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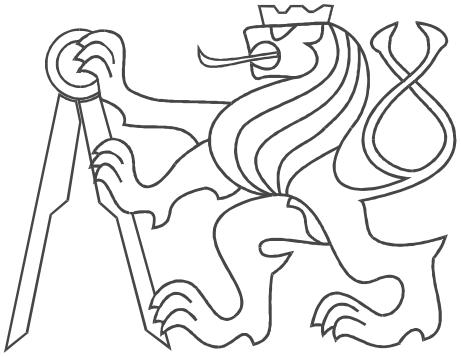

TEZE K DISERTAČNÍ PRÁCI

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České vysoké učení technické v Praze
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Katedra řídicí techniky

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Dynamic system identification methods for fMRI data processing

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Oponenti .....
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Teze byly rozeslány dne: .....

Obhajoba disertace se koná dne ..... v ..... hodin před komisí pro obhajobu disertační práce ve studijním oboru Řídicí technika a robotika, v zasedací místnosti č. ..... Fakulty elektrotechnické ČVUT v Praze.

S disertací je možno se seznámit na děkanátě Fakulty elektrotechnické ČVUT v Praze, na oddělení pro vědu, výzkum a zahraniční styky, Technická 2, Praha 6.

Prof. Ing. Michael Šebek, DrSc.
předseda komise pro obhajobu disertační práce
ve studijním oboru
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Abstract

The thesis deals with application of system identification methods for fMRI data processing. The main goal of this thesis is to define the complex dynamic system represented by brain areas within the context of the systems theory, and to cast it as a task for system identification procedures. The system, as interpreted by the systems theory, is a complex object consisting of interconnected subsystems and components which transforms inputs into outputs and this transformation can be characterized by a mathematical model, usually in the form of differential equations. The key issue is to look for these models by identification methods and to consider them as a certain alternatives for fMRI data processing to commonly used statistical methods. We focus especially to DCM procedure for detection of the brain intrinsic structure and we review that from user's point of view within Writer's cramp study. Then we propose application of modern multidimensional systems identification algorithms of the subspace identification theory in the context of fMRI data analysis. The methods originated in 1990s in the field of process control and identification and yield robust linear model parameter estimates for systems with many inputs, outputs and states. Our ultimate goal was to establish an alternative to the DCM analysis procedure which would eliminate its main drawbacks, namely the need to predefine the models structure.

1 Goals and objectives

Specific goals of this dissertation were set as follows

1. Develop a comprehensive review of techniques and procedures used in the fMRI area from the systems and process identification viewpoint. Focus on the process of fMRI measurement, discuss the fMRI data structure and present other issues concerning fMRI which could be helpful for the application of systems identification procedures in this area.

2. Get familiar with the "State of the Art" techniques used in fMRI data processing, namely with Dynamic Causal Modeling (DCM). Verify them with experimental data coming from a clinical study. Established partnership with Department of Neurology, 1^{st} Faculty of Medicine, Charles University in Prague is supposed to be exploited. Discuss the results and identify advantages and drawbacks of the standard fMRI modeling techniques.

3. Develop alternatives to fMRI data processing procedures, namely to Dynamic Causal Modeling, based on process identification and estimation techniques. Demonstrate them with simulated and experimental fMRI data.

2 Motivation

The main goal of the dissertation thesis is to formulate advanced concepts and procedures/algorithms commonly used in process identification for fMRI research field and to apply the system identification methods for fMRI data modeling. Human brain can be described as a system consisted of many

subsystems representing constituent brain areas which represents a dynamical system with characteristic dynamics. By means of fMRI technique it is even possible to measure output signals of this complex system so we know the input-output behavior of the system and we suppose it is possible to use identification and estimation methods to describe that by linear system with a certain accuracy. This approach could provide an important information about some crucial parameters of the brain system and it could be a certain alternative to available statistical techniques which are commonly used for fMRI data processing at present. The thesis reports on some attempts to approach the problem of modeling of simple system including just one brain area and looking for dynamics description of more complex system with several brain areas. It also brings a comprehensive survey of related literature, mainly out of the systems and control field.
The thesis was partly created in cooperation with Department of Neurology, 1^{st} Faculty of Medicine, Charles University in Prague (professor Evžen Růžička, Dr. Robert Jech).

3 Outline of thesis

The following second chapter gives the specific goals and objectives of the dissertation thesis. All of them are then discussed in further chapters.

The third and fourth chapters contain the basic information about fMRI technique and data processing by commonly used tool for Matlab called SPM toolbox and they bring some details necessary to comprehension of the other chapters.

Next fifth chapter deals with the case study - Writer's cramp study - completed in cooperation with Department of Neurology, 1^{st} Faculty of Medicine, Charles University in Prague. Our personal experience with SPM toolbox for DCM procedure is discussed with real fMRI data giving some details, advantages and drawbacks.

The sixth chapter deals with fMRI data modeling by system identification methods. It discusses the results of the modeling depending on fMRI data quality. It also considers the subspace identification methods as an alternative to DCM procedure for intrinsic structure detection.

In the seventh chapter, the results of the thesis are summed up and confronted with the goals and objectives set. There are also summarized the scientific achievements of this thesis and outlines immediate opportunities for improvement and further research.

Chapter 8 contains the publications of the authors, related directly to the thesis, and other references used throughout the text.

4 Writer's cramp study

This section summarizes the Writer's cramp study - project of the Department of Neurology, 1^{st} Faculty of Medicine, Charles University in Prague. We participated in the study by DCM analysis of fMRI data acquired during second phase of the project - Advanced study. The final result of the

project was joint paper published in NeuroEndocrinology Letters (HAVRANKOVA, P. et al., 2010). The writer's cramp is a common type of focal dystonia which manifests by involuntary spasm of the hand and forearm muscles (HAVRANKOVA, P. et al., 2010). The conventional therapy is the botulotoxin medication, sometimes without clinical effect unfortunately. The next alternative for some patients is an experimental therapy by rTMS - repetitive Transcranial Magnetic Stimulation. rTMS applies the sequence of magnetic pulses by coil focused on defined cortex area causing symptoms suppression. Within the writer's cramp study, we processed fMRI data sets measured before and after rTMS therapy for comparison. We completed DCM analysis as one part of an objective assessment of rTMS therapy effect.

4.1 Materials and methods

12 patients (8 women and 4 men) with right hand writer's cramp were included in the study. The duration of their disorder was 2-11 years. Each patient underwent two five-day blocks of rTMS, the first was real rTMS, the second was sham (placebo) rTMS. The rTMS took 30 minutes every day. The fMRI measurement was carried out before the therapy began (the first day) and after the therapy was finished (the fifth day).
rTMS was done by 70-mm double coil connected to stimulator. One pulse set contained 1800 pulses. The coil was focused on sulcus postcentralis. fMRI procedure was related to the task with active movement of right hand fingers. The patients were required to perform about ten movements during 6 minutes, each movement with 3 seconds duration. The movements were captured by the video-fMRI monitoring (JECH, R. et al., 2008). As a result, two vectors were obtained for each patients and they contained the onsets (start instants) and durations of movements. The vectors served for fMRI analysis (the detection of statistical significant areas with hemodynamic response) in SPM toolbox ver.5 (SPM toolbox, 2012). All related information on the fMRI procedure and fMRI analysis are described in (JECH, R. et al., 2008).

4.2 DCM

The main task of DCM analysis was to quantitatively approve an effect of the rTMS therapy. All the patients passed clinical examination before and after the therapy. The clinical examination consisted in a subjective assessment by a patient himself, and objective assessments by raters, for instance evaluation of cribbing of text for two minutes see Figure 1. The subjective and objective assessments showed significant improvement of writer's cramp symptoms for 9 patients who finished the therapy. For detailed results concerning all assessment, in addition to DCM analysis, see (HAVRANKOVA, P. et al., 2010).
The DCM analysis was called to confirm these results. 9 patients finished the rTMS therapy and their fMRI data was put subject to the overall processing. DCM analysis was created only for fMRI data related to real stimulation and measured before and after the therapy. The data was processed separately and then particular connections and their strength were compared. Next to the

results themselves, our goal was also to describe experience with the DCM tools of SPM ver.5 for Matlab (SPM toolbox, 2012), based on a specific medical experiment data processing.

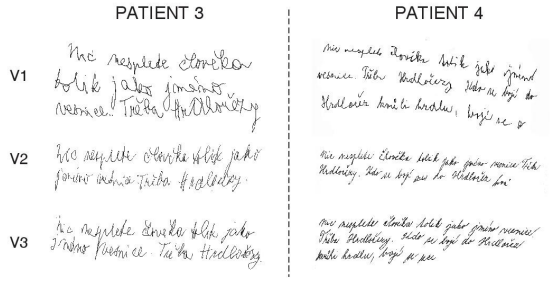

Figure 1: The handwriting of patient 3 and patient 4 before rTMS (V1), immediately after the last session of rTMS (V2), and one week later (V3) - adopted from (HAVRANKOVA, P. et al., 2010)

4.2.1 Models

The first step of DCM analysis was the definition of models which were confronted with real data. The definition usually results from clinical experience and from knowledge in functional brain organization. Originally, models which differed in number of connections for data measured before and after the therapy were considered for these reasons. The reasoning behind was a presumption that rTMS could have some influence on functional brain organization and more connections could be detected for data measured after therapy. The problem here was however that the results of DCM analysis for data measured before and data measured after are not easily and directly comparable in this case. Since the DCM approach is based on hypotheses testing, one must ensure the same structure - all connections considered - for both the ”before” and ”after” presumed models. Based on this observation a new set of 11 models depicted in the Figure 2 was created. All the models featured equal number of areas for data measured before and after the therapy and contained just extrinsic input namely into LS1, LSM1, and SMA area - input representing right hand fingers movement and extrinsic input for coil position (there was not any modulatory input).

4.2.2 Areas

The next stage of DCM analysis was selection of substantial brain areas. Also in this case the clinical experience helps. But the other clue can be fMRI analysis result with significant active areas detection.

Here were selected five brain areas with significant activity related to the required task (finger movement), based on the second level analysis as provided by (SPM toolbox, 2012). In the case of LS1,

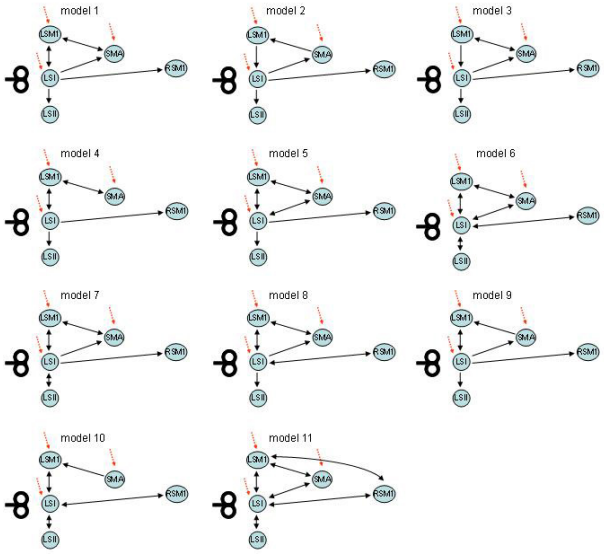

Figure 2: Models for DCM procedure

stimulated directly by the rTMS coil, the question was however whether to apply the same second level analysis result for the coordinates estimation, or whether to define the coordinates explicitly as the coil target. In terms of medical experience it seems more logical to consider location of the coil as the stimulation area. The DCM results with this particular coordinate set also include more significant connections as well which proves this assumption.

4.3 Results

4.3.1 Individual assessment

The data set resulting from the medical experiment described in section 5.2 was restricted for practical reasons in terms of number of patients (9 in total). Consequently we will have some problems with statistical processing.
On the other hand, the DCM analysis results for particular patients can be qualitatively analyzed easily to reveal some basic rules appearing in all models for one particular patient, or appearing across the whole patient group for one particular model. In our case there was for instance the connection $LS1a \rightarrow LSM1$ included in majority of models. Interestingly, the strengths of this connection for a particular patient across the whole set of models were roughly equal. This observation can serve as a kind of ”cross-check” when deducing about a particular connection significance.

4.3.2 Statistical processing: Non-parametric statistical tests

The drawbacks of the parametric T-test discussed above can be eliminated by calling alternative non-parametric statistical tests. The Wilcoxon test and Sign test were applied, leading to similar

Table 1: Significant connections across the whole patient group - LS1 is location of the coil

connection	t statistic probability
LS1a-SMA - model 2	0.0381
LS1a-RSM1 - model 6	0.0109
LS1a-LS2 - model 6	0.0109
LS1a-SMA - model6	0.0858
RSM1-LS1a - model 6	0.0663
LS2-LS1a - model 6	0.0284

conclusions. Only Wilcoxon test results are therefore discussed further.
The non-parametric tests show significant changes of six connections. The positive result is that five connections of those six are in the (reciprocal) model number 6, see section 5.4.4 for details. The non-parametric test results are summarized in Table 1. Four connections appear as significant (probability of t-statistic smaller than significance level 5% (three of them in model No. 6), two others are slightly above.

4.4 Conclusion

The chapter deals with DCM analysis of fMRI data measured on patients suffering from writer's cramp and subjected to an rTMS therapy. The main result is identification of a DCM model structure based on a non-parametric test performed on a reduced measured data set. Practical experience with DCM tools of the SPM toolbox is also discussed. The detailed description of the writer's cramp study from medical point of view and summary of all results (objective and subjective assessment) are given in (HAVRANKOVA, P. et al., 2010).

5 System identification and fMRI data processing

The main goal of this section is to define the complex dynamic system represented by brain areas within the context of the systems theory, and to cast it as a task for system identification. The system, as interpreted by the systems theory, is a complex object consisting of interconnected subsystems and components which transforms inputs into outputs and this transformation can be characterized by a mathematical model, usually in the form of differential equations. The input stimulus signals that enter into the brain system reflect the particular fMRI neurological experiment, and can be modeled as rectangular signals (on/off or active/inactive) as they correspond to hand motion, pictures projection, electrical stimulation etc. The measured outputs are BOLD signals which are usually visualized as volumetric 3D plots. They can also be viewed as rectangular for which at every time instance the measured value assumes a shape of a 3-dimensional array (cube). Hence the input-output behavior of the brain system can be measured experimentally. However the brain system is

characterized by specific intrinsic structure comprised of two different parts called neurodynamics and hemodynamics, see Figure 3. The input (stimulus) signals enter the faster dynamics (neurodynamics) representing the intrinsic interconnections among brain areas. Neurodynamics could be modeled by several first order systems, each corresponding to a given brain area and their intrinsic connections as is done by DCM in fact (FRISTON, K. J. et al., 2003). The neuronal response of every brain area is only observed in the fMRI data after passing through the slower hemodynamics part, which can be modeled as a simple system (filter) for each brain area separately. In contrast to the nonlinear balloon model used within DCM, higher order hemodynamic linear filters (at least order two) are necessary to capture the oscillatory behavior as shown in the next section concerning subspace identification methods used for fMRI data fitting.

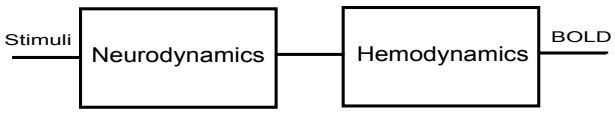

Figure 3: Brain dynamics system structure - two types of dynamics, at first faster dynamics, slower dynamics forms output BOLD signal in each activated brain area

5.1 MIMO identification - fMRI data fitting

This section summarizes first results of subspace identification experiments for fMRI simulated data. We focused on subspace N4SID identification methods implemented in System Identification Toolbox for Matlab (version 2007b). Subspace methods combine results of systems theory, geometry and numerical linear algebra (KATAYAMA, T., 2005) (FAWOREEL, W. et al., 2000). They seem suitable for our task especially for their fine numerical reliability for MIMO system identification. In addition, they give rise to models in the state-space form directly. The simulated data sets differ in the signal-to-noise ratio factor (SNR) and in number of samples. Other parameters are the number of areas, interscan interval, and the number of conditions, see (SPM toolbox, 2012) for details. The data parameters are presented in the tables below for particular cases. Related tables show the vector of onsets and vector of duration (definition of inputs, stimulation signal). The last piece of information for the SPM simulator is the matrix A defining the strength of connections, and the input matrix C. The results for particular parameters choices are the identified matrix A acquired from SPM toolbox by DCM estimation and then the (linear dynamic) model of simulated data acquired from the Identification Toolbox by help of subspace identification method (Identification toolbox, 2012).

5.1.1 Case 1

This example tests the quality of identification for simulated data with "good" parameters, see BOLD signals in Figure 4. The data set has enough samples and the signal-to-noise ratio is high,

Table 2: The simulated data parameters - case 1,2

SNR	areas	TR	scans	cond.		
50	3	1.7	256	1		
onsets	20	45	113	154	203	240
duration	3	4	3	3	2	3

see Table 2. The input data is defined by vectors and the matrix of connection strength as well as the input matrix are also presented below in Equation 1.

$$A = \begin{pmatrix} -1 & 0 & 0 \\ 1 & -1 & 1 \\ 2 & 0 & -1 \end{pmatrix} \qquad C = \begin{pmatrix} 1 \\ 0 \\ 0 \end{pmatrix} \tag{1}$$

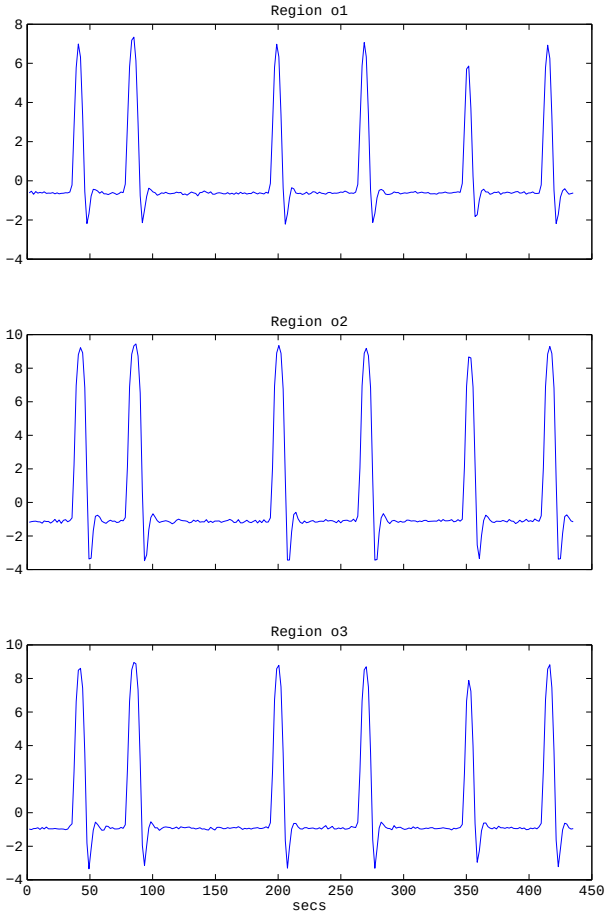

Figure 4: The simulated data for three areas - case 1 - created in SPM toolbox

The DCM procedure gives fairly good results in terms of the identified matrix A which corre-

sponds to the simulation model's A, see Equation 2 and 1 for comparison. The identification toolbox also proves useful here and fits successfully the simulated data by the identified linear model of order five, see Figure 5. We also bring the transfer function of model identified by subspace identification method in zero-pole-gain format, see Equation 3.

$$A = \begin{pmatrix} -1 & 0 & 0 \\ 0.872 & -1 & 1.0716 \\ 1.9955 & 0 & -1 \end{pmatrix} \tag{2}$$

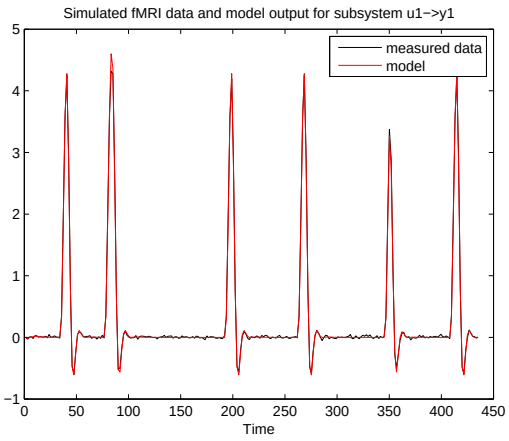

Figure 5: The simulated data and model for case 1

$$G_{u_1y_1} = \frac{-0.52202(s-1.631)(s+0.1145)(s^2+0.6438s+1.364)}{(s+0.1115)(s^2+0.7257s+0.3925)(s^2+0.8288s+0.7242)} \tag{3}$$

5.1.2 Case 2

Simulated data with smaller signal-to-noise ratio equal to one are processed now. Other parameters remain unchanged from the previous case. The DCM procedure naturally embodies worse results than in the previous case which is shown in the matrix A again, see Equation 4. The system identification toolbox identifies the model with order three and the identified output series is confronted with simulated data in the Figure 6.

$$A = \begin{pmatrix} -1 & 0 & 0 \\ 0.5057 & -1 & 0.5106 \\ 0.9121 & 0 & -1 \end{pmatrix} \tag{4}$$

$$G_{u_1y_1} = \frac{-0.54433(s-1.527)(s+0.1644)}{(s+0.1663)(s^2+0.4181s+0.2268)} \tag{5}$$

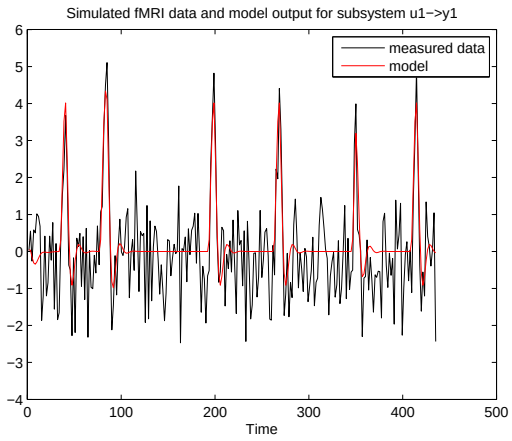

Figure 6: The simulated data and model for case 2

5.1.3 Conclusion

The simulation experiments carried out for various combinations of important parameters in the cases 1-4 prove applicability of subspace identification methods for fitting simulated fMRI data by linear dynamic higher-order models, without the necessity to pre-define the model structure. On basis of identified models we can say that every output hemodynamics filter should be modeled as at least a second order system with complex conjugate eigenvalues, reflecting the oscillatory response as shown in continuous transfer functions. At this moment it is not clear however how to interpret those dynamical models in terms of functional brain organization unfortunately, the DCM is certainly considerably farther in this regard. This issue will be therefore the direction of further research: how to interpret the linear identified model parameters in, say, a DCM-like manner.

5.2 Intrinsic structure detection

The next idea behind our approach is to estimate the significance of interconnections among the brain areas (so called intrinsic structure) by identifying the coupling among the states of an underlying linear state-space model. This is done by finding the state matrices describing the dynamics of neuronal states through the measured hemodynamic responses, using conventional linear system identification techniques, subspace identification methods here (N4SID especially). However, these methods do not apply constraints on the form of the state matrix. We finesse this problem by modeling the data with a number of hidden states that is greater than the number of observed brain areas. We then find a transformation of the hidden states that conforms to the known expected block structure of the state matrix appropriate for our problem. This transformation relies on the numerically reliable Schur decomposition of the original state matrix and related eigen decompositions. We can then interpret the transformed states in terms of neuronal and hemodynamic states. The transformed state matrix gives direct information on couplings between particular neuronal states,

and also defines the mapping from neuronal to hemodynamic subsystems.
The subspace identification proves useful here and fits successfully the simulated data by the identified linear model as is shown in previous section; just for the last data set with smaller signal-to-noise ratio and number of samples the model is not able to fit data sufficiently. We can summarize that subspace identification methods are a promising technique for hemodynamic response fitting. So we attempt to extend the identification procedure to the system including intrinsic structure detection.

5.2.1 Identification procedure for brain system structure

Subspace identification methods return a linear state space model in form Equation 6. The matrix A represents the dynamics, B is related to the inputs and C characterizes the outputs. The matrix D indicates direct connection from input to output in general. Choosing the linear model Equation 6 instead of the bilinear model used in DCM procedure (see chapter 4 for details) for brain area system description is intentional, ignoring so-called modulatory inputs motivated by simplicity. The hidden states x include certain transformation of all the neuronal and hemodynamic states in our model. This means the number of hidden states is much greater than the number of observations y (and that C is not a square matrix).

$$\begin{aligned} \dot{x}(t) &= \boldsymbol{A}x(t) + \boldsymbol{B}u(t) \\ y(t) &= \boldsymbol{C}x(t) + \boldsymbol{D}u(t) \end{aligned} \tag{6}$$

If we had the state space description in suitable form we could see intrinsic connections among selected brain areas directly. Unfortunately matrices A, B and C as a result of subspace methods are usually full and inappropriate to the specific structure of the brain system. Apparently it is necessary to transform the state space model into a realization reflecting separation of neurodynamics and hemodynamics. Matrix D of identified state space description is zero because there is no direct connection from input to output. One way to enforce this structure into the state space realization is a similarity transformation with a suitable transformation matrix T. The next section illustrates construction of the T matrix in a simple case which corresponds to the special brain structure according to Figure 7.

5.2.2 First order hemodynamics filter case

We consider a system including one input (stimulus) signal, two brain areas and two output (BOLD) signals, see Figure 7. The output filters for hemodynamics modeling are considered as first order systems only for this moment (note that it does not fully correspond to orders necessary to model accurately hemodynamic filters as identified in the previous section 6.2., so it is not possible to use SPM toolbox as the data generator, and we use the generator according to system matrices Equation 8 instead). The subspace identification methods yield the full matrices A, B, and C, see

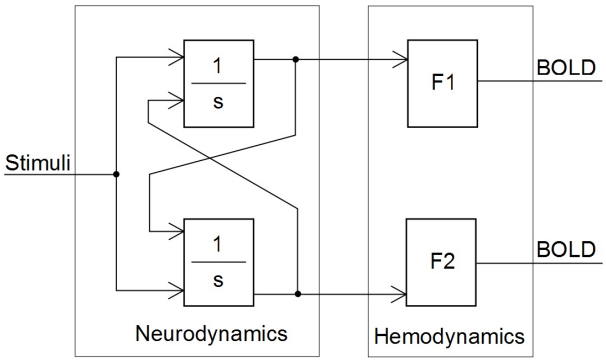

Figure 7: The detailed structure of brain system - neurodynamics is modeled by reciprocally connected first order systems. Each area has also own hemodynamics represented by higher order system

Equation 7. The matrix D is zero (no direct throughputs are present in the system considered).

$$A = \begin{pmatrix} a_1 & a_2 & a_3 & a_4 \\ a_5 & a_6 & a_7 & a_8 \\ a_9 & a_{10} & a_{11} & a_{12} \\ a_{13} & a_{14} & a_{15} & a_{16} \end{pmatrix} \qquad B = \begin{pmatrix} b_1 \\ b_2 \\ b_3 \\ b_4 \end{pmatrix} \qquad C = \begin{pmatrix} c_1 & c_2 & c_3 & c_4 \\ c_5 & c_6 & c_7 & c_8 \end{pmatrix} \tag{7}$$

$$A = \begin{pmatrix} e_1 & 0 & g_1 & 0 \\ 0 & e_2 & 0 & g_2 \\ 0 & 0 & e_3 & c_{12} \\ 0 & 0 & c_{21} & e_4 \end{pmatrix} \qquad B = \begin{pmatrix} 0 \\ 0 \\ 1 \\ 1 \end{pmatrix} \qquad C = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \end{pmatrix} \tag{8}$$

However, the desired form is in Equation 8. This form reveals the specific structure of the brain system with the neuronal dynamics affected directly by the inputs and the hemodynamics projected immediately into the measured outputs. Matrix A contains the eigenvalues e_1, e_2 and the gain coefficients g_1, g_2 defining the hemodynamic SISO filters associated to a particular brain area. The lower right submatrix represents the (much faster) neurodynamics. The coefficients c_{12} and c_{21} are the crucial parameters which determine the intrinsic neuronal interconnections between the two modeled brain areas. The matrix B represents the structure of inputs and matrix C corresponds to the structure of outputs, in agreement with Figure 7.

Now we describe the sequence of similarity transformations steps leading from the full state-space model see Equation 7 to the structured form realization Equation 8 from which the coupling parameters c_{12} and c_{21} can be detected. We consider a system with one input and two brain areas, each modeled by first order dynamics and with corresponding two output BOLD signals. Each similarity transformation follows the conventional rule in Equation **??**. The first step is Schur decomposition applied to the identified dynamic matrix A. It yields zero elements under the main diagonal on which the eigenvalues are displayed. These are then ordered to separate the eigenvalues of hemody-

namics (slow) and neurodynamics (fast). The subsequent steps are devised to impact the remaining parts of state space description and to preserve the effect of the previous transformation steps. In this way, the eigenvectors of a selected submatrix of the new dynamic matrix A are calculated and used for diagonalization of the submatrix representing hemodynamics filters, and the null space of output matrix C is used for zeroing its selected elements. We also use inverse submatrix for adjustment of parts concerning gain coefficients of output (hemodynamic) filters. All steps are detailed in a Matlab pseudocode-form see Figure 8, and are illustrated by a numerical example in the case study in the next section.

```
>>[T1,A1] = schur(A)
>>[T2,A2] = ordschur(T1,A1,[1,2,3,4])
>>G2 = ss(T2\A*T2, T2\B, C*T2, 0);

>>[t1,aj1] = eig(G2.a(1:2,1:2));
>>C2 = G2.c*blkdiag(t1,eye(2));
>>T3 = T2*blkdiag(t1,eye(2))*[eye(4,2), null(C2)];
>>G3 = ss(T3\G2.a*T3, T3\G2.b, G2.c*T3, 0);

>>t2 = inv(G3.a(1:2,3:4));
>>T4 = [eye(2) zeros(2);zeros(2) t2];
>>G4 = ss(T4\G3.a*T4, T4\G3.b, G3.c*T4, 0);}
```

Figure 8: Matlab pseudo-code for similarity transformation

6 Contribution of the thesis

6.1 Main results

In accordance with the stated objectives, the thesis brings the following concrete contributions.

- We provide a comprehensive review of techniques and procedures commonly used in fMRI area especially from systems identification point of view. We present elementary terminology of fMRI area, basic principle of fMRI measurement and we also mention some basic methods of fMRI data modeling, see State-of-the-Art, chapters 3 and 4.

- We present commonly used tool for fMRI processing called SPM toolbox in chapter 4. We also give a description of Dynamic Causal Modeling technique for intrinsic structure detection and discuss some advantages and drawbacks of that from user's viewpoint within cooperation with Department of Neurology, 1^{st} Faculty of Medicine, Charles University in Prague and project called Writer's cramp study. We develop joint paper "Repetitive TMS of the somatosensory cortex improves writer's cramp and enhances cortical activity" published in Neuro Endocrinology Letters. The results and our experience with DCM implemented in SPM toolbox are shown in chapter 5.

- We present subspace identification methods for fMRI data modeling and consider them as certain alternative to DCM procedure. We show intrinsic structure detection on simplified case - paper "Dynamic causal modeling and subspace identification methods" is published in Biomedical Signal Processing.

7 Publications and references

Publications

7.1 Publications of the author related directly to the thesis

Journal Papers

[1] Tauchmanová J.; Computer controlled switching device for deep brain stimulation, *Acta Polytechnica*, 2007, vol. 47, p.4-5.(100%)

[2] Nováková J., Hromčík M. and Jech R.; Dynamic Causal Modeling and subspace identification methods, *Biomedical Signal Processing and Control*, 2012, vol.7, p. 365-370. ISSN 1746-8094. (Impact factor 2012 is 1.000). (45%)

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8 Anotace

Funkční magnetická rezonance (fMRI) je moderní metoda používaná neurology pro získání trojrozměrného obrazu aktuálního lokálního průtoku krve v mozku, na základě čehož je tak možné usuzovat na lokální neurální aktivitu. Například je tak možné detekovat mozková centra zapojená do tzv. hemodynamické odezvy na konkrétní podněty.

Cílem práce je aplikovat metody z oboru identifikace a odhadování dynamických systémů pro získání modelu mozkové aktivity. Nejprve je však nutné seznámit se se základními principy a metodami používanými při měření a zpracování fMRI dat.

Velká část práce je věována tzv. DCM proceduře, která detekuje vazby mezi vybranými oblastmi mozku. Procedura je posuzována i z uživatelského hlediska na reálných fMRI datech a to v rámci studie s pacienty s písařskou křečí prováděné na Neurologické klinice při 1. Lékařské fakultě UK.

Na toto zhodnocení DCM procedury pak navazuje formulování úlohy detekce vazeb mezi vybranými oblastmi mozku jako úlohy pro metody modelování dynamických systémů. Použity jsou subspace identifikační metody a na jednoduchém příkladu jsou použity jako slibná alternativa k DCM proceduře.