Balázs Ligeti

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EDUCATION

PhD in Bioinformatics

2011 — Present

Roska Tamás Doctoral School of Sciences and Technology, PPKE ITK, Budapest

Microbiom research

Drug combination prediction

Network analysis

Network mining

Data integration

Data warehousing

Erasmus scholarship, internship

2009 - 2010

Katholieke Universiteit Leuven

Data mining

Machine learning

Statistics - linear models

Biological databases

Introduction to genetics

Msc in Electronic and Computer

2005 - 2011

Engineering

Pázmány Péter Catholic University, Faculty of Information Technology and Bionics

Sensing computers and robots

Neuromorphic information technology

Bionics

RESEARCH EXPERIENCE PPKE (Budapest) - SE (Budapest) -

2011 — Present

ICGEB (Trieste, Italy)

Drug combination prediction

Large-scale, data-driven prediction of efficient drug combinations

Personal tasks: developing and applying new paradigms for designing drug combinations in a data-driven way; data integration; statistical evaluation of the data

Skills acquired or improved:

- data warehousing (JBioWH, developing an ETL-based framework for bioinformatics data integration): Oracle, MySQL, PL/SQL, XML
- NoSQL graph databases (Neo4j)
- programming in: Matlab, R, Python, Java
- network mining
- sparse linear algebra
- Markov processes and Monte Carlo methods

PPKE (Budapest) - SE (Budapest) - ICGEB (Trieste, Italy)

Sep 2011 — Sep 2013

Text mining

Revealing unexpected relationship between biological entities such as diseases and genes based on the analysis of biomedical corpora and by using text and other data networks Personal tasks: Statistical evaluation of the biomedical hypothesis generated by the algorithm; improving the ranking performance by using network-mining techniques Skills acquired or improved:

- cloud computing

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- network data mining
- assessing the significance of the ranking
- text mining
- programming in Matlab

PPKE (Budapest) - ICGEB (Trieste, Italy)

Sept 2014 — Jun 2016

Microbial research

Developing an algorithm for the interpretation and analysis of high-throughput sequencing data

Personal tasks: classifying large number of experimental data item with high sensitivity Typical data size: 30 gigabyte / experiment

Skills acquired or improved:

- programming in C
- Python framework for testing and data visualization
- handling complex data structure such as taxonomy

PROGRAMMING SKILLS

python (expert), R (expert), SQL (expert), Matlab (expert), C++ (intermediate), Java (intermediate), C (intermediate), Unix Shell Script (intermediate), JavaScript (beginner)

LANGUAGE SKILLS

English: fluent (in written and spoken)

French: intermediate (in written and spoken)

Dutch: beginner (in written and spoken)

SCIENTIFIC PUBLICATIONS

Ligeti, B., Menyhárt, O., Petrič I., Győrffy, B.; Pongor, S. (2016). Prediction of Effective Drug Combinations and Biomarkers via Propagation on Molecular Interaction Networks. *Current Pharmaceutical Design*, in press.

Ligeti, B.; Vera, R.; Juhász, J.; Pongor, S. (2016). CX, DPX and PCW: Web servers for the visualization of interior and protruding regions of protein structures in 3D and 1D. *Springer Protocols: Methods in Molecular Biology*, in press.

Ligeti, B.; Pénzváltó, Z.; Vera, R.; Győrffy, B.; Pongor, S. (2015). A Network-Based Target Overlap Score for Characterizing Drug Combinations: High Correlation with Cancer Clinical Trial Results. *PLoS One.* 10 (9), e0129267.

Hudaiberdiev, S.; Choudhary, K.; Vera, R.; Gelencsér, Zs.; **Ligeti**, B.; Lamba, D.; Pongor, S. (2015); Census of solo LuxR genes in prokaryotic genomes. *Front. Cell. Infect. Microbiol.* 5:20. doi:10.3389/fcimb.2015.00020

Pongor, L. S.; Vera, R.; **Ligeti** B. (2014). Fast and Sensitive Alignment of Microbial Whole Genome Sequencing Reads to Large Sequence Datasets on a Desktop PC: Application to Metagenomic Datasets and Pathogen Identification. *PLOS ONE*, published 31 Jul 2014, 10.1371/journal.pone.0103441

Petric, I.; **Ligeti**, B.; Gyorffy, B.; Pongor, S. (2014). Biomedical Hypothesis Generation by Text Mining and Gene Prioritization. *Protein Pept Lett.* 20, 1-1.

Ligeti, B.; Vera, R.; Lukacs, G.; Gyorffy, B.; Pongor, S. (2013). Predicting effective drug combinations via network propagation. *Biomedical Circuits and Systems Conference*, 378-381.

Vera, R.; Perez-Riverol, Y.; Perez, S.; **Ligeti**, B.; Kertész-Farkas, A.; Pongor, S. (2013). JBioWH: an open-source Java framework for bioinformatics data integration. *Database*. 2013, bat051.

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OTHER PUBLICATIONS

- S. Pongor, J. Juhász , **B. Ligeti**, "Valós és virtuális társadalmak a baktériumoknál" (Real world and virtual societies in bacteria), *Élet és Tudomány*, vol. 71, no. 2,pp. 41-43., Jan. 2016. (in Hungarian)
 - S. Pongor, J. Juhá**s**z, **B. Ligeti**, "Háború és béke a baktériumoknál" (War and peace in bacteria), $Term\acute{e}szet~Vil\acute{a}ga$, vol. 147, no. 5, May. 2016. (in Hungarian)

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