Barbara Piasecka

CONTACT INFORMATION	ul. Toruńska 15 80-747 Gdańsk Poland	*Phone:* +48 662 001 727 *E-mail:* piasecka.barbara@gmail.com

EDUCATION

Ph.D., Bioinformatics   **October 2008 - November 2012**
University of Lausanne, Lausanne, Switzerland
Faculty of Biology and Medicine

M.S., Applied Mathematics   **October 2003 - September 2008**
Adam Mickiewicz University, Poznań, Poland
Faculty of Mathematics and Computer Science

M.S., Biotechnology   **October 2004 - October 2006**
Adam Mickiewicz University, Poznań, Poland
Faculty of Biology

B.A., Biotechnology   **October 2001 - July 2004**
Adam Mickiewicz University, Poznań, Poland
Faculty of Biology

EXPERIENCE

Institut Pasteur, Paris, France

Biostatistician   **January 2015 - January 2017**

Experimental design and statistical analyses in a population-based study of the impact of genetics and environment on the human immune system (`www.milieuinterieur.fr`).
- Importing electronic case report form (eCRF) into relational database (LabKey).
- Normalisation and quality control of gene expression data.
- Identifying expression quantitative trait loci (eQTL) and their interactions with environment.
- Custom made visualisation of multimodal and multidimensional data.
- Biostatistical service.

IntegraGen, Boulogne Billancourt, France

Biostatistician   **January 2014 - November 2014**

- Performing statistical analyses to discover biomarkers of treatment effect in patients with metastatic colorectal cancer. This includes survival analysis using the Kaplan-Meier estimator and multivariate Cox regression models.
- Studying polygenic nature of autism spectrum disorder. This includes genome wide association analyses using, e.g., standard logistic regression, lasso, ridge and elastic-net penalized logistic regression.
- Biostatistical service.

University of Lausanne & Swiss Institute of Bioinformatics, Lausanne, Switzerland

Postdoctoral Researcher   **November 2012 - March 2013**

Member of a team studying gene expression changes associated with beta-adrenergic responses in mouse. This involved statistical analyses of RNA-Seq data and associating the results with genotype and phenotype data from 22 inbred mouse strains.

Teaching Assistant   **October 2008 - March 2013**

- Assisted in the course of Integrative Analysis of Large-scale Data at SystemsX.ch/SIB joint Summer School - From Data to Models in Biological Systems.

- Prepared syllabus of the Bioinformatics for Genomics course and managed the work of other assistants.
- Prepared teaching materials and assisted in the courses of: Introduction to Bioinformatics, Bioinformatics for Genomics, Statistics for Biologists, and Experimental Design.
- Supervision of master students from the Biology Department.

Doctoral Researcher   **October 2008 - November 2012**

- Theoretical and numerical study on similarity measures of gene expression profiles commonly used in the field of Evo-Devo.
- Study of gene expression conservation by means of modular analysis of large-scale data (Iterative Signature Algorithm, ISA, and Ping-Pong Algorithm, PPA).
- Development of ISA and PPA, and application of these algorithms in several side projects.
- Assembly of Amphioxus transcriptome from RNA-seq data.
- Communication of results in the form of conference talks, posters and journal articles.

PUBLICATIONS

Piasecka B. et al., In preparation. Independent impacts of age, sex and genetics on human transcriptional responses to bacterial, viral and fungal challenges.

Patin E. et al., Submitted. Natural variation in innate immune cell parameters is driven by genetic factors.

Urrutia A. et al., 2016. Standardized whole-blood transcriptional profiling enables the deconvolution of complex induced immune responses. *Cell Reports* **16**(10): 2777-2791.

Piasecka B. et al., 2012. The hourglass and the early conservation models - co-existing evolutionary patterns in vertebrate development. *PLoS Genetics* **9**(4): e1003476.

Piasecka B. et al., 2012. Correcting for the bias due to expression specificity improves the estimation of constrained evolution of expression between mouse and human. *Bioinformatics* **28**(14): 1865-1872.

Piasecka B. et al., 2012. Comparative modular analysis of gene expression in vertebrate organs. *BMC Genomics* **13**:124.

HONORS AND
AWARDS

- 2nd Best Poster Award at 11th European Conference on Computational Biology (ECCB), 2012
- Swiss Institute of Bioinformatics (SIB) Competitive Fund for Conference Attendance, 2012
- Best Poster Award at SIB Days, 2012
- Scholarship of the Adam Mickiewicz University for outstanding academic accomplishments, 2007/2008

COMPUTER SKILLS

- Languages: R, Matlab, BASH scripts.
- Bioinformatics tools: Bioconductor packages, PLINK.
- Applications: LaTeX, Microsoft Office, iWorks, Adobe Lightroom.
- Operating Systems: Mac OS, Linux, Windows.
- Cluster computing: SLURM, SGE.

LANGUAGES

- Polish: Native
- English: Very good
- French: Very good

PERSONAL
INTERESTS

- Hiking
- Traveling
- Photography