

Rodoniki Athanasiadou, M.Res., Ph.D.

Programming skills

Python (numpy, pandas, scikit-learn, matplotlib, seaborn, Jupyter notebooks), R (dplyr, rpart, ggplot2, EdgeR, limma, BiomaRt, Rstudio, R Shiny), bash (Tuxedo suite, Plink), SQL (mySQL, psycopg2), APIs (Twitter, Google Maps, Entrez programming utilities), High Performance Computing (HPC), cloud computing (AWS), LaTeX, markdown.

Data science skills

Supervised and unsupervised classification, hypothesis testing (parametric and non-parametric), natural language processing (TF-IDF, word embeddings), feature engineering, signal detection, bootstrapping, Bayes theorem.

Molecular Biology expertise

Epigenetics (global DNA methylation changes, histone modification, and chromatin composition analysis), global gene expression regulation, transcriptome stability, genome-wide SNP detection, protein assays, physicochemical properties of nucleic acids, biochemical and biophysical molecular assays.

Other skills

Hypothesis generation, experimental design, methodology and protocol development, project and team management, data visualization, science communication and results dissemination (oral, written).

EDUCATION

Ph.D. in Cellular and Molecular Biology , University of Edinburgh, UK.	2008
M. Res. in Biomolecular Sciences , University of York, UK.	2002
Ptychio (B.Sc.) in Biology , Aristotle University of Thessaloniki, Greece.	2001

INDEPENDENT DATA SCIENCE PROJECTS

Visiting bioinformatician fellow NCBI, National Institutes of Health, Bethesda, USA.	10/2017 - 11/2017
<ul style="list-style-type: none"><i>Proposed a computational pipeline in python for the combination of genetic, clinical and behavioral data in predictive models of complex disease onset (github.com/NCBI-Hackathons/Complex_Phenogeno).</i>	
Data Science consultant Downtown Alliance, New York, USA.	06/2017 - 07/2017
Data science fellow Fast Forward labs, Cloudera, New York, USA.	06/2017 - 09/2017
<ul style="list-style-type: none"><i>Compared different word embedding algorithms (word2vec, GloVe) using different lexicographic ground truth datasets and python.</i>	
Data Science fellow Insight Data Science, New York, USA.	06/2016 - 08/2016
<ul style="list-style-type: none"><i>Employed algorithms for the prediction of 10-year tree survival by species, in different city neighborhoods (plant-wise.com). Utilized publicly available census data from 2005 and 2015 on half a million trees in the streets of New York and CART algorithms, among others. This work was recognized by the NYC Office of the Mayor for the creative use of NYC OpenData in a data science project.</i>	
Board of directors Future of Research (non profit), Boston, USA.	05/2016 - 06/2017
<ul style="list-style-type: none"><i>Analyzed quantitative trends in a sample of 13,000 postdocs shared with the organization by 52 public universities across the US. The work has been accepted by a peer-reviewed journal as an important contribution to understanding the academic workforce.</i>	

ACADEMIC RESEARCH

Researcher

01/2018 - Present

Langone Health/Courant Institute of Mathematical Sciences, New York University, New York, USA.

- *Conducting research on the application of machine learning algorithms for the prediction of obesity from electronic health records and behavioral surveys using python and NYU's HPC clusters.*
- *Designed and currently leading the generation of preliminary data on the extraction and utilization of behavioral 'digital footprints' for the surveillance of complex disease prevalence in US populations. Coordinating with National Institutes of Health for the submission of a corresponding grant proposal.*
- *Extracting behavioral information from Twitter streams using python interfaces to Twitter's API. Prototyping the analytical pipeline on a 90 million entries data subset in JSON format. Developing novel methodology for the removal of bot and cyborg noise from the dataset.*
- *Leading liaison for the acquisition of data from IBM Watson, Google's Sidewalk Labs, and the OCHIN network.*

Researcher

09/2016 - 06/2017

Courant Institute of Mathematical Sciences, New York University, New York, USA.

- *Initiated and coordinated an interdisciplinary, collaborative research program between NYU Courant, NYU Tandon, and NYU Langone Health on the utilization of computational approaches in population health.*
- *Used RStudio and R Shiny to create interactive visualizations of data obtained from the US Census Bureau, the Center for Disease Control (CDC), and other online sources (rdna.shinyapps.io/RiskEconApp).*

Postdoctoral researcher

05/2011 - 06/2016

Center for Genomics and Systems Biology, New York University, New York, USA.

- *Studied the effect of cellular growth rate on gene expression and post-transcriptional RNA stability.*
- *Developed the experimental design and quantitative basis for a new calibration method of RNA-seq data from samples where the assumption of equal transcriptome sizes is violated. This novel approach creates the foundation for the experimental acquisition of absolute quantities of transcripts per cell.*
- *Built an analytical pipeline for the custom processing of RNA-seq data in yeast using R, bash, Bowtie, and EdgeR, hosted at NYU's High Performance Computing clusters.*
- *Mentored three graduate students and two high-school students. The work of the latter on the mutagenic effect of nucleotide analogues was selected for the Finals Round, 2015 New York City Science and Engineering Fair.*

Postdoctoral researcher

09/2008 - 04/2011

Albert Einstein College of Medicine, New York, USA.

- *Studied the role of epigenetic regulation on the onset and molecular response to disease.*
- *Developed the experimental approach and analytical pipeline for the detection of rare RNA:DNA hybrids in the human genome. Led a team of two graduate students and one technician for the completion of the award-winning study.*
- *Identified altered DNA binding patterns of the REST transcription factor in brains after stroke that supported a collaborative published study. Created and implemented an algorithm in R for the detection of signal from noisy microarray data from Chromatin Immunoprecipitation assays.*

Doctoral student

10/2003 - 08/2008

Wellcome Trust Center for Cell Biology, University of Edinburgh, Edinburgh, U.K.

- *Studied the establishment of DNA methylation during embryonic differentiation and lineage specification.*
- *Identified nucleation centers that control the spreading of methylation in the regulatory elements of pluripotency genes. Dissected the role of different components of the methylation machinery in the phenomenon, in a work recognized by the British Biochemical Society.*
- *Designed custom oligonucleotide microarrays for the identification of CpG islands that are enriched after affinity purification of methylated genomic regions. Performed the experiments and analyzed the results using R.*
- *Created primary fibroblast cell lines from mouse tail tips, maintained somatic and embryonic cell lines of murine and insect origin. Conducted in vitro differentiation experiments of embryonic stem (ES) cells.*

SCHOLARSHIPS AND AWARDS

Data Science OpenData project award, NYC Office of the Mayor, 2018.
 Best paper award, Epigenetics & Chromatin journal, 2015.
 Illumina research proposal competition first place, Department of Biology, NYU, 2014.
 Promega Young Biochemist Award, Biochemical Society, UK, 2008.
 Scholarship by the Darwin Trust of Edinburgh, UK, 2003-2006.
 Scholarship by the Lilian Voudouri Foundation, Greece, 2001-2002.
 Honors for academic performance from the Greek Scholarship Foundation, 1996-1998.

TEACHING

Invited lecturer Department of Biology, New York University, New York, USA. • “The binomial distribution”.	02/2016
Invited lecturer , “Advanced Genomics” Department of Biology graduate course, New York University, New York, USA. • “High-throughput RNA-sequencing”.	09/2013
Invited lecturer , “Pillars in Biology” Albert Einstein College of Medicine graduate course, New York, USA. • “The epigenetics of cancer”.	11/2010
Teaching assistant , Biology Teaching Organization University of Edinburgh, Edinburgh, UK. • “Origin and diversity of life 1” • “Molecules and cells 1” • “Genes and Gene Action 2” • “The dynamic cell 2”	2004 - 2006

OTHER TRAINING

Fundamentals of teaching Sackler institute of graduate studies, New York University, New York, USA.	09/2013 - 11/2013
Advanced science communication (by invitation) Arthur L. Carter Journalism Institute, New York University, New York, USA.	10/2013 - 12/2013
Science communication Arthur L. Carter Journalism Institute, New York University, New York, USA.	10/2012 - 12/2012
Advanced R programming and Bioconductor Wellcome Trust advanced course, Cambridge, UK.	03/2007 - 04/2007

OTHER EXPERIENCE

Science communication • Guest on the popular podcast DataSkeptic on the topic of personalized medicine. • Writer on current next generation sequencing topics (bitesizebio.com/profile/niki-athanasiadou). • Delivered popularized lectures on the principles of experimental design, in venues ranging from the New York Public Library to Brooklyn’s Genspace, in collaboration with various New York city non-profit organizations. • Contributed ‘yeast dice’ to the exhibit “Not everything that counts can be counted: Microbe Monopolies Game” at the art community space FLUX Factory, NYC.	2015 - 2017
Symposium organizer • Lead the organization of the 1st NYU Interdisciplinary Postdoc Symposium (PoIntS). Formulated an organizational structure for the completion of all tasks. Coordinated five assignment-based teams of 4-6 volunteers.	02/2015 - 05/2015

INVITED RESEARCH TALKS

- Graduate Women in Science (GWIS), New York, USA.** 03/2018
 “The Landscape of U.S. Postdoctoral Salaries”
- University Medical Center, Gröningen, Netherlands.** 06/2015
 “Global tuning of gene expression through regulated RNA synthesis and degradation as a function of growth rate”
- New York University, School of Biology retreat, Wave Hill, USA.** 09/2014
 “Towards absolute quantification of mRNA (a better way to do RNA-seq)”
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RESEARCH PAPERS

- Athanasiadou R.**, Neymotin B., Brandt N., Wang W., Christiaen L., Gresham D., Tranchina D. (2018) “A Complete Statistical Model for Calibration of RNA-seq Counts using External Spike-ins and Maximum Likelihood Theory”. PLOS Computational Biology (submitted).
- Hammond R., **Athanasiadou R.**, Curado S., Aphinyanaphongs Y., Abrams C., Messito M.J., Gross R., Katzow M., Jay M., Razavian N., Elbel B. (2018) “Predicting childhood obesity using electronic health records and publicly available data”. PLOS Computational Biology (submitted).
- Athanasiadou R.**, Bankston A., Carlisle McK., Niziolek C., McDowell G.S. (2018) “Assessing the Landscape of U.S. Postdoctoral Salaries”. Studies in Graduate and Postdoctoral Education (accepted, preprint: doi.org/10.1101/227694).
- Airoldi E.M., Miller D., **Athanasiadou R.**, Brandt N., Abdul-Rahman F., Neymotin B., Hashimoto T., Bahmani T., Gresham D. (2016) “Steady-state and dynamic gene expression programs in *Saccharomyces cerevisiae* in response to variation in environmental nitrogen”. Mol. Biol. Cell, 27(8): 1383.
- Nadel J., **Athanasiadou R.**, Lemetre C., Wijetunga A.N., O. Broin P., Sato H., Zhang Z., Jeddelloh J., Montagna C., Golden A., Seoighe C., Greally J.M. (2015) “RNA:DNA hybrids in the human genome have distinctive nucleotide characteristics, chromatin composition, and transcriptional relationships”. Epigenetics & Chromatin, 8(1): 46 (Epigenetics & Chromatin Best Paper Award 2015).
- Neymotin B., **Athanasiadou R.**, Gresham D. (2014) “Determination of *in vivo* RNA kinetics using RATE-seq”. RNA, 20(10): 1645.
- Noh K.-M., Hwang J.-Y., Follenzi A., **Athanasiadou R.**, Miyawaki T., Greally J.M., Bennett M.V.L., Zukin R.S. (2012) “Repressor element-1 silencing transcription factor (REST)-dependent epigenetic remodeling is critical to ischemia-induced neuronal death”. PNAS, 109(16): E962.
- Athanasiadou R.**, de Sousa D., Myant K., Merusi C., Stancheva I., Bird A. (2010) “Targeting of *de novo* DNA methylation throughout the *Oct-4* gene regulatory region in differentiating embryonic stem cells”. PLOS ONE, 5 (4): e9937.
- Athanasiadou R.**, Polidoros A.N., Mermigka G., Nianiou-Obeidat I., Tsiftaris A.S. (2005) “Differential expression of *CmPP16* homologues in pumpkin (*Curcubita maxima*), winter squash (*C. moschata*) and their interspecific hybrid”. The Journal of Horticultural Science and Biotechnology, 80 (5): 643.