matrix

All the non-diagonal elements in the flow matrix Q are defined earlier as the interconnecting flows q_{ij}. The diagonal elements q_{ii} are given by

$$q_{ii} = - q_{it} = - q_{ti} \qquad (i=1,n) \qquad (2.7)$$

which can be seen from the equations (2.1-4). The flow matrix Q has the following properties:

1. The summation of all row elements in row i are equal or less than zero, if zero then $q_{iu} = 0$ (no inflow from outside to cell i).

2. The summation of all colomn elements in colomn i are equal or less than zero, if zero then $q_{ui} = 0$ (no outflow to outside from cell i).
3. All non-diagonal elements are non-negative.
4. All diagonal elements are negative.

The number of model parameters in a multiple cell model of order n are n(n+2), consisting of n volumes, n(n-1) interflows, n inflows, and n outflows.

However, n parameters are linear dependant on the others which follows from the equations (2.4). The number of model parameters becomes n(n+1).

3. MODEL PARAMETER IDENTIFICATION

A general question is how to determine the model parameters in a multiple cell model from measurements of tracer gas concentration and tracer gas inlet in each cell.

The model (2.6) can be rewritten on a more common form as follows:

$$\dot{c}(t) = V^{-1}Q\, c(t) + V^{-1}p(t) \tag{3.1}$$

This continuous time model is then transformed into a discrete time model as follows:

$$c(t+1) = Fc(t) + Gp(t) \tag{3.2}$$

This is done under the assumption that the tracer gas production p(t) is constant during the time interval (t,t+1).

The matrixes F and G are given by

$$F = e^{V^{-1}Q} \tag{3.3}$$

$$G = \int_0^1 e^{V^{1-}Qs}\, ds V^{-1} \tag{3.4}$$

The matrixes F and G can now be determined from the measurements. The volume matrix V and the flow matrix Q can then be determined from the equations (3.3-4).

However, there is no guarantee that a solution determining V and Q from F and G exists. A simple counterexample is a single cell system with a negative $F = f_{11}$ which is impossible with real V and Q.

One method could be to fit the discrete time model to measurement data by varying the parameters in V and Q and fulfilling the actual constraints. The problem can be regarded as a non-linear constrained optimization problem. The number of parameters can be large. There may be several local minima.

Another method is to use the continuous time model. The only problem is that the time derivatives of the tracer gas concentration is unknown. Then, the idea is to calculate the derivatives directly from the measurements.

Now a large linear equation system can be formulated containing m x n equations, describing the tracer gas mass balances for n cells and for m measurements. The major advantage of this method is that the equations are linear in the model parameters.

Linear programming is a method that can be used to solve this problem. One advantage of this method is that it works with only non-negative free parameters. Another advantage is that all free parameters can be restricted to given intervals. A third advantage is that linear relations between free parameters can be introduced into the equation system.

The linear programming problem can be stated as follows, minimizing the function y with respect to x

$$y = c^T x \tag{3.5}$$

under the constraints

$$Ax = b \tag{3.6}$$

and

$$x_i \geq 0 \tag{3.7}$$

where A constant matrix (mxn)
b constant vector (mx1)
c constant vector (nx1)
x vector (nx1)
y scalar function

Application

The problem has been solved with the following free parameters:

V_i		volume
q_{ij}	$i \neq j$	interflow
q_{iu}		inflow from the outside
q_{ui}		outflow from the outside

All are non-negative. All the abovementioned free parameters are sorted into a model parameter vector x_m. The number of parameters are denoted $p = n(n+2)$.

Mass balance equations

All the mass balance equations can now be stated as a normally over-determined equation system given as

$$A_m x_m = b_m \tag{3.8}$$

The dimensions are as follows with q = mn

A_m q x p
x_m p x 1
b_m q x 1

The elements in the matrix A_m are given by $\dot{c}(t)$, $c_j(t)$ and the differences $c_i(t) - c_j(t)$. The elements in the vector b_m are given by the tracer gas inlets $p_i(t)$.

The equation system (3.8) can be fulfilled by introducing two non-negative error vectors x_p and x_n for positive and negative equation errors, both with the dimension q. This gives

$$A_m x_m + x_p - x_n = b_m \tag{3.9}$$

Model parameter relations

The model parameter relations given by equation (2.4) can be stated as follows:

$$A_r x_m = 0 \tag{3.10}$$

The dimensions of the matrix A_r are n x p. The elements in the matrix A_r are -1, 0 or +1. Each row contains n times -1 and n times +1.

Bounded model parameters

All free parameters x_i are non-negative in linear programming. All model parameters can be given a lower and an upper bound. The lower bound is introduced as

$$x_{im} = b_{il} + x_{iv} \quad (i=1,p) \tag{3.11}$$

or on the vector form as

$$x_m = b_l + x_v \tag{3.12}$$

where b_{il} is the lower bound and x_{iv} is the variable part (non-negative).

The equation systems given by (3.9) and (3.10) can now be rewritten by replacing the model parameter vector x_m with $b_l + x_v$.

$$A_m x_v + x_p - x_n = b - A_m b_l \tag{3.13}$$

$$A_r x_v = -A_r b_l \tag{3.14}$$

An upper bound for each model parameter x_i is introduced by the following equation

$$b_{il} + x_{iv} + x_{is} = b_{iu} \quad (i=1,p) \tag{3.15}$$

or on the vector form as

$$b_l + x_v + x_s = b_u \tag{3.16}$$

where b_{iu} is the upper bound and x_{is} is the non-negative slack variable used by the linear programming method to fulfill the equation (3.15). The upper bound equations given by (3.16) can be added to the problem in the form of

$$x_v + x_s = b_u - b_l \tag{3.17}$$

It should be noted that the lower and upper bounds cannot be chosen arbitrary because the parameter relation given by (3.14) can be impossible to fulfill.

The complete linear equation system is given by

$$Ax = b \tag{3.18}$$

where

$$A = \begin{bmatrix} A_m & I_q & -I_q & 0 \\ A_r & 0 & 0 & 0 \\ I_p & 0 & 0 & I_p \end{bmatrix}$$

$$b = \begin{bmatrix} b_m - A_m b_l \\ -A_r b_l \\ b_u - b_l \end{bmatrix}$$

$$x = \begin{bmatrix} x_v \\ x_p \\ x_n \\ x_s \end{bmatrix} \begin{matrix} \text{variable parameter} \\ \text{positive error} \\ \text{negative error} \\ \text{slack variable upper bound} \end{matrix}$$

and where in turn I_q and I_p are unit matrixes with the dimensions $q = mn$ and $p = n(n+2)$.

The number of equations are easily calculated for the full problem to $mn+n+n(n+2) = n(m+n+3)$.

The number of variables are $n(n+2)+m+n+n(n+2) = 2n(m+n+2)$.

Loss function

The loss function y is a weighted summation of the errors in the mass balance equations

$$y = c_p^T x_p + c_n^T x_n \tag{3.19}$$

The penalty vectors c_p and c_n can be given different values.

However, if all measurements and all cells are assumed to be equally important then the loss function can be given as

$$y = \sum_{i=1}^{mn} (x_{pi} + x_{ni}) \tag{3.20}$$

There should of course be no penalty on the variable part of the model parameter vector x_v and the slack variable x_s, used for the upper bound.

Calculation of time derivatives

Four methods based on simple interpolation are used. Two methods are of first order and two of second order. The calculation formulas are given by

$$dc_F(t) = c(t+1) - c(t) \tag{3.21}$$

$$dc_B(t) = c(t) - c(t-1) \tag{3.22}$$

$$dc_{FB}(t) = (c(t+1) - c(t-1))/2 \tag{3.23}$$

$$dc_{FF}(t) = (-c(t+2) + 4\,c(t+1) - 3\,c(t))/2 \tag{3.24}$$

It is easily seen that $dc_F(t) = dc_B(t+1)$ and $dc_{FB}(t) = (dc_F(t) + dc_B(t))/2$.

In a fifth method, proposed by Mr Björn Hedin, research engineer, the time derivatives are calculated from the earlier estimated or guessed model parameters and different observations in time. The tracer gas input p(t) is eliminated in (3.1) by using (3.2). The matrixes F and G are calculated as given by (3.3) respectively (3.4). This gives

$$\dot{c}(t) = V^{-1}Qc(t) + V^{-1}G^{-1}(c(t+1) - Fc(t))$$

This equation can be simplified by eliminating the matrixes F and G which gives the fifth time derivative calculation method denoted A below.

$$dc_A(t) = A(e^A - I)^{-1}(c(t+1) - c(t)) \tag{3.25}$$

where the matrix A is given by $A = V^{-1}Q$. This method A and the method F are similar when the matrix A is diagonal and has small elements. This is the case when the multiple cell system dynamics is slow compared with the sampling rate.

The method A can be used iteratively and the starting values for the V and Q matrixes can be estimated with one of the four simple interpolation methods or just guessed. It can be shown that the estimated model parameters will converge to the actual ones for a single cell system.

4. SIMULATED EXPERIMENTS

Test model

A three cell model is simulated with a flow matrix Q given as

$$Q = \begin{bmatrix} -5 & 2 & 0 \\ 1 & -11 & 3 \\ 0 & 4 & -9 \end{bmatrix}$$

It follows from the flow matrix Q that the inflows q_{iu} are $q_{1u} = 3$, $q_{2u} = 7$, and $q_{3u} = 5$, and the outflows q_{ui} are $q_{u1} = 4$, $q_{u2} = 5$, and $q_{u3} = 6$. The cell volumes are $V_1 = 10$, $V_2 = 20$, and $V_3 = 15$.

PRBS experiments

Three PRBS experiments and one decay experiment have been simulated. A PRBS (Pseudo Random Binary Sequence) assumes only two values (normally 0 and 1). The sequence is determined by its order o and the basic period T_b time units. The sequence is constant for T_b up to oT_b time units. The sequence has got the total period $T_t = NT_b$ time units where $N = 2^o - 1$.

The PRBS signal u(t) is generated as follows:

$$u(t) = \begin{cases} 1 & \text{of U odd} \\ 0 & \text{of U even} \end{cases} \qquad (4.1)$$

where $U = \sum_{i=1}^{o} f_i \, u(t-i)$ (4.2)

The feedback polynomial f_i is given by

Order o	f_i (i=1,o)						
2	1	1					
3	1	0	1				
4	1	0	0	1			
5	0	1	0	0	1		
6	1	0	0	0	0	1	
7	0	0	1	0	0	0	1
8	0	1	1	1	0	0	0	1

The autocovariance function r(s) for a PRBS signal u(t) of order o is given by

$$r(s) = \begin{cases} 1 & s=0,\pm N,\pm 2N, \ldots \\ -1/N & \text{else} \end{cases} \qquad (4.3)$$

The autocovariance function becomes almost uncorrelated for a high sequence order o and similar to white noise.

Measurements are made at t = 1(1)15 time units for all experiments. The initial tracer gas concentrations are $c_1(1) = 0.8$, $c_2(1) = 1.2$, and $c_3(1) = 1.0$ in all experiments.

The tracer gas inlets are controlled by a PRBS signal as follows:

Experiment	Signal min	Signal max	Order o	Basic period T_b	Total period T_t
P25	0	10	2	5	15
P32	0	15	3	2	14
P41	0	15	4	1	15

The same PRBS signal is used for all tracer gas inlets, but with different phase or time delay as follows:

$$p_3(t+2T_b) = p_2(t+T_b) = p_1(t) \qquad (4.4)$$

The decay experiment is denoted DEC and it is without tracer gas inlets.

The tracer gas inlets $p_i(t)$ (i=1,3), the tracer gas concentrations $c_i(t)$ (i=1,3), and the corresponding time derivative $\dot{c}_i(t)$ (i=1,3) are given i FIG 4.1 for the experiment P25.

All the four time derivatives estimated and the actual time derivative are given in FIG 4.2 for each cell and for the experiment P25. The time derivatives estimated from the method F are also given together with the actual time derivative in FIG 4.3.

Model parameter identification

The four experiments have been used together with the five time derivative calculation methods given by (3.21-25) and denoted F, B, FB, FF and A. All model parameters have been free and unbounded except for the decay experiment in which the volumes have been fixed to correct values.

The found model parameters, the loss function y, and the number of iterations k are presented in one table for each time derivative calculation method. The tables are numbered 4.1-5 and correspond to the method F, B, FB, FF and A. The method A is used with only five iterations and it is started from the method F.

Remarks on results

The five time derivative calculation methods can be ordered as follows: A, F, FF, FB and B with respect to the smallest loss function for all four experiments, except for the experiment P41 where the method F is better than the method A.

The loss function for the experiment P25 and the method A is about 1 and corresponds to an average error in the 42 (=n·m=3·14) mass balance equations of about 0.03.

The model parameters obtained from the experiment P25 are close to the real ones for all five methods.

Model parameters determined by the method A are close to the real ones except for the experiment P41. But the cell volumes V_i are very close to the real ones. It should be noticed that only five iterative calculations of the time derivatives are made.

The model parameters obtained from the experiment P32 och P41 deviate more from the real ones for all methods. The method B and the experiment P41 fail completely. The second order methods FB and FF fail partly for the experiment P41. The obtained models have no interflows. One explanation is that the PRBS signal is changing 8 times out of 15 measurement times.

The estimated cell volumes are the model parameter with the largest deviation. The second order methods have cell volumes close to the real ones. The cell volumes are overestimated for the method F and underestimated for the method B.

The loss function is almost zero for the decay experiment and for all four methods. The second order models have model parameters more close to the real ones for this experiment. Note that the cell volumes have to be fixed, otherwise all model parameters will become zero. This is due to the fact that $b_m = 0$ (no tracer gas inlets) and $b_l = 0$ (no lower bounds). The mass balance equations (3.13) and the flow relations (3.14) are then turned into homogenous equations with the trivial solution $x_v = 0$, $x_p = 0$, and $x_n = 0$. Then it is impossible to determine all model parameters from decay experiments.

Other experiments without tracer gas inlet in some cells, indexed i, have the same behaviour as a decay experiment. All model parameters containing index i tend to zero. Then it is also impossible to determine all model parameters from experiments without tracer gas inlet in some cells.

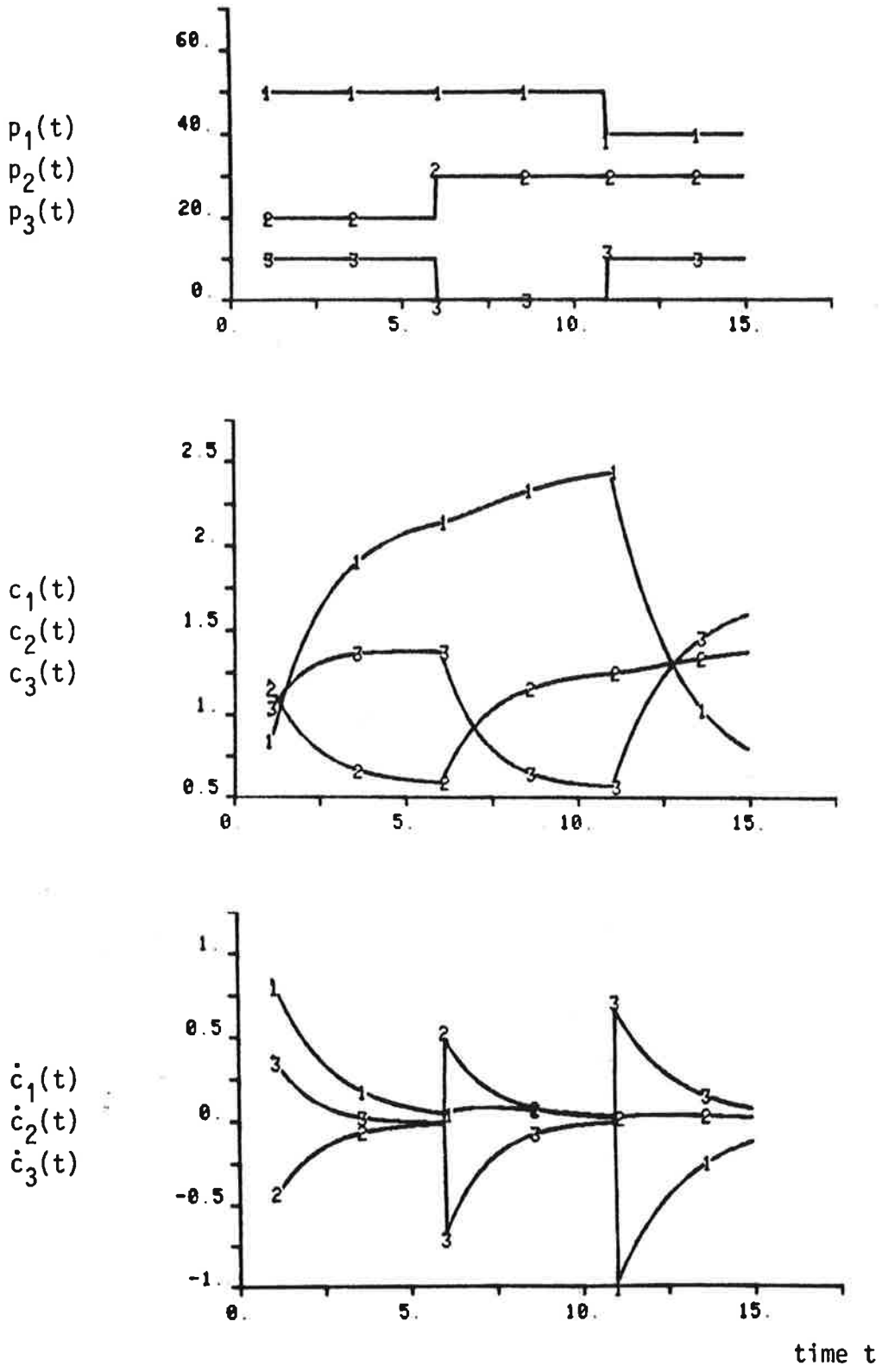

FIG 4.1 Tracer gas inlets $p_i(t)$ (i=1,3), tracer gas concentration $c_i(t)$ (i=1,3) and its time derivative $\dot{c}_i(t)$ (i=1,3) as a function of time t for experiment P25.

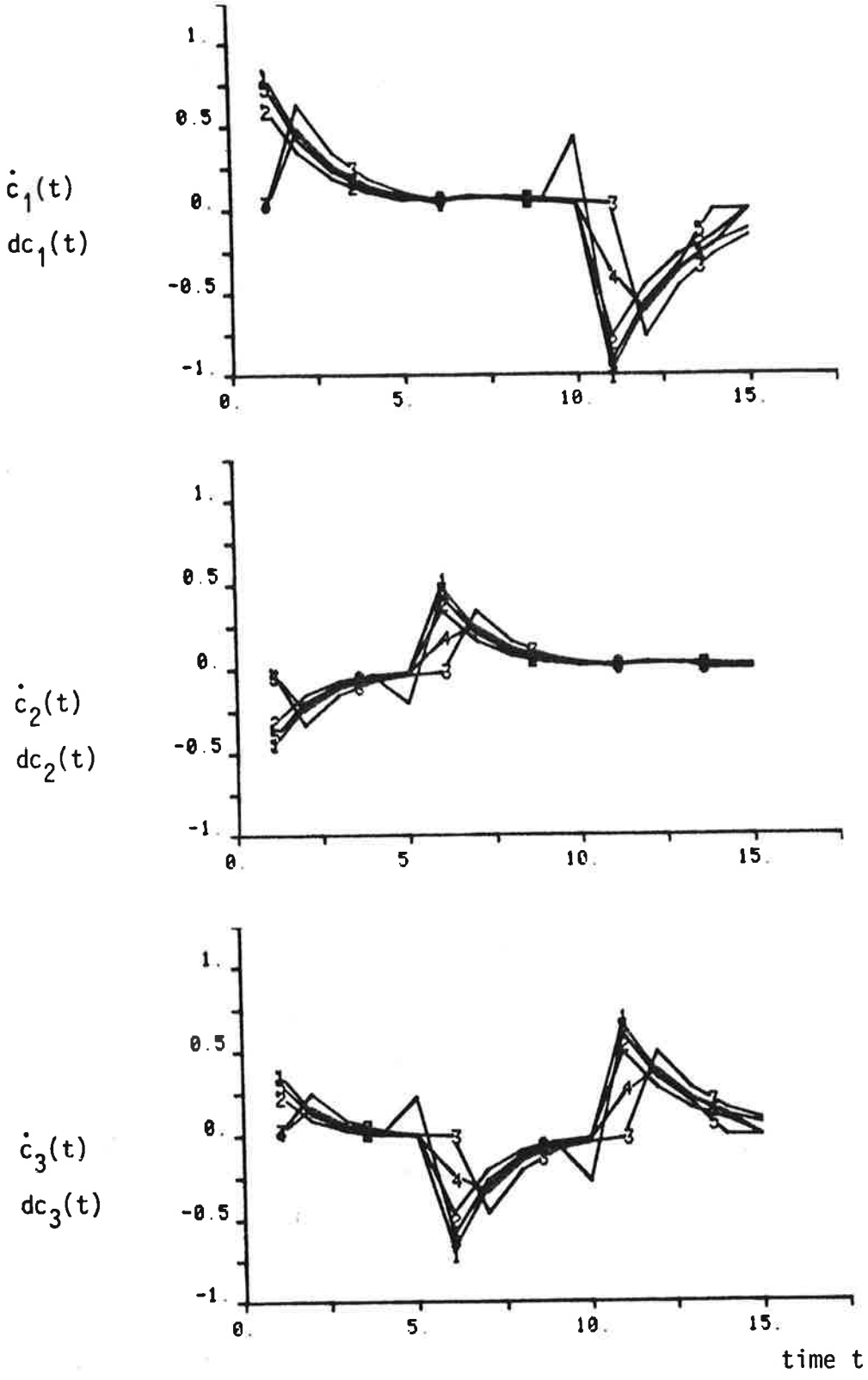

FIG 4.2 Actual time derivative $\dot{c}_i(t)$ (i=1,3) marked (1) and calculated time derivatives $dc_i(t)$ (i=1,3) for the methods F, B, FB, and FF marked (2-5) as a function of time t for the experiment P25.

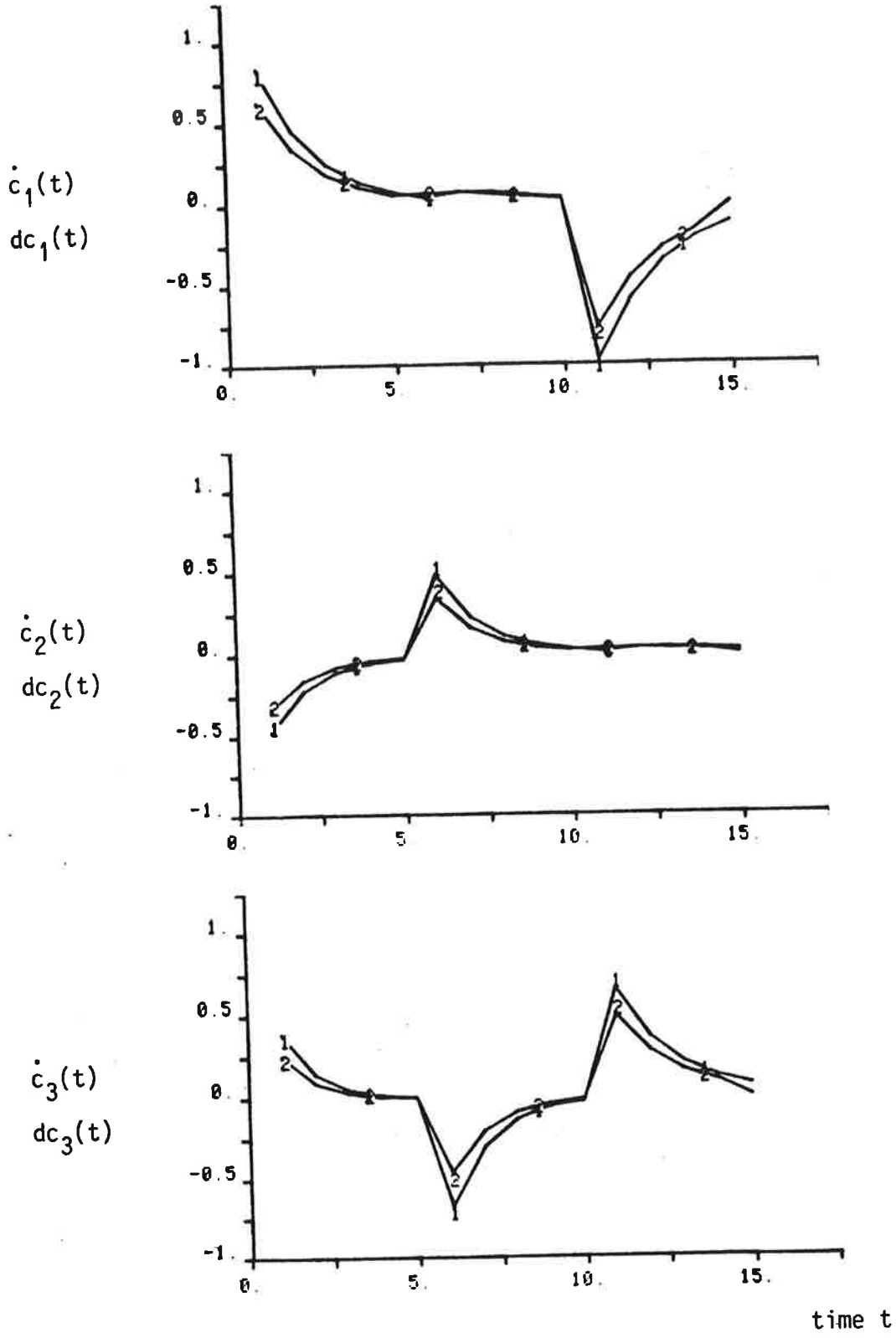

FIG 4.3 Actual time derivative $\dot{c}_i(t)$ (i=1,3) marked (1) and calculated time derivative $dc_i(t)$ (i=1,3) for the method F marked (2) as a function of time t for the experiment P25.

TABLE 4.1 Model parameters, the loss function y, and the number of iteration k. The time derivative method F (3.21), m = 14.

Parameters	Real	Experiments			
		P25	P32	P41	DEC
q_{11}	-5.00	-4.90	-4.60	-4.37	-3.90
q_{12}	2.00	1.84	2.26	0.92	1.19
q_{13}	0.00	0.00	0.09	0.06	0.09
q_{21}	1.00	0.96	1.86	1.66	0.60
q_{22}	-11.00	-10.86	-10.67	-10.31	-8.17
q_{23}	3.00	2.96	1.88	1.27	1.70
q_{31}	0.00	0.00	0.66	1.27	0.06
q_{32}	4.00	4.22	3.19	2.85	2.27
q_{33}	-9.00	-9.13	-9.14	-9.77	-6.60
q_{1u}	3.00	3.06	3.25	3.39	2.62
q_{2u}	7.00	6.92	6.93	7.37	5.88
q_{3u}	5.00	4.91	5.28	5.65	4.27
q_{u1}	4.00	3.94	2.08	1.44	3.25
q_{u2}	5.00	4.80	6.22	6.53	4.71
q_{u3}	6.00	6.14	7.16	8.44	4.81
V_1	10.00	13.16	12.70	12.67	-
V_2	20.00	28.20	29.96	27.53	-
V_3	15.00	20.48	20.32	20.78	-
y	-	4.98	11.05	5.77	0.00
k	-	53	64	20	114

TABLE 4.2 Model parameters, the loss function y, and the number of iterations k. The time derivative method B (3.22), m = 14.

Parameters	Real	Experiments			
		P25	P32	P41	DEC
q_{11}	-5.00	-5.04	-4.99	0.00	-6.68
q_{12}	2.00	2.01	1.65	0.00	3.26
q_{13}	0.00	0.05	0.29	0.00	0.00
q_{21}	1.00	1.04	0.00	0.00	1.70
q_{22}	-11.00	-11.11	-9.01	0.00	-15.54
q_{23}	3.00	2.98	2.37	0.00	5.38
q_{31}	0.00	0.00	0.16	0.00	0.00
q_{32}	4.00	3.64	0.00	0.00	7.38
q_{33}	-9.00	-8.74	-5.72	0.00	-13.26
q_{1u}	3.00	2.98	3.04	0.00	3.42
q_{2u}	7.00	7.08	6.64	0.00	8.46
q_{3u}	5.00	5.10	5.56	0.00	5.87
q_{u1}	4.00	3.99	4.83	0.00	4.97
q_{u2}	5.00	5.46	7.36	0.00	4.90
q_{u3}	6.00	5.71	3.06	0.00	7.88
V_1	10.00	7.41	7.63	0.00	-
V_2	20.00	13.53	13.28	0.00	-
V_3	15.00	10.70	10.18	0.00	-
y	-	42.30	173.16	300.00	0.02
k	-	40	57	22	83

TABLE 4.3 Model parameters, the loss function y, and the number of iterations k. The time derivative method FB (3.23), m = 13.

Parameters	Real	Experiments P25	P32	P41	DEC
q_{11}	-5.00	-4.99	-4.32	-3.70	-5.27
q_{12}	2.00	1.96	0.00	0.00	2.25
q_{13}	0.00	0.02	0.89	0.00	0.00
q_{21}	1.00	1.04	0.00	0.00	1.15
q_{22}	-11.00	-11.07	-5.77	-6.12	-11.86
q_{23}	3.00	2.98	0.00	0.00	3.54
q_{31}	0.00	0.00	0.44	0.00	0.00
q_{32}	4.00	3.87	0.00	0.00	4.79
q_{33}	-9.00	-8.91	-5.77	-3.15	-9.86
q_{1u}	3.00	3.01	3.43	3.70	3.02
q_{2u}	7.00	7.06	5.77	6.12	7.17
q_{3u}	5.00	5.04	5.34	3.15	5.07
q_{u1}	4.00	3.96	3.88	3.70	4.12
q_{u2}	5.00	5.23	5.77	6.12	4.82
q_{u3}	6.00	5.91	4.89	3.15	6.32
V_1	10.00	9.60	10.54	10.65	-
V_2	20.00	18.34	25.34	21.07	-
V_3	15.00	13.99	14.83	22.51	-
y	-	27.40	88.20	193.69	0.01
k	-	47	59	23	86

TABLE 4.4 Model parameters, the loss function y, and the number of iterations k. The time derivative method FF (3.24). m = 13.

Parameters	Real	Experiments P25	P32	P41	DEC
q_{11}	-5.00	-4.90	-4.82	-3.34	-4.69
q_{12}	2.00	1.83	1.61	0.00	1.66
q_{13}	0.00	0.00	0.09	0.00	0.07
q_{21}	1.00	0.95	0.00	0.00	0.83
q_{22}	-11.00	-10.88	-8.24	-6.16	-10.01
q_{23}	3.00	3.00	1.88	0.00	2.42
q_{31}	0.00	0.32	0.00	0.00	0.05
q_{32}	4.00	3.36	0.00	0.00	3.23
q_{33}	-9.00	-8.91	-5.63	-5.49	-8.15
q_{1u}	3.00	3.07	3.11	3.34	2.95
q_{2u}	7.00	6.93	6.36	6.16	6.76
q_{3u}	5.00	5.23	5.63	5.49	4.87
q_{u1}	4.00	3.63	4.82	3.34	3.81
q_{u2}	5.00	6.69	6.64	6.16	5.12
q_{u3}	6.00	5.92	3.66	5.49	5.65
V_1	10.00	10.73	10.61	6.82	-
V_2	20.00	22.39	19.14	12.74	-
V_3	15.00	16.32	12.73	9.25	-
y	-	18.58	45.19	65.61	0.00
k	-	56	39	38	99

TABLE 4.5 Model parameters, the loss function y, and the number of iterations k. The time derivative method A (3.25), m = 14.

Para-meters	Real	Experiments P25	P32	P41	DEC
q_{11}	-5.00	-5.00	-4.98	-4.94	-5.00
q_{12}	2.00	2.00	1.96	1.86	2.00
q_{13}	0.00	0.00	0.01	0.04	0.00
q_{21}	1.00	1.00	1.02	2.33	1.00
q_{22}	-11.00	-11.00	-10.99	-12.51	-10.99
q_{23}	3.00	3.00	2.97	2.47	2.99
q_{31}	0.00	0.01	0.00	0.38	0.00
q_{32}	4.00	3.99	4.00	3.19	3.99
q_{33}	-9.00	-9.01	-9.00	-8.74	-8.99
q_{1u}	3.00	3.00	3.01	3.04	3.00
q_{2u}	7.00	7.00	7.00	7.71	7.00
q_{3u}	5.00	5.01	5.00	5.17	5.00
q_{u1}	4.00	3.99	3.97	2.23	4.00
q_{u2}	5.00	5.01	5.04	7.47	5.00
q_{u3}	6.00	6.01	6.01	6.23	6.00
V_1	10.00	10.01	10.02	10.05	-
V_2	20.00	20.02	20.11	20.00	-
V_3	15.00	14.97	14.97	14.95	-
y	-	0.98	3.30	13.11	0.03
k	-	330	357	433	658

5. FURTHER RESEARCH

The method presented in this paper is still more an idea than a method. It remains to investigate noise sensivity, to use real measurements, other combined inlet and measurement patterns, other calculation methods for time derivatives or even other model parameter identification methods.

One possible approach is to use the discrete time model given by (3.2) and identify the matrixes F and G under suitable constraints so that the corresponding matrixes V and Q will describe a multiple cell system. The linear programming method could also be used in this approach.

The presented method assumes that the tracer gas concentration in all cells are measured simultaniously. This is almost impossible. One solution is to use a single device continuously measuring the tracer gas concentration in different cells in sequence. Then the time differences between the measurements can be small in comparison with the sampling interval for the model and can therefore be neglected. Interpolation can be used to compute simultanious tracer gas concentrations.

Another practical problem is the tracer gas inlet. The inlet is assumed to be constant over the model sampling interval. The tracer gas inlet is normally on-off-controlled. One solution would be to distribute several equal pulses evenly over the model sampling interval.

It should also be stated that so far the research work has not been part of any national research project. The work effort has been about two man-months during a period of two years.

ABSTRACT

Determination of flows and volumes in multiple cell systems

A new method to determine flows and volumes in multiple cell systems with a single tracer gas in one experiment is described. The tracer gas concentration is measured in each cell. The same tracer gas is released in each cell in a certain pattern in time. The pattern is such that the influence of different tracer gas inputs can be separated. Pseudo Random Binary Sequences (PRBS) can be used. The multiple cell model assumes ideal mixing in each cell.

A large equation system can be formulated based on the multiple cell model structure and its parameters, the measured tracer gas concentrations and its time derivatives calculated from measurements, and the tracer gas inputs. The equation system is linear in the model parameters which are flows and volumes.

The linear equation system has normally more equations than model parameters. The LP-method is used to determine the model parameters. All model parameters can be restricted to a given interval or even be given a fixed value.

The method is tested on four simulated experiments with a three cell system together with five different time derivative calculation methods.