

gáborcsárdi

computer scientist

334 Harvard street L3,
Cambridge, MA
02139 USA

+1 (857) 259-0417
csardi.gabor@gmail.com
@gaborcsardi
gaborcsardi.org
github.com/gaborcsardi

skills

Algorithms, data structures.
Graph algorithms,
network analysis.

expert

♥ R, C, Linux/Unix, Shell.

experienced

C++, Python, JavaScript,
Java, HTML/CSS, \LaTeX .

SQL and noSQL databases.

Software engineering tools,
git, Jenkins CI, etc.

education

- 2003–2008 **PhD**, *Eötvös University*, Budapest, Hungary, Computer Science.
Dissertation: Modeling complex systems as evolving networks
Summa cum laude.
- 1998–2003 **MSc**, *Eötvös University*, Budapest, Hungary, Computer Science.
Graduated with distinction (single in class).
Specialized in Programming Languages, Databases, Machine Learning and Economics.

experience

- 2011–2015 **Postdoctoral researcher**, Department of Statistics, Harvard University, Cambridge, MA, USA.
- 2008–2011 **Postdoctoral researcher**, Computational Biology Group, Department of Medical Genetics, University of Lausanne, Lausanne, Switzerland.
- 2006–2007 **Research Fellow**, Department of Biophysics, Research Institute for Particle and Nuclear and Physics, Hungarian Academy of Sciences., Budapest, Hungary.
- 2003–2006 **Research Assistant**, Department of Biophysics, Research Institute for Particle and Nuclear and Physics, Hungarian Academy of Sciences., Budapest, Hungary.
- 2002, 2004, 2005, 2006 **Research and teaching assistant**, Three months each, Center for Complex Systems Studies, Kalamazoo College, Kalamazoo, MI, USA., Kalamazoo, MI, USA.
- 2002 **Erasmus student**, Department of Biomedical Engineering, Eindhoven University of Technology, Eindhoven, The Netherlands..

applications

- 2005– **igraph**, Library for network analysis and graph algorithms, C/C++/R/Python <http://igraph.org>.
- 2014– **METACRAN**, Tools for the CRAN R package repository, R/JavaScript <https://github.com/metacran/metacran>, <http://www.r-pkg.org>.
- 2011–2015 **MISO**, Mixture of isoforms model for RNA-Seq isoform quantitation, Python/C <http://genes.mit.edu/burgelab/miso/index.html>.
- 2011– **Other software**, See <http://github.com/gaborcsardi>.
<http://www.r-pkg.org/maint/csardi.gabor@gmail.com>

selected awards

- 2015 Winner of the W. J. Youden Award in Interlaboratory Testing.
- 2012 Best 5 minute postdoc presentation at the Harvard Symposium of Applied Statistics.
- 2004 Scholarship to the Santa Fé Complex Systems Summer School.
- 2003–2006 Young researcher scholarship of the Hungarian Academy of Sciences.
- 2003 Graduated in computer science with distinction, Eötvös University, Faculty of Science.

service

Associate Editor of Journal of Statistical Software.

Reviewing for Journal of Statistical Software, Journal of Machine Learning Research, Physical Review E, Bioinformatics, Physica A, Biosystems, Computational Statistics and Data Analysis, Neural Information Processing Systems, International Conference on Artificial Intelligence and Statistics.

selected publications

books

- Csárdi, G, T Nepusz, and EM Airolidi. *Network Analysis with R/igraph*. In preparation. Springer, 2015.
- Kolaczyk, ED and G Csárdi. *Statistical Analysis of Network Data with R*. Springer, 2014.

articles

- Csárdi, G, AM Franks, DS Choi, EM Airolidi, and DA Drummond. “Accounting for experimental noise reveals that mRNA levels, amplified by post-transcriptional processes, largely determine steady-state protein levels in yeast”. In: *PLoS genetics* 11.5 (2015), e1005206.
- Franks, AM, G Csárdi, DA Drummond, and EM Airolidi. “Estimating a structured covariance matrix from multi-lab measurements in high-throughput biology”. In: *Journal of the American Statistical Association* (2014).
- Verdier, V, G Csárdi, AS de Preux-Charles, JJ Médard, AB Smit, MHG Verheijen, S Bergmann, and R Chrast. “Aging of myelinating glial cells predominantly affects lipid metabolism and immune response pathways”. In: *Glia* 60 (2012), pp. 751–760.
- Brawand, D, M Soumillon, A Necsulea, P Julien, G Csárdi, P Harrigan, M Weier, A Liechti, A Aximu-Petri, M Kircher, FW Albert, U Zeller, P Khaitovich, F Grützner, S Bergmann, R Nielsen, S Pääbo, and H Kaessmann. “The evolution of gene expression levels in mammalian organs”. In: *Nature* 478 (2011), pp. 343–348.
- Henrichsen, CN, G Csárdi, MT Zabot, C Fusco, S Bergmann, G Merla, and A Reymond. “Using Transcription Modules to Identify Expression Clusters Perturbed in Williams-Beuren Syndrome”. In: *PLoS computational biology* 7 (2011), e1001054.
- Csárdi, G, Z Kutalik, and S Bergmann. “Modular analysis of gene expression data with R”. In: *Bioinformatics* 26 (2010), pp. 1376–1377.
- Csárdi, G, KJ Strandburg, L Zalányi, J Tobochnik, and P Érdi. “Modeling innovation by a kinetic description of the patent citation system”. In: *Physica A: Statistical Mechanics and its Applications* 374 (2007), pp. 783–793.
- Csárdi, G and T Nepusz. “The igraph software package for complex network research”. In: *InterJournal Complex Systems* (2006), p. 1695.