Robert Piskol

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Summary

Expert in high-throughput data analysis, with extensive expertise in genomic variant discovery, expression analysis, comparative genomics and population genetics, paired with proficiency in high-level programming languages and excellent understanding of statistical principles.

Postdoctoral work is focused on the development of computational methods for the genome-wide discovery of RNA editing and their combination with high-throughput, targeted sequencing approaches for the spatio-temporal profiling of RNA editing.

Professional Experience

05/2011–present Postdoctoral Research Scholar, Department of Genetics, Stanford University, Stanford, USA

- Development of computational approaches for *de novo* identification of RNA editing variants from RNA-seq experiments.
- Development of a comprehensive atlas of RNA editing sites in human and mouse using a high throughput microfluidic-based, targeted sequencing approach.
- Identification of functional RNA editing targets using comparative genomics.

01/2008–04/2011 PhD Student, Evolutionary Biology, Ludwig-Maximilian-University, Munich, Germany

- Development of a logistic regression approach to analyze the evolutionary dynamics of RNA molecules.
- Identification of structural and population genetic determinants of RNA secondary structure evolution.

06/2010–08/2010 Visiting Researcher, Graduate University for Advanced Studies (SOKENDAI), Hayama, Japan

- Study of the evolution of complexity in *Arabidopsis* and mouse miRNA gene regulation systems.

2008–present Reviewer for Molecular Biology and Evolution, PLoS One, FEBS letters, Journal of Molecular Evolution and Journal of Theoretical Biology

10/2005–11/2006 Research Assistant, Evolutionary Biology, Ludwig-Maximilian University Munich, Munich, Germany

- Design and implementation of web interfaces for computational tools used in evolutionary genomic studies (Perl/CGI & PHP).
- Design of a database system for microarray and primer data (Perl/CGI & MySQL).

1999–2003 Summer intern, Landeskuratorium der Erzeugerringe für tierische Veredelung in Bayern e.V., Munich, Germany

- Application programming (Informix - r4gl)
- Interface programming (Oracle - PL/SQL)

Technical Experience and Acquired Skills

Scripting and Programming languages	Perl, Java
Statistics	R, Mathematica
Software development	Emacs, Eclipse, git
Database development	MySQL, ORACLE
Bioinformatics / Computational Biology	RNA-seq/WGS/exome-seq analysis, SNP calling, expression analysis, transcriptome assembly
Bioinformatic tools	bwa, novoalign, tophat, cufflinks, GATK, samtools, Sun Grid Engine

Education

01/2008–04/2011	PhD Biology, (*magna cum laude*) Ludwig-Maximilian-University, Munich, Germany
10/2002–11/2007	Diploma Bioinformatics (corresponds to M.S.), (*with high distinction*) Ludwig-Maximilian-University & Technical University, Munich, Germany

Principal fields of study:

Biology	Evolutionary Biology, Population Genetics
Bioinformatics	Machine Learning, Structural Bioinformatics
Computer science	Database Development, Knowledge Discovery in Databases

Awards and Scholarships

07/2013–06/2013	Dean's Fellowship, Stanford University
05/2012–04/2014	Postdoctoral Fellowship, German Academic Exchange Service (DAAD)
06/2010–08/2010	Japan Society for the Promotion of Science (JSPS) Summer Program 2010 Scholarship
04/2010	Evolution Ecology and Systematics (EES) Travel Award; Visit of the 2nd EMBO Workshop on Computational RNA Biology in Cargèse (France)
06/2009	International travel award from the Society for the Study of Evolution
10/2008	Evolution Ecology and Systematics (EES) Award for distinguished Diploma Thesis, Ludwig-Maximilian-University Munich, Germany

Publications

Piskol, R., Ramaswami, G., and Li, J.B. (2013). Reliable identification of genomic variants using RNA-seq data. ***AJHG*** 93(4), 641–651.

Ramaswami, G.*, Zhang, R.*, Piskol, R., Keegan, L.P., Deng, P., O'Connell, M.A., and Li, J.B. (2013). Identifying RNA editing sites using RNA sequencing data alone. ***Nature methods*** 10, 128–132.

Piskol, R.*, Peng, Z.*, Wang, J., and Li, J.B. (2013). Lack of evidence for existence of non-canonical RNA editing. ***Nature biotechnology*** 31, 19–20.

Ramaswami, G.*, Lin, W.*, Piskol, R.*, Tan, M.H., Davis, C., and Li, J.B. (2012). Accurate identification of human *Alu* and non-*Alu* RNA editing sites. ***Nature methods*** 9, 579–581.

Lin, W.*, Piskol, R.*, Tan, M.H., and Li, J.B. (2012). Comment on "Widespread RNA and DNA sequence differences in the human transcriptome". ***Science*** 335, 1302; author reply 1302.

Piskol, R., and Stephan, W. (2011). The role of the effective population size in compensatory evolution. ***Genome Biology and Evolution*** 3, 528–538.

Piskol, R., and Stephan, W. (2011). Selective constraints in conserved folded RNAs of drosophilid and hominid genomes. ***Molecular Biology and Evolution*** 28, 1519–1529.

Aguilar, A.L., Piskol, R., Beitzinger, M., Zhu, J.Y., Kruspe, D., Aszodi, A., Moser, M., Englert, C., and Meister, G. (2010). The small RNA expression profile of the developing murine urinary and reproductive systems. ***FEBS letters*** 584, 4426–4434.

Piskol, R., and Stephan, W. (2008). Analyzing the evolution of RNA secondary structures in vertebrate introns using Kimura's model of compensatory fitness interactions. ***Molecular Biology and Evolution*** 25, 2483–2492.

* these authors have contributed equally

Presentations

Piskol, R. (Poster)
A Quantitative Atlas of RNA Editing Sites in Mammals
Gordon Research Conference on RNA Editing, Galveston TX, U.S.A., 01/2013

Piskol, R. (Talk)
Discovery of genomic variants from RNA-sequencing data
Annual Meeting of the Society of Human Genetics, San Francisco CA, U.S.A., 11/2012

Piskol, R. (Talk)
What are the Factors that Govern the Evolution of RNA Secondary Structures - Insights from Kimura's Model of Compensatory Evolution
Annual Meeting of the Society for the Study of Evolution (SSE), Moscow ID, U.S.A., 06/2009

Piskol, R., Stephan, W. (Poster)
Analyzing the Evolution of RNA Secondary Structures in Vertebrate Introns Using Kimura's Model of Compensatory Fitness Interactions
Annual Meeting of the Society for Molecular Biology and Evolution (SMBE), Iowa City IA, U.S.A., 06/2009

Piskol, R. (Talk)
What are the Factors that Govern the Evolution of RNA Secondary Structures - Insights from Kimura's Model of Compensatory Evolution
First VW Status Symposium, Muenster, Germany, 02/2009

Piskol, R. (Talk)
Evolution of RNA Structures in Introns
EES Conference '08, Munich, Germany, 10/2008

Piskol, R., Stephan, W. (Poster)
Analyzing the Evolution of RNA Secondary Structures in Vertebrate Introns Using Kimura's Model of Compensatory Fitness Interactions
German Conference on Bioinformatics (GCB), Dresden, Germany, 09/2008

References

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Hideki Innan
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Advanced Studies (SOKENDAI)
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