Introduction to Bioinformatics:  
*Biological Networks*  

Spring 2010

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**Lectures:**

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<thead>
<tr>
<th>Time</th>
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<tbody>
<tr>
<td>LEC: Thursdays 16:00 - 18:00</td>
<td>Huxley 331</td>
</tr>
<tr>
<td>TUT: Thursdays 11:00 – 12:00</td>
<td>Huxley 145</td>
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**Office Hours:** By appointment. The best way to reach me is by e-mail.

**Marking Scheme:**

1. About 17% two coursework (30 marks)  
2. About 83% final exam (150 marks)

<table>
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<tr>
<th>Mark range (%)</th>
<th>Grade</th>
<th>Undergraduates</th>
<th>MSc Postgraduates</th>
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<tr>
<td>[90-100]</td>
<td>A+</td>
<td>PASS</td>
<td>PASS</td>
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<tr>
<td>[70-90)</td>
<td>A</td>
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<tr>
<td>[60-70)</td>
<td>B</td>
<td>PASS</td>
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<td>[50-60)</td>
<td>C</td>
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<td>[40-50)</td>
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<td>FAIL</td>
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<td>[30-40)</td>
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<td>FAIL</td>
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<td>[0-30)</td>
<td>F</td>
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**Recommended Texts and Readings:**

e) A list of papers selected by Dr. Pržulj (see below).
Course Overview and Goals:

Vast amounts of biological network data have recently been generated due to advances in experimental biology. These data sets are increasingly being studied to obtain systems-level understanding of biological structures and processes. Various mathematical and computational tools are being used and developed to analyze and model these data aiming to achieve a better description and understanding of biological processes, disease, and contribute to the time and cost effectiveness of biological experimentation.

This course will give an overview of the existing types of biological network data, point to sources of errors and biases in the data, and introduce the current methods, models and literature on graph theoretic modeling and discrete algorithmic analyses applied to these data. The course will also present an overview of the works of several major network biology labs around the world (e.g., U. Alon, M. Vidal, M. Tyers, M. Stumpf, J. Doyle, A.-L. Barabasi etc.).

Topics Outline:

The course will cover the following topics:

a) Types of biological networks: metabolic, signaling, protein-protein interaction, etc.

b) Major databases storing biological network data (e.g. MINT, DIP, HPRD, GRID, MIPS, KEGG).

c) Sources of noise and biases in various types of the biological network data (e.g., biotechnological biases and limitations, effects of sampling).

d) Computational challenges in network analysis: introduction to basic graph theoretic and computational complexity concepts such as subgraph isomorphism and NP-completeness.

e) Properties of large networks: global (e.g., degree distribution, clustering coefficient, average diameter) and local (e.g., network motifs and graphlets).

f) Network models: various types of random graphs (e.g., Erdos-Renyi, small-world, scale-free, hierarchical, geometric) and network growth models (e.g., preferential attachment).

g) Network motifs: techniques for their detection (exhaustive and heuristic network search algorithms) and biological function (e.g., feed-forward loops in transcriptional regulation networks).

h) Interplay of network topology and function (e.g., “lethality” and “centrality,” “synthetic lethality” and network “redundancy,” graph theoretic pathway models).

i) From models to heuristic algorithms (e.g., exploiting network model properties for “optimal” walks through a network, or detection of small network substructures).

j) Graph alignment heuristics (e.g., PathBLAST, IsoRank, GRAAL).

k) Network evolution (e.g. gene duplication and divergence in biological network growth models).

l) Clustering problems in biological networks (e.g., detection of protein complexes).

m) Software tools and libraries for network analysis (e.g., LEDA, Cytoscape, Pajek).

Some Additional Reading Materials:

Review Papers:


**Research Papers:**


23. N. Przulj, D. G. Corain, and I. Jurisica, "Modeling Interactome: Scale-Free or Geometric?" 
*Bioinformatics* 20 (18), 2004.


**Research Papers on Network Alignment:**

44. B. P. Kelley *et al.*, "Conserved pathways within bacteria and yeast as revealed by global protein network alignment", *PNAS* 100 (20), 2003.