NETWORK MODEL INSPIRED BY THE REAL DATA – FUNCTIONAL BRAIN NETWORKS

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Abstract. In this paper we studied degree distributions of functional brain networks, which a re extracted from the real fMRI measurements of young healthy participants at three different correlation thresholds of voxel activity. To explain how the degree distribution changes with the decreasing threshold, we created a dynamic network model. The model reflects how initially scale-free networ ks change their structure, manifested in the degree distribution, due to the processes of the network growth and edge addition.

1 Introduction

1.1 fMRI

Functional Magnetic Resonance Imaging (fMRI) is a technique capturing high-resolution images of the brain neural activity, based on the blood-oxygen-level-dependent (BOLD) signal [4]. Images in the fMRI method are captured in a series of 3-d slices. A single slice is comprised of a grid of discrete 3D regions known as voxels. Spatial resolution of a single fMRI image is around 3 mm^3 per each voxel. fMRI is an ideal technique for deriving functional brain connectivity, defined by the extent to which spatially distinct regions of the brain exhibit similar behavior over time. By modelling this functional connectivity as a network (functional brain network), we can explore the ways in which regions of the brain interact, and use techniques from the graph theory to evaluate their topological characteristics. Voxels, are represented in a network as nodes, and interaction between voxels as edges [3, 8, 13].

1.2 Graph theoretical concepts

Graph $G(V, E)$ consists of $N = |V|$ nodes, connected by $M = |E|$ edges [18], while V and E denote node and edge sets, respectively. Network is a graph that has some dynamics. Binary network is a network having undirected unweighted edges. If there are no multiple edges and no node is connected to itself in a binary network, it can be represented as a simple

graph [18]. All the following definitions are for simple, binary networks. The node degree is the number of edges incident with the node. The degree distribution shows how many nodes in the network has certain degree. To measure clustering of nodes clustering coefficient of the node i is defined as:

$$C_i = \frac{2m_i}{k_i\,(k_i - 1)}\ ,$$ (1)

where m_i denotes the number of edges among neighbors of the node i and k_i is its degree. Average network clustering coefficient is denoted as C. Average shortest path l, is defined as an average of shortest paths (measured in the number of edges) between all pairs of nodes [18]. As shown by [1] and others [5, 9], real-world networks developed by self-organized processes, have usually scale-free structure. Scale-free property is reflected in the power law degree distribution (2). The normalized number of nodes with the degree k, $P(k)$, decreases as a power law with the scaling exponent γ,

$$P(k) \propto k^{-\gamma}.$$ (2)

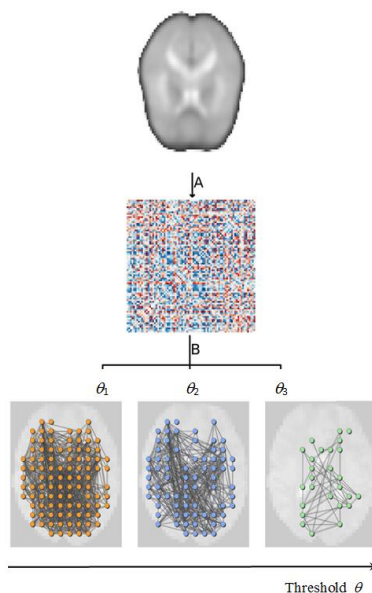As shown in [1], the scale-free structure develops due to a preferential node linking.

Fig. 1. Steps in functional network creation. A: Correlation matrix for the fMRI volume of each participant. B: From each correlation matrix, three unweighted, undirected networks were created, using three correlation thresholds $\theta_1 \pi \theta_2 \pi \theta_3$. So the resulting networks contain different number of nodes and edges.

1.3 The goals

The aim of this paper is to study and model real world networks by means of the graph theoretical methods. For this purpose, the functional brain networks derived from the brain fMRI data of healthy young (HY) participants collected by Buckner et al. [2] were used. We

analyze how degree distributions of functional brain networks change due to the correlation threshold changes. Based on this analysis we developed a network model that links the underlying network dynamics with the network structure manifested as the degree distribution at different thresholds. We test how the model fits the data by its numerical simulation.
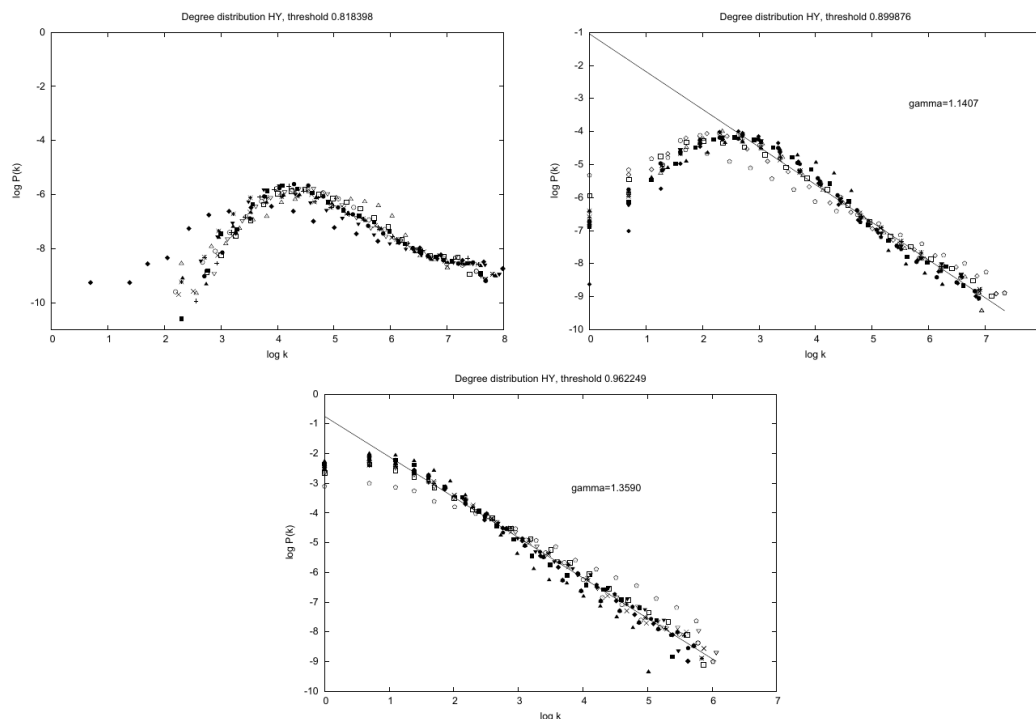

Fig. 2. Degree distributions from left to right: distribution at the threshold $\theta_1 = 0.818398$, the threshold $\theta_2 = 0.899876$, and the threshold $\theta_3 = 0.962249$. See how the scale-free network structure is destroyed, as the correlation threshold gets lower and lower.

2 The data

2.1 The fMRI datasets

The raw fMRI data were collected by Buckner et al. [2] and are publicly available (data set no. 2-2000-118W from the fMRI Data Center: http://www.fmridc.org). Structural and functional MRI data were acquired from 41 subjects in total. The participants were divided into three groups: healthy young (HY) participants, healthy elderly (HE) participants and elderly participants with diagnosed Alzheimer's disease (AE). The HY group used for our studies has 14 subjects (9 females/5 males) with the mean age 21.1 years. The data are preprocessed before being used in this and other studies [13]. Preprocessing applied to the data is described in detail in [11].

2.2 Functional brain networks

For each participant in each group the prepossessed fMRI data were used to create functional brain networks [11]. Functional brain networks, contrary to the neuronal brain networks, are based on the temporal correlation of signals between the voxels over some time. Thus, the functional brain network reflects the functional cooperation of different brain areas. Because the smallest unit of the measured fMRI signal is an integrated signal of the neurons contained

in one voxel, voxels are natural candidates for the nodes of the functional brain network. If the two voxels functionally cooperate, the measured BOLD signal is highly correlated over time. The Pearson correlation coefficient is calculated for all the voxel pairs:

$$r(i, j) = \frac{\langle V(i,t)V(j,t)\rangle - \langle V(i,t)\rangle\langle V(j,t)\rangle}{\sigma(V(i))\sigma(V(j))} , \tag{3}$$

where $r(i, j)$ is the correlation coefficient between the pair of nodes, $V(m,t)$, $m = i, j$ is the measured activity in the m-th voxel at time t, $\langle.\rangle$ denotes the time average, and $\sigma^2(V(m)) = \langle V^2(m,t)\rangle - \langle V(m,t)\rangle^2$. A link between the voxel pair (nodes) is established, if $|r(i, j)| \phi \theta$, where θ is a prescribed correlation threshold (Fig.1). We opted for an absolute value of correlation that is both strongly positively and strongly negatively correlated voxels to be included in the functional network. Thus, the networks are unweighted and undirected, because correlation $r(i, j)$ is a symmetric function.
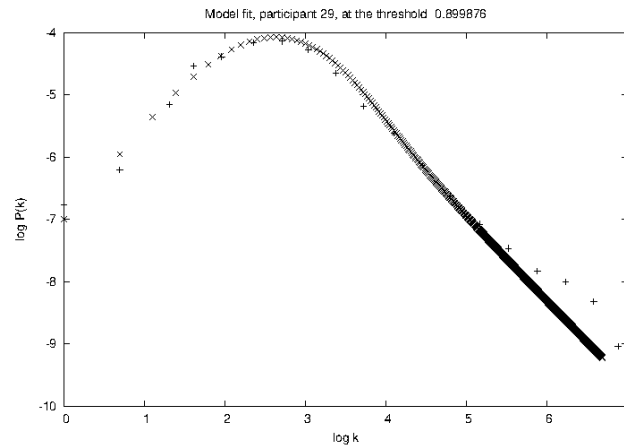

Fig. 3. The best fit for the threshold θ_2. Model fit for the participant No.29, `+' -- data, `x' -- simulation. 800 iterations, b=3.7479, a=1.3958, $b_1 = 243.14$, $a_1 = 0.0$, mse=0.086.

2.3 Towards the model of functional network dynamics

We used the degree distributions extracted from the HY functional networks for different correlation thresholds, in order to get an insight into the network changes as the value of the threshold changes from high to low. The data for HY group were chosen because of their coherence and the smallest differences among subjects. Based on this analysis we built our dynamic network model. We are aware, that to speak about "dynamics" in the context of our model is not quite correct, because the independent variable is not time. Nevertheless, we believe, to use this term with respect to the model iteration steps, is not misleading.

Character of the degree distribution is an indicator whether the functional brain networks are scale-free or not. The scale-free property means that the model should incorporate preferential linking, while the loss of the scale-free structure with the changing correlation threshold,

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means that there are random link additions present too. As the power law degree distribution gradually changes, each intermediate stage reflects the ratio of preferential versus random linking. All of this should be incorporated into the formal mathematical model.
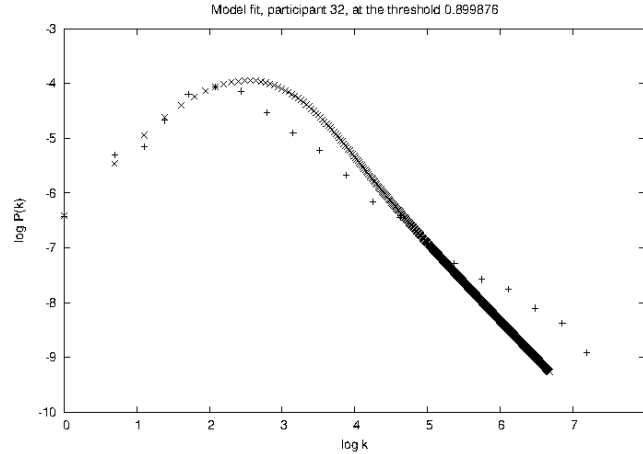

Fig. 4. The worst fit for the threshold θ_2, `+' -- data, `x' -- simulation. Model fit for the participant No. 32 , 800 iterations, $b = 3.61$, $a = 1.87$, $b_1 = 528,52$, $a_1 = 0.0$, $mse = 0.28$.

3 Results

3.1 Data analysis – whole brain network

In this section, a basic network analysis of the measured data is presented. The networks are constructed at the three different correlation thresholds $\theta_1 = 0.819398$, $\theta_2 = 0.899876$ and $\theta_3 = 0.962249$. The reason for these threshold values are explained in [11]. For the lowest correlation threshold $\theta_1 = 0.819398$, the average number of network nodes is $N_1^{HY} = 10487$ (interval of the individual values is $[9850, 11140]$). The average group clustering coefficient is $C_1^{HY} = 0.4594$; and the average group shortest path is $l_1^{HY} = 2.5677$. All individual values of the average clustering coefficients are in the interval $[0.4029, 0.5593]$ and that of the shortest paths are in the interval $[2.3519, 2.6877]$, respectively. For the lowest correlation threshold, the degree distribution does not have a power law character (Fig. 2).

For the threshold $\theta_2 = 0.899876$, the group average number of nodes is somewhat lower, i.e. $N_2^{HY} = 10426$ with the individual values in the interval $[9842, 11140]$. The average group clustering coefficient is $C_2^{HY} = 0.3982$, with individual values in the interval $[0.36128, 0.4822]$ and the average group shortest path is $l_2^{HY} = 3.7981$ with the individual values in the interval $[3.3168, 4.015]$. The degree distribution reveals a more pronounced power law tail, with the average group exponent $\gamma_2^{HY} = 1.41$ (see Fig. 2).

The situation changes for the correlation threshold $\theta_3 = 0.962249$. The functional brain networks have a well-defined scale-free structure, reflected in the power law degree distribution with the average scaling exponent $\gamma_3^{HY} = 1.36$ (Fig. 2) with the individual values in the interval $[0.9346, 1.7812]$. Other characteristics are $N_3^{HY} = 7280$, $C_3^{HY} = 0.3616$ and $l_3^{HY} = 7.3596$, with the individual values in the intervals $[6482, 8582]$, $[0.3366, 0.4049]$, and $[5.6129, 9.6049]$, respectively.
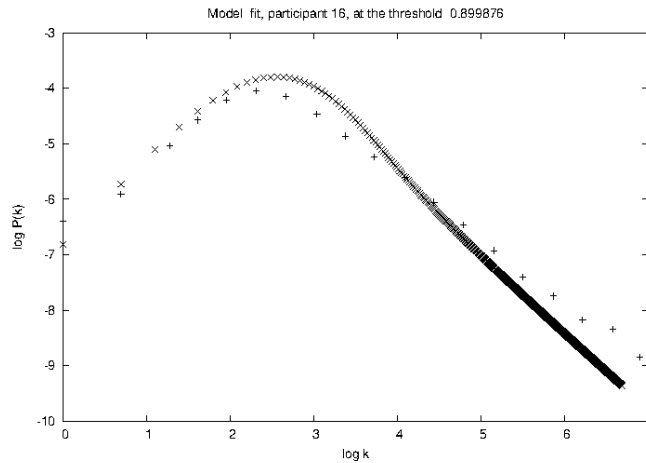

Fig. 5. Typical fit for the threshold θ_2, `+' -- data, `x' -- simulation. Model fit for the participant No. 16, 800 iterations, $b = 4.9$, $a = 0.0$, $b_1 = 255.48$, $a_1 = 0.0$, $mse = 0.19$.

4 The model

Recently, several papers proposed models of functional brain networks using various principles [7, 14, 16]. Our data analysis has shown that the properties of the functional brain networks depend mainly on the correlation threshold. For the lower correlation thresholds, the degree distributions do not have a power law character, but rather have a shape more resembling the degree distribution of the random graph [18]. As the threshold increases, the distributions develop power law tails (Fig. 2). Similar scenario is described in Scholz et al. [15] for the noisy scale-free networks. The authors started from an initially scale free network, disturbed by several types of noise: i.e. random link removal, random link exchange and random link addition. They have studied how the degree distribution drifts from the power law character with the increasing noise.

We adopted the idea of the random link addition noise to reflect degree distribution changes while lowering the threshold of correlation. Unlike the original model, we allow the network to grow and we also allow preferential link addition. We suppose, it is possible to lower the threshold by such a slow way, that at each threshold jump one new node comes to the system. Thus, each network growth step or iteration is marked by an addition of a new node. The situation, can be described as follows: One starts at the highest threshold θ_3, where the network is scale-free having N_0 nodes, L_0 edges and the power law degree distribution. Then the threshold is lowered. New nodes and edges are added to the network by both -

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preferential and random linking. New node is added due to the fact, that the signal of such a new node (voxel) is now correlated with some node (voxel) signal already present in the network, which were not previously correlated at the higher threshold. Each new node brings a_1 new edges, which are linked preferentially and a edges linked randomly. Simultaneously another process takes place. As the threshold decreases, some correlations between the pairs of nodes already present in the network become significant. Therefore new edges are distributed randomly (b) and preferentially (b_1) among the nodes being already in the network. Thus, our network grows in the number of nodes and edges. Because the network at the highest threshold is scale-free, we suppose, that the real correlations between voxels construct the scale-free structure, which is, as the threshold lowers, disturbed by the accidental correlations (edges). These correlations are caused either by the real similarity between the two voxel signals or by their accidental resemblance.
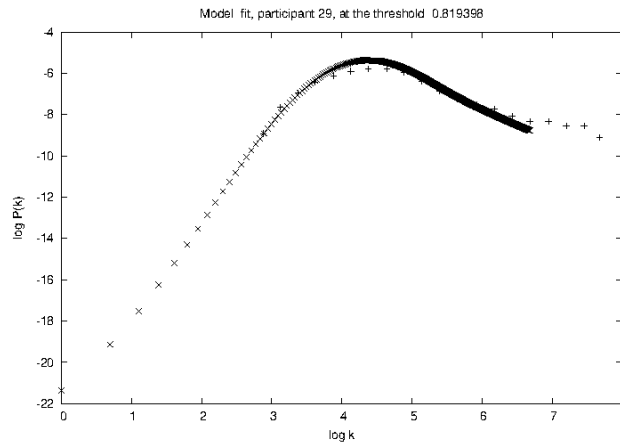

Fig. 6. The best fit for the threshold θ_1. Model fit for the participant No. 29, `+' -- data, `x' – simulation, 800 iterations, parameters b=14.44, a=12.24, $b_1 = 888.39$, $a_1 = 1.77$, mse=0.29.

The rate equation describing the above-mentioned dynamic processes in the model is:

$$P(k, n+1) = p_{k,k-1}(n)P(k-1,n) + \left((1 - p_{k+1,k}(n))P(k,n)\right) . \qquad 4$$

The transition term $p_{k,k-1}(n)$ is defined as

$$p_{k,k-1}(n) = \frac{a + 2b}{N_0 + n} + \frac{(a_1 + 2b_1)(k-1)}{2L_0 + A(n)} \qquad , \qquad 5$$

where $A(n) = 2n(a + b + a_1 + b_1)$. In equation (4), $P(k,n)$ is the normalized number of nodes having the degree k at the iteration n. At each iteration, this number changes, due to the fact, that some nodes having at the previous iteration n the degree $k-1$, gain a new edge. This is expressed in the first term of the equation (4). The second term expresses, that some nodes have the degree k already at iteration n and with the probability $1 - p_{k+1,k}(n)$ no new edges are added. In equation (5), N_0, L_0 denote initial number of nodes and edges, a, b are the number of randomly added edges per iteration, where a is the number of edges fetched by a

new coming node and b is the number of edges added between older network nodes. Similarly, a_1 denotes the number of edges by which a new node links preferentially to the network and b_1 is the number of edges linking older nodes preferentially. Factor two denotes, that some edges are linked by both of their ends, unlike those edges, which have one edge end linked to the new coming node. The transition term $p_{k+1,k}(n)$ describes how the number of nodes having the degree k changes due to the above-mentioned dynamic processes. The first term of $p_{k+1,k}(n)$ says that $a + 2b$ edge ends are linked randomly, with equal probability $\dfrac{1}{N_0 + n}$ to the node in the network. The number of nodes in the network at iteration n is $N_0 + n$, because, as stated before, at each iteration (threshold step) exactly one new node appears. The second term of $p_{k+1,k}(n)$ describes preferential attachment of $a_1 + 2b_1$ edge ends with the probability proportional to the node degree. The normalization factor is a sum of all node degrees $2L_0 + A(n)$.
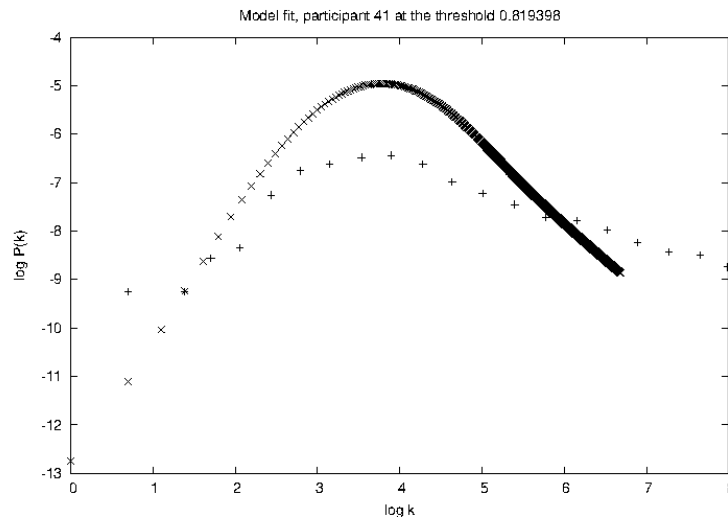

Fig. 7. The worst fit for the threshold θ_1. Model fit for the participant No 41, `+' -- data, `x' -- simulation. 800 iterations, $b = 6.97$, $a = 6.88$, $b_1 = 824.46$, $a_1 = 0.06$, $mse = 1.38$.

5 Results of numerical simulations

We simulated the proposed model (4, 5) numerically. Each simulation was done for all appropriate functional brain HY networks and compared to the data at the thresholds θ_2 and θ_1. Here we present the best, the worst and the typical fit for the threshold θ_2 (Fig 3, Fig 4, Fig 5) and the same for the threshold θ_1 (Fig 6, Fig 7, Fig 8).

First, we used the experimental data to find the parameters in the power law distributions at threshold θ_3 (6). This threshold corresponds to the initial number of iterations $n_0 = 0$. Thus, the initial degree distribution is power law i.e.:

$$P(k) = ck^{-\gamma} . \tag{6}$$

Both parameters c and γ are derived from the data. The power law distribution at the highest threshold was normalized by the constant z calculated from the equation

$$z = \int_{1}^{\infty} P(k)\,dk , \tag{7}$$

and it was checked whether the sum of all probabilities of the initial distribution is close to one after the normalization. We excluded the networks, for which the integral (7) does not converge (case $0.0 \, \pi \, \gamma \, \pi \, 1.0$). The model (4, 5) was first applied to model the transition between the two highest correlation thresholds θ_3 and θ_2. Each model has been iterated $N_2 - N_0$ times for the defined set of parameters a, a_1, b, b_1. N_0, N_2 denote the number of nodes at the initial network state (threshold θ_3) and at the network state corresponding to the correlation threshold θ_2, respectively. In each network growth step (a discrete small threshold change), a fixed number of edges is added, namely $\dfrac{L_2 - L_0}{N_2 - N_0}$, where L_2 is the number of network edges gained from the measured data at the threshold θ_2 and L_0 is the initial number of edges. To find the best set of parameters a, b, a_1, b_1 we used the hill climbing algorithm, in which the mean square error between the measured and simulated data is calculated. From the best fit parameters in the current simulation, fifteen new sets of parameters were derived by the slight perturbations of the currently best fit parameter set. This is a standard procedure in the hill climbing algorithm. The hill climbing algorithm was iterated 800 times. Second, the same job as before has been done to model the data at the threshold θ_1. The only difference is, that the model was iterated $N_1 - N_0$ times, where N_1 is the number of nodes at the threshold θ_1. Also the number of edges added in each threshold (network growth) step is different, namely $\dfrac{L_1 - L_0}{N_1 - N_0}$, where L_1 is the number of edges in the functional brain network created at the lowest threshold θ_1.

5. 1 Results for the HY group

In the HY group we excluded one participant (number 39), since the γ exponent is such that the normalization (7) does not converge. In Fig 3, the best fit at the θ_2 threshold is presented. The participant number is 29 and for this participant the overall best fits have been achieved. We got the worst fit at the θ_2 threshold for the participant number 32 (Fig.4). For illustration also a typical results (Fig.5) in the HY group are presented. Next results are for the lowest threshold θ_1 (Fig.6). We show the best fits again for the participant (No. 29). The worst fit has been achieved for the participant 41 (Fig. 7). The typical results at this threshold are presented at Fig. 8.

6 Summary

In this paper, the degree distributions of functional brain networks were analyzed. We found that:

1. At the threshold θ_3 the degree distributions are scale-free (Fig.2). This is in agreement with previous studies [10, 6] on different fMRI data sets.
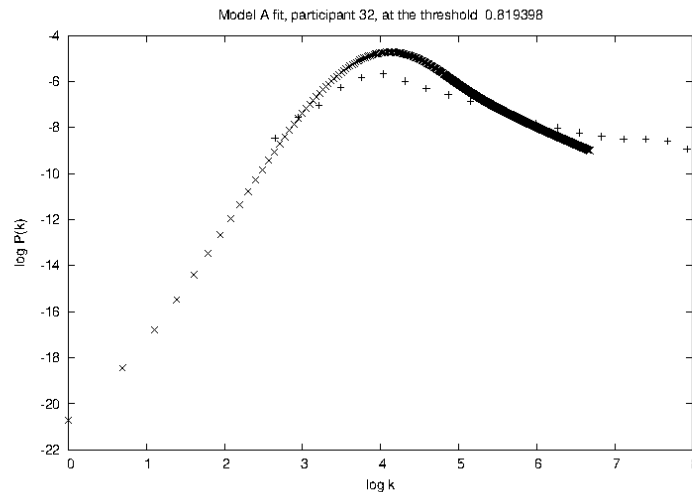
Fig. 8. The typical fit for the threshold θ_1. Model fit for the participant No. 32, `+' -- data, `x' -- simulation. 800 iterations, $b = 22.43$, $a{=}5.34$, $b_1 = 867.64$, $a_1 = 0.97$, $mse{=}0.87$.

2. The character of the degree distribution changes with the threshold. As the threshold decreases, the degree distributions are losing their scale-free character.
3. There are individual differences in the degree distributions at each threshold.
4. Our model is successful in fitting the different correlation thresholds.

The distribution analysis formed a prerequisite for the model addressing the question which dynamical processes causes the scale-free functional brain networks to change their structure.

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