

Special Topics in Computational Network Biology Fall 2016

Syllabus

1 Background

1.1 Foundations

- Introductory graph theory
- Introductory probability theory
- Introduction to molecular networks

1.2 Readings

- L. Hunter. Life and Its Molecules: A Brief Introduction. AI Magazine 25(1):9-22, 2004.

2 Graph structure learning for network inference

2.1 Foundations

- Probabilistic graphical model representation of molecular networks
- Bayesian networks
- Dependency networks
- Bootstrap and stability selection
- Statistical Regression

2.2 Readings

- F. Markowetz and R. Spang, "Inferring cellular networks a review," BMC Bioinformatics, vol. 8, no. Suppl 6, pp. S5+, 2007. [Online]. Available: <http://dx.doi.org/10.1186/1471-2105-8-s6-s5>
- N. Friedman, M. Linial, I. Nachman, and D. Pe'er, "Using bayesian networks to analyze expression data," Journal of Computational Biology, vol. 7, no. 3-4, pp. 601-620, Aug. 2000. [Online]. Available: <http://dx.doi.org/10.1089/106652700750050961>
- V. A. Huynh-Thu, A. Irrthum, L. Wehenkel, and P. Geurts, "Inferring regulatory networks from expression data using Tree-Based methods," PLoS ONE, vol. 5, no. 9, pp. e12 776+, Sep. 2010. [Online]. Available: <http://dx.doi.org/10.1371/journal.pone.0012776>
- E. Segal, D. Pe'er, A. Regev, D. Koller, and N. Friedman, "Learning module networks," Journal of Machine Learning Research, vol. 6, pp. 557-588, Apr. 2005. [Online]. Available: <http://www.jmlr.org/papers/volume6/segal05a/segal05a.pdf>

3 Integrative network inference

3.1 Foundations

- Models for integrating diverse data types
- Prior-based approaches
- Regularized regression

3.2 Readings

- A. V. Werhli and D. Husmeier, "Reconstructing gene regulatory networks with bayesian networks by combining expression data with multiple sources of prior knowledge." *Statistical applications in genetics and molecular biology*, vol. 6, no. 1, Jan. 2007. [Online]. Available: <http://dx.doi.org/10.2202/1544-6115.1282>
- N. Novershtern, A. Regev, and N. Friedman, "Physical module networks: an integrative approach for reconstructing transcription regulation," *Bioinformatics*, vol. 27, no. 13, pp. i177-i185, Jul. 2011. [Online]. Available: <http://dx.doi.org/10.1093/bioinformatics/btr222>
- A. Greenfield, C. Hafemeister, and R. Bonneau, "Robust data-driven incorporation of prior knowledge into the inference of dynamic regulatory networks." *Bioinformatics (Oxford, England)*, vol. 29, no. 8, pp. 1060-1067, Apr. 2013. [Online]. Available: <http://dx.doi.org/10.1093/bioinformatics/btt099>

4 Dynamics and context-specificity of networks

4.1 Foundations

- Models to represent dynamics in networks
- Dynamic Bayesian networks
- Hidden Markov Models
- Multi-task learning
- Graphical Gaussian models.

4.2 Readings

- T. Ideker, O. Ozier, B. Schwikowski, and A. F. Siegel, "Discovering regulatory and signalling circuits in molecular interaction networks," *Bioinformatics*, vol. 18, no. suppl 1, pp. S233-S240, Jul. 2002. [Online]. Available: http://dx.doi.org/10.1093/bioinformatics/18.suppl_1.s233
- Bayesian Inference of Signaling Network Topology in a Cancer Cell Line. <http://bioinformatics.oxfordjournals.org/content/28/21/2804.full.pdf>
- Reconstructing dynamic regulatory maps DREM. Jason Ernst, Oded Vainas, Christopher T. Harbison, Itamar Simon, Ziv Bar-Joseph. <http://msb.embopress.org/content/3/1/74>
- Sharing and Specificity of Co-expression Networks across 35 Human Tissues. Emma Pierson, the GTEx Consortium, Daphne Koller, Alexis Battle, Sara Mostafavi. <http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004220>

5 Graph clustering to detect network modules

5.1 Foundations

- Introductory linear algebra
- Clustering
- Modularity measures on graphs
- Spectral clustering
- Dense subgraph mining/attributed subgraph mining
- Hierarchical agglomerative graph clustering

5.2 Readings

- Similarity network fusion for aggregating data types on a genomic scale. <http://www.nature.com/nmeth/journal/v11/n3/full/nmeth.2810.html>
- Resolving the structure of interactomes with hierarchical agglomerative clustering. <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3044301/>
- Identification of functional modules using network topology and high-throughput data <http://bmcysystbiol.biomedcentral.com/articles/10.1186/1752-0509-1-8>

6 Graph comparison and alignment

6.1 Foundations

- Types of graph alignment problems
- Scoring and seeding in graphs
- Matrix completion and factorization

6.2 Readings

- B. P. Kelley, R. Sharan, R. M. Karp, T. Sittler, D. E. Root, B. R. Stockwell, and T. Ideker, "Conserved pathways within bacteria and yeast as revealed by global protein network alignment," *Proceedings of the National Academy of Sciences*, vol. 100, no. 20, pp. 11 394-11 399, Sep. 2003. [Online]. Available: <http://dx.doi.org/10.1073/pnas.1534710100>
- R. Singh, J. Xu, and B. Berger, "Global alignment of multiple protein interaction networks with application to functional orthology detection," *Proceedings of the National Academy of Sciences*, vol. 105, no. 35, pp. 12 763-12 768, Sep. 2008. [Online]. Available: <http://dx.doi.org/10.1073/pnas.0806627105>
- V. Gligorijevi?, N. Malod-Dognin, and N. Pr?ulj, "Fuse: multiple network alignment via data fusion," *Bioinformatics*, vol. 32, no. 8, pp. 1195-1203, Apr. 2016. [Online]. Available: <http://dx.doi.org/10.1093/bioinformatics/btv731>
- J. Hu and K. Reinert, "LocalAli: an evolutionary-based local alignment approach to identify functionally conserved modules in multiple networks," *Bioinformatics*, vol. 31, no. 3, pp. 363-372, Feb. 2015. [Online]. Available: <http://dx.doi.org/10.1093/bioinformatics/btu652>

7 Information flow on graphs for prioritization, integration and interpretation

7.1 Foundations

- Random walk on the graph
- Nested effect models
- Factor graphs
- Steiner tree, max flow

7.2 Readings

- S. Khler, S. Bauer, D. Horn, and P. N. Robinson, "Walking the interactome for prioritization of candidate disease genes." *American journal of human genetics*, vol. 82, no. 4, pp. 949-958, Apr. 2008. [Online]. Available: <http://dx.doi.org/10.1016/j.ajhg.2008.02.013>
- C. J. Vaske, C. House, T. Luu, B. Frank, C.-H. H. Yeang, N. H. Lee, and J. M. Stuart, "A factor graph nested effects model to identify networks from genetic perturbations." *PLoS computational biology*, vol. 5, no. 1, pp. e1 000 274+, Jan. 2009. [Online]. Available: <http://dx.doi.org/10.1371/journal.pcbi.1000274>
- S.-s. C. Huang, D. C. Clarke, S. J. C. Gosline, A. Labadorf, C. R. Chouinard, W. Gordon, D. A. Lauffenburger, and E. Fraenkel, "Linking proteomic and transcriptional data through the interactome and epigenome reveals a map of oncogene-induced signaling," *PLoS Comput Biol*, vol. 9, no. 2, pp. e1 002 887+, Feb. 2013. [Online]. Available: <http://dx.doi.org/10.1371/journal.pcbi.1002887>
- F. Vandin, E. Upfal, and B. J. Raphael, "Algorithms for detecting significantly mutated pathways in cancer." *Journal of computational biology : a journal of computational molecular cell biology*, vol. 18, no. 3, pp. 507-522, Mar. 2011. [Online]. Available: <http://dx.doi.org/10.1089/cmb.2010.0265>