

# Efficient Markov Chain Monte Carlo Estimation of Exponential Random Graph models

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# Introduction

**We have developed efficient Markov chain-based algorithm to perform Maximum Likelihood parameter estimation for probability distributions with intractable normalizing constants**

ERGMs are exponential family of probability distributions for dependent network data

$$\pi(x, \theta) = \frac{1}{k} \exp\left(\sum_A \theta_A z_A(x)\right)$$

$$k = \sum_x \exp\left(\sum_A \theta_A z_A(x)\right)$$

$z_A(x)$  are networks statistics (number of ties, triangles, starts ..)

Robins G, Snijders T, Wang P, Handcock M, & Pattison P (2007) Recent developments in exponential random graph ( $p^*$ ) models for social networks. *Social Networks* 29(2):192-215.

# Introduction

We want to find MLE of the model parameters  $\theta$

$$E_{\pi(\theta)}(z_A(x)) = z_A(x_{obs})$$

$E_{\pi(\theta)}(z_A(x)) = \sum_x z_A(x)\pi(x, \theta)$  are expected statistics

Metropolis-Hastings algorithm may be used to compute  $E_{\pi(\theta)}(z_A(x))$  and to generate **simulated data**  $x(\theta)$

And we want to solve inverse problem: find  $\theta(x_{obs})$

# Introduction

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Why we want to find  $\theta(x_{obs}) : E_{\pi(\theta)}(z_A(x)) = z_A(x_{obs})$

$$\partial E_{\pi(\theta)}(z_A(x)) / \partial \theta_A > 0$$



If  $\theta_A(x_{obs}) > 0$  then  $z_A(x_{obs})$  is larger than expected by chance only



By estimating  $\theta_A(x_{obs})$  we study structural features in empirical network data

Geyer CJ & Thompson EA, Constrained Monte Carlo Maximum Likelihood for dependant data, Journal of the Royal Statistical Society (1992)

Snijders, Tom AB. Markov chain Monte Carlo estimation of exponential random graph models, Journal of Social Structure, 1-40 (2002)

# Existing estimation approaches

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- 1) Bayesian
- 2) Geyer-Thompson MCMCMLE
- 3) Method of Moments  
(Stochastic approximation)

- Iteratively update  $\theta_A$
- At many different  $\theta_A$  values perform MCMC simulations to draw simulated data  $x(\theta_A)$



MLE is computationally expensive

Geyer CJ & Thompson EA, Constrained Monte Carlo Maximum Likelihood for dependant data, Journal of the Royal Statistical Society (1992)

Snijders, Tom AB. Markov chain Monte Carlo estimation of exponential random graph models, Journal of Social Structure, 1-40 (2002)

# New approaches for MLE

**We can find MLE without MCMC simulation**

Given the state  $x$  the state  $x'$  is proposed with probability  $q(x \rightarrow x')$

Acceptance probability  $\alpha(x \rightarrow x', \theta_A) = \min \left\{ 1, \frac{q(x' \rightarrow x)\pi(x', \theta_A)}{q(x \rightarrow x')\pi(x, \theta_A)} \right\}$

Transition probability  $P(x \rightarrow x', \theta_A) = q(x \rightarrow x')\alpha(x \rightarrow x', \theta_A)$

Metropolis N, Rosenbluth AW, Rosenbluth MN, Teller AH, & Teller E Equation of state calculations by fast computing machines. *The journal of chemical physics* 21, 1087-1092 (1953)  
Hastings WK, Monte Carlo sampling methods using Markov chains and their applications. *Biometrika* 57, 97-109 (1970)

# New approaches for MLE

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We can find MLE from the following **Equilibrium Expectation** condition:

$$\sum_{x'} P(x_{obs} \rightarrow x', \hat{\theta}) (z_A(x') - z_A(x_{obs})) = 0$$

It may be shown that if  $x_{obs}$  is a simulated data, drawn from  $\pi(x, \theta^*)$  then we can estimate true  $\theta^*$  from EE

# MLE for simulated data

**And we obtain very fast MLE!**

We have to find  $\hat{\theta}$  such that

$$dz_A(x_{obs}, \hat{\theta}) = 0$$

$$dz_A(x_{obs}, \theta) = \sum_{x'} P(x_{obs} \rightarrow x', \theta_A) (z_A(x') - z_A(x_{obs}))$$

$dz_A(x_{obs}, \theta)$  may be computed by Monte Carlo integrations,  
without time consuming MCMC simulation

We have developed iterative algorithm to solve  $dz_A(x_{obs}, \hat{\theta}) = 0$



# New approaches for MLE

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How to apply this theory if  $x_{obs}$  is not drawn from  $\pi(x, \theta)$  ?

We can perform MCMC simulation constraining the values of statistics  $z_A(x)$  to the observed values  $z_A(x_{obs})$

# Efficient MCMC sampler for complex networks

Let one of statistics is the number of network ties  $L(x)$

$$\pi(x, \theta) = \frac{1}{k} \exp \left( \sum_{A \neq L} \theta_A z_A(x) + \theta_L L(x) \right)$$

**IFD sampler**

$L(x)$  may be constrained by a special proposal:

$$q(x \rightarrow x') = \begin{cases} \text{Fill randomly selected null dyad if } L(x) = L_{obs} \\ \text{Delete randomly selected tie if } L(x) > L_{obs} \end{cases}$$

$$\alpha(x \rightarrow x') = \min \left\{ 1, \exp \left( \sum_{A \neq L} \theta_A \Delta z_A(x) + \Delta z_L \left( \theta_L + \log \left( \frac{L_{\max} - L_{obs}}{L_{obs} + 1} \right) \right) \right) \right\}$$

**The corresponding parameter  $\theta_L$  is found from EE**

# Motivation for new estimation method

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When IFD sampler is applied the parameter  $\theta_L$  is found from EE

Byshkin M, Stivala A, Mira A, Krause R, Robins G, Lomi A, Auxiliary Parameter MCMC for Exponential Random Graph Models J. Stat. Phys. 165: 740-754 (2016)

If we manage to estimate all the parameters in a similar way then we can suggest **very efficient estimation method**

# EE algorithm for empirical data

We can apply this methodology for empirical data if we can draw simulated data  $x$  so that  $z_A(x) = z_A(x_{obs})$

$$\left. \begin{aligned} \sum_{x'} P(x \rightarrow x', \theta_A) (z_A(x') - z_A(x)) &= 0 \\ z_A(x) &= z_A(x_{obs}) \end{aligned} \right\} \Rightarrow E_{\theta} (z_A(x)) = z_A(x_{obs})$$

We have developed MCMC algorithm to solve this system of equation

# EE algorithm for empirical data

## MCMC to constrain the values of all the statistics

- 1: Initialization:  $t=0$ ;  $x = x_{obs}$ ;  $\theta_A(t=0) = \tilde{\theta}_A(t=M1)$ ;  $dz_A = 0$
- 2: **for**  $k=1$  to  $m$  **do**
- 3:     Propose move  $x \rightarrow x'$  with probability  $q(x \rightarrow x')$
- 4:     Using [4] calculate Metropolis-Hastings acceptance probability  $\alpha(x \rightarrow x', \theta(t))$
- 5:     **If**  $\alpha(x \rightarrow x', \theta(t)) > Unif([0,1])$  **then**  $dz_A = dz_A + z_A(x') - z_A(x)$  **and perform this move:**  $x = x'$
- 6: **end for**
- 7: Update of parameters  $\theta_A(t+1) = \theta_A(t) - K_A \cdot \text{sgn}(dz_A)(dz_A)^2$
- 8: Increment  $t$ . Save sequences  $dz_A(t) = dz_A$ ; **If**  $t < M$  **then** go to step 2

# EE algorithm for empirical data

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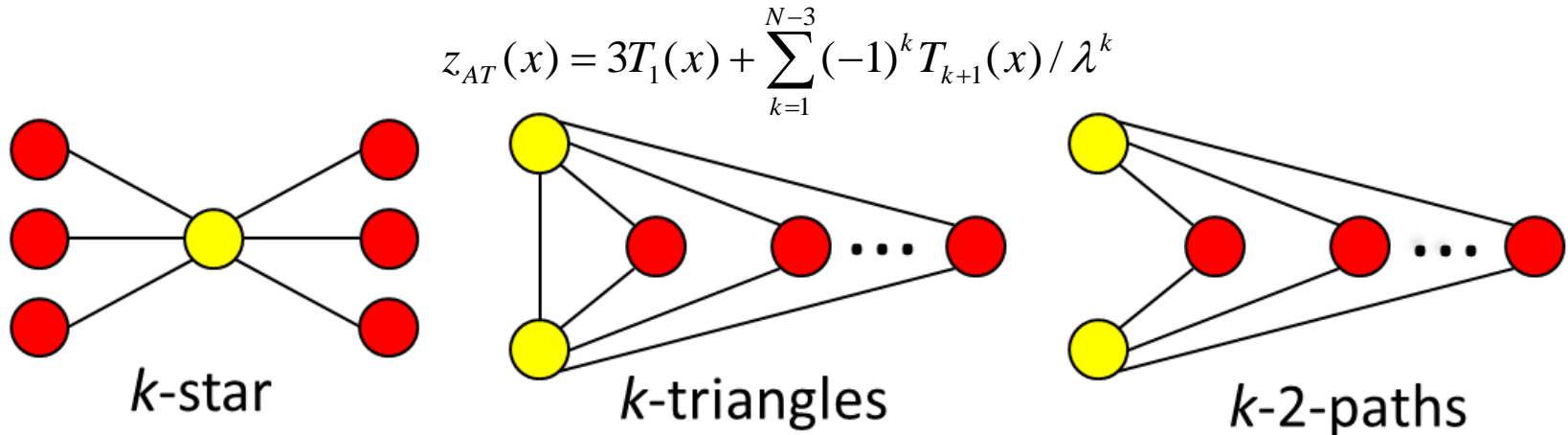
MoM (Snijders 2002) and MCMCMLE (Geyer CJ & Thompson 1992) require many converged outputs of Metropolis-Hastings algorithm

EE algorithm does not need such outputs. Instead it generates one converged output

EE algorithm is similar to Metropolis-Hastings algorithm, but allows Monte Carlo simulation to be performed while constraining the values of statistics  $z_A(x)$  and in such a way that the EE condition is satisfied

# Tests and applications

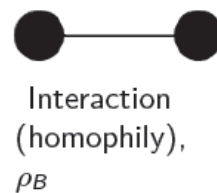
## Networks statistics typical for social networks



Node attributes



$$z_{\rho} = \sum_{i,j} a_i x_{ij}$$



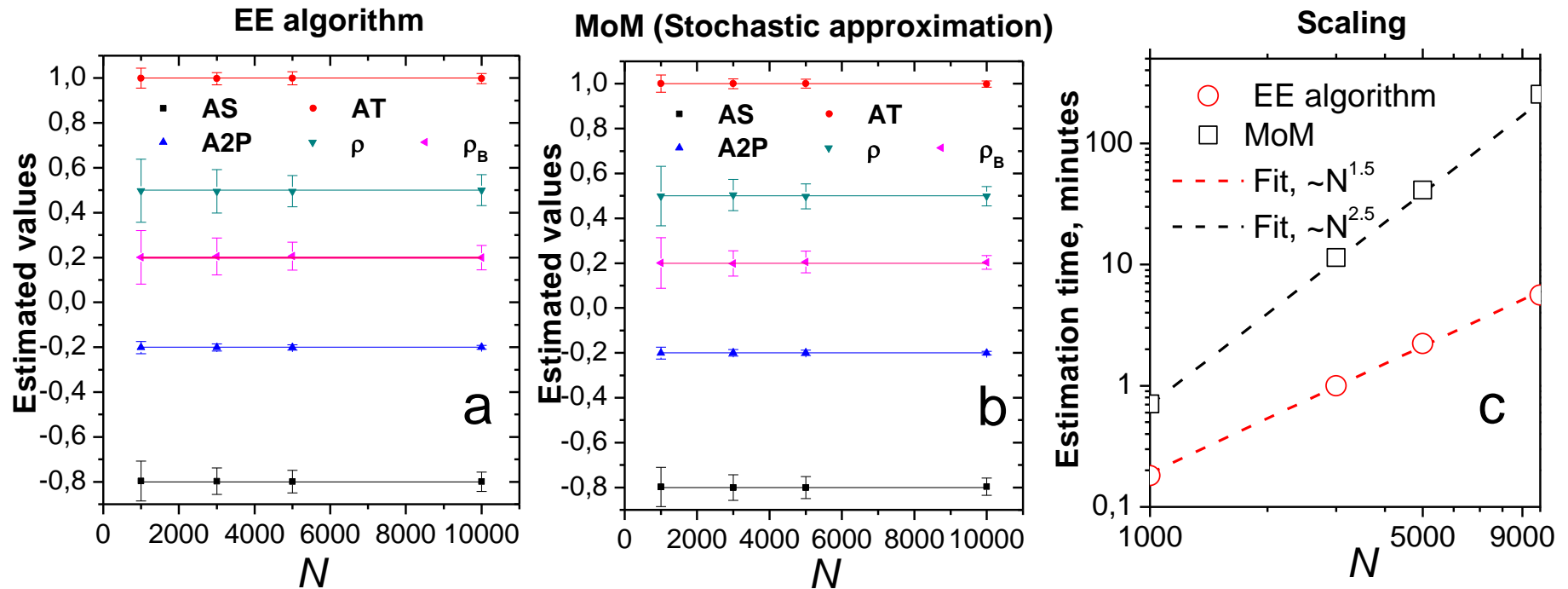
$$z_{\rho_B} = \sum_{i,j} x_{ij} a_i a_j$$

$$z_{Match} = \sum_{i,j} x_{ij} \delta_{a_i, a_j}$$

Snijders T.A., Pattison P.E., Robins G.L., Handcock M.S., New specifications for exponential random graph models, *Sociological Methodology* **36**(1), 99-153 (2006)

# Tests and applications

We use EE algorithm to estimate parameters of ERGMs



With EE algorithm the estimation time grows with number of nodes  $N$  almost linear



# Tests and applications. Biological networks

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Arabidopsis Interactome Mapping Consortium. *Science*, 333(6042):601–607, 2011.

C. von Mering, et al. Comparative assessment of large-scale data sets of protein–protein interactions. *Nature*, 417(6887):399–403, 2002

T. Rolland et al. A proteome-scale map of the human interactome network. *Cell*, 159(5):1212–1226, 2014.

X.-T. Huang, et al An integrative *C. elegans* protein–protein interaction network with reliability assessment based on a probabilistic graphical model. *Molecular BioSystems*, 12(1):85–92, 2016.

S.-y. Takemura, et al. A visual motion detection circuit suggested by *Drosophila* connectomics. *Nature*, 500(7461):175–181, 2013

S. S. Shen-Orr et al, Network motifs in the transcriptional regulation network of *Escherichia coli*. *Nature Genetics*, 31(1):64–68, 2002.

# Tests and applications. Biological networks

Method	Network	Average sample size	$N_c$	Avg. estim. time (m)	Elapsed time
EE (IFD sampler)	<i>A. thaliana</i> PPI	2160	20	1.1	01 m 50 s
EE (IFD sampler)	Yeast PPI	2617	20	6.6	09 m 07 s
EE (IFD sampler)	Human PPI	4303	20	7.6	10 m 49 s
EE (IFD sampler)	<i>C. elegans</i> PPI	5038	20	6.8	09 m 35 s
EE (IFD sampler)	<i>E. coli</i> regulatory	418	20	0.6	00 m 43 s
EE (IFD sampler)	<i>Drosophila</i> optic medulla	1781	20	4.3	06 m 22 s
SA (IFD sampler)	<i>A. thaliana</i> PPI	2160	20	9.2	0 h 34 m 02 s
SA (IFD sampler)	Human PPI	4303	20	49.2	2 h 46 m 54 s
SA (IFD sampler)	Yeast PPI	2617	20	45.6	2 h 02 m 38 s
SA (IFD sampler)	<i>C. elegans</i> PPI	5038	20	766.5	25 h 07 m 44 s
SA (IFD sampler)	<i>E. coli</i> regulatory	418	20	0.0	0 h 00 m 06 s
SA (IFD sampler)	<i>Drosophila</i> optic medulla	1781	20	824.6	72 h 40 m 00 s
SA (basic sampler)	<i>A. thaliana</i> PPI	2160	0	—	(time limit)
SA (basic sampler)	Yeast PPI	2617	0	—	(time limit)
SA (basic sampler)	Human PPI	4303	0	—	(time limit)
SA (basic sampler)	<i>C. elegans</i> PPI	5038	3	204.5	7 h 40 m 20 s
SA (basic sampler)	<i>E. coli</i> regulatory	418	20	1.1	0 h 04 m 06 s
SA (basic sampler)	<i>Drosophila</i> optic medulla	1781	0	—	(time limit)
Snowball sampling	<i>A. thaliana</i> PPI	490.6	19	26.3	2 h 08 m 24 s
Snowball sampling	Yeast PPI	264.8	19	30.2	3 h 40 m 34 s
Snowball sampling	Human PPI	822.5	18	47.0	3 h 50 m 27 s
Snowball sampling	<i>C. elegans</i> PPI	496.4	16	270.7	40 h 00 m 33 s
Snowball sampling	<i>Drosophila</i> optic medulla	649.7	15	118.0	7 h 22 m 48 s

This research was supported by Melbourne Bioinformatics at the University of Melbourne, grant number VR0261

# Tests and applications. Biological networks

Network	Effect	Estimate (95% C.I.)			
		EE (IFD sampler)	SA (IFD sampler)	SA (basic sampler)	Snowball
<i>A. thaliana</i> PPI	AS	2.33 (2.24,2.42)	2.32 (2.23,2.42)	—	2.88 (1.72,3.10)
<i>A. thaliana</i> PPI	AT	1.28 (1.24,1.31)	1.27 (1.23,1.32)	—	0.00 (-0.01,0.01)
<i>A. thaliana</i> PPI	Edge	-14.99 (-15.01,-14.96)	-14.97	—	-14.76 (-16.26,-13.36)
<i>A. thaliana</i> PPI	Isolates	-7.14 (-7.58,-6.69)	-7.12 (-7.58,-6.66)	—	-10.49 (-11.21,-7.95)
Yeast PPI	AS	-0.05 (-0.10,0.01)	-0.05 (-0.10,0.01)	—	0.56 (-0.48,1.29)
Yeast PPI	AT	1.86 (1.81,1.91)	1.86 (1.82,1.90)	—	0.85 (0.18,1.07)
Yeast PPI	Edge	-7.76 (-7.81,-7.71)	-7.76	—	-6.57 (-13.42,-4.88)
Human PPI	AS	1.32 (1.29,1.35)	1.32 (1.29,1.35)	—	1.29 (0.67,2.04)
Human PPI	AT	1.37 (1.35,1.38)	1.37 (1.34,1.39)	—	0.03 (0.02,0.07)
Human PPI	Edge	-11.77 (-11.82,-11.73)	-11.77	—	-9.04 (-13.21,-7.21)
<i>C. elegans</i> PPI	AS	1.04 (1.01,1.07)	1.04 (1.01,1.07)	1.14 (1.03,1.25)	1.06 (0.83,2.16)
<i>C. elegans</i> PPI	AT	1.59 (1.58,1.61)	1.59 (1.57,1.61)	1.52 (1.47,1.57)	0.35 (0.19,0.41)
<i>C. elegans</i> PPI	Edge	-11.03 (-11.08,-10.98)	-10.99	-11.41 (-11.78,-11.04)	-8.82 (-13.40,-7.24)
<i>E. coli</i> regulatory	AS	0.45 (0.32,0.59)	0.44 (0.31,0.57)	0.44 (0.19,0.69)	—
<i>E. coli</i> regulatory	AT	0.78 (0.64,0.93)	0.79 (0.66,0.92)	0.79 (0.61,0.96)	—
<i>E. coli</i> regulatory	Edge	-6.55 (-6.63,-6.47)	-6.53	-6.53 (-7.24,-5.82)	—
<i>Drosophila</i> medulla	AS	0.23 (0.17,0.30)	0.24 (0.18,0.30)	—	1.17 (-0.64,1.58)
<i>Drosophila</i> medulla	AT	1.62 (1.56,1.67)	1.61 (1.57,1.65)	—	1.09 (0.86,1.29)
<i>Drosophila</i> medulla	Edge	-8.14 (-8.19,-8.09)	-8.16	—	-7.70 (-12.51,-5.12)

# Tests and applications. Large networks

With good scaling of EE algorithm we can obtain MLE for large dependent data

Citation networks of coauthors working on condensed matter physics  
40421 nodes and 175693 ties

Newman, M.E.: The structure of scientific collaboration networks. PNAS, 98(2), 404-409 (2001)

	$\theta_L$	AT	2-star	3-star	A2P	CPU time
Mean	-12.49	5.1	-0.011	$7.6 \cdot 10^{-5}$	-0.013	30 minutes
SD	0.018	0.014	0.00044	$4.3 \cdot 10^{-6}$	0.00057	

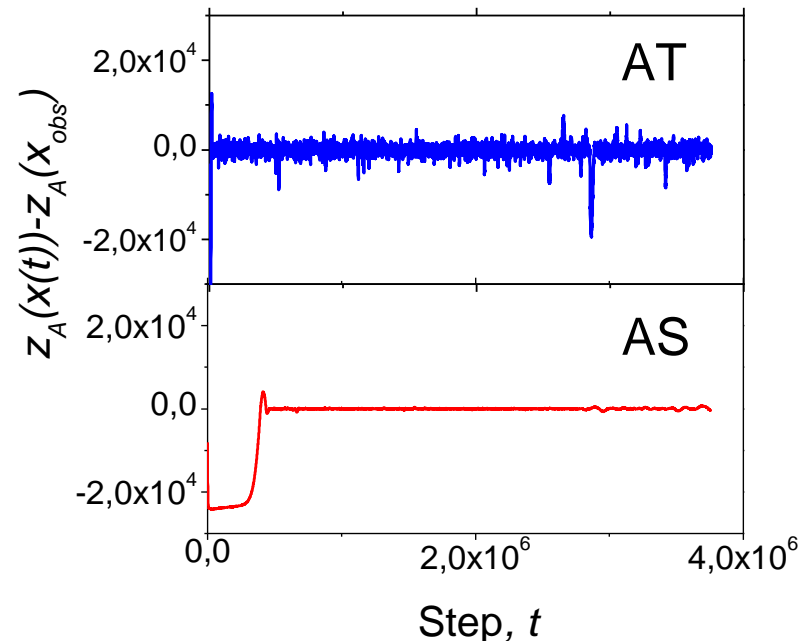
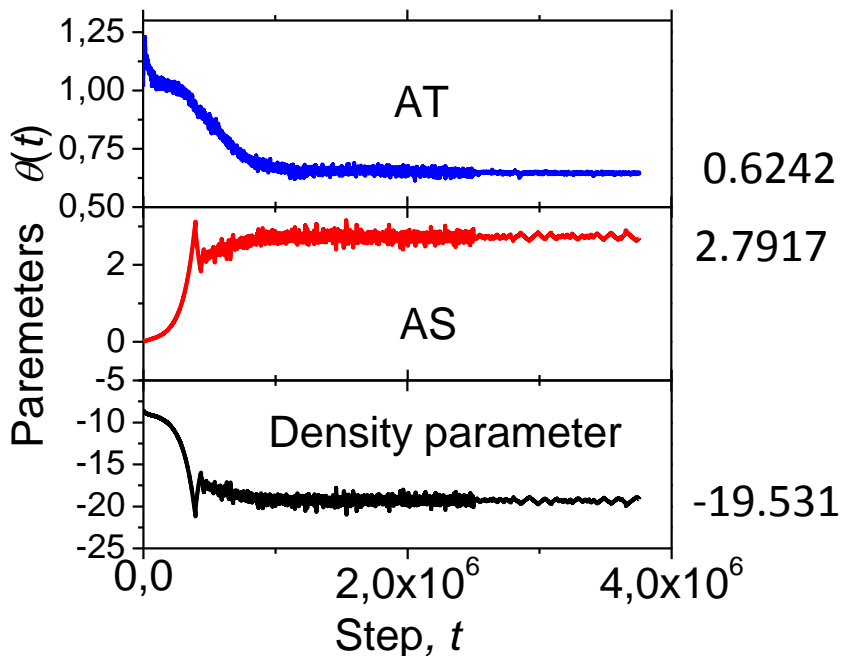
# Tests and applications. Large networks



was a social network for language learning  
104103 nodes and 2193083 ties

Output of EE algorithm with IFD sampler (in 12 hours)

Statistics is constrained to the observed values



# Tests and applications. Large networks



Networks with 104103 nodes and 2193083 ties

**Both convergence tests are passed**

Our convergence test

$$\left| \frac{\overline{z_A(x) - z_A(x_{obs})}}{SD(z_A(x) - z_A(x_{obs}))} \right| < 0.1$$

$\theta_A(t)$  converge



$$\sum_{x'} P(x \rightarrow x', \theta_A) (z_A(x') - z_A(x)) = 0$$

$$z_A(x) = z_A(x_{obs})$$

Convergence test of T. Snijders

$$t_A = \frac{E_{\pi(\theta)}(z_A(x)) - z_A(x_{obs})}{SD_{\pi(\theta)}(z_A(x))}$$

$$|t_A| < 0.3$$



$$E_{\pi(\theta)}(z_A(x)) = z_A(x_{obs})$$

# More presentations

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- Complex Networks, March 20-24, 2017, Dubrovnik, Croatia
- Sunbelt INSNA Conference, May 30-June 4, 2017, Beijing, China
- Cambridge Networks Day, 13th June 2017, Cambridge, UK
- PASC17, June 26 - 28, 2017, Lugano, Switzerland
- International Conference on Monte Carlo Methods and Applications, July 3-7, 2017, Montreal, Canada
- International Conference on Computational Social Science, July 10-13, 2017, Cologne, Germany
- Third European Conference on Social Networks, September 26 to 29, 2017, Mainz, Germany

The code will be available free of charge

[www.sonarcenter.eco.usi.ch](http://www.sonarcenter.eco.usi.ch)