

MARIA SECRIER

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CURRENT POSITION

Lecturer, Computational Genetics *11/2017 - present*
UCL Genetics Institute, Department of Genetics, Evolution and Environment, London, UK
• Research programme in computational cancer genomics and immunology.

EDUCATION

PhD, Computational Biology - *magna cum laude* (4 publications, 3 first author) *10/2009 - 06/2013*
European Molecular Biology Laboratory (EMBL) and the University of Heidelberg, Germany
-Mentors: Dr. Reinhard Schneider, Dr. Wolfgang Huber
• Thesis topic: Visualization and analysis strategies for dynamic gene-phenotype relationships

BSc, Bioinformatics and Computational Biology (2 publications, 1 first author) *08/2006 - 06/2009*
Jacobs University, Bremen, Germany
• Thesis topic: Paths towards large basins of attraction underlying robustness in gene regulatory networks

RESEARCH EXPERIENCE

Senior Scientist: Bioinformatics and Immuno-oncology (3 manuscripts, *in prep*) *07/2016 - 10/2017*
AstraZeneca, Cambridge, UK
• Led projects in the area of immuno-oncology, disease bioinformatics and CRISPR-Cas9 screens.

Visiting Scientist: Cancer Genomics (1 manuscript, *under review*) *07/2016 - 07/2017*
Cancer Research UK Cambridge Institute, UK
• Led the genomic analyses of the first ever derived oesophageal adenocarcinoma organoids.

Research Associate: Cancer Genomics (9 publications, 2 first author) *01/2014 - 07/2016*
Cancer Research UK Cambridge Institute, University of Cambridge, UK
- Mentors: Prof. Simon Tavaré, Prof. Rebecca Fitzgerald
• Headed the computational analysis efforts of the group on whole-genome sequencing data from >100 samples of oesophageal adenocarcinoma, as part of the International Cancer Genome Consortium (ICGC).

Short-term Postdoc: Cancer Bioinformatics *07/2013 - 10/2013*
European Molecular Biology Laboratory (EMBL), Heidelberg, Germany
- Mentors: Dr. Reinhard Schneider, Dr. Wolfgang Huber, Dr. Toby Gibson
• Evaluated the impact of perturbing motif-mediated protein interactions in different types of cancer.

Internship: Systems Biology of Neuronal Migration (1 publication) *08/2009- 09/2009*
Hamilton Institute, University of Maynooth, Ireland
• Performed mathematical modelling of neuronal migration in the early stages of cortical development.

Internship: Microbial Genomics *02/2009 - 05/2009*
Max Planck Institute of Marine Microbiology, Bremen, Germany
• Worked on programming tasks involving self-organizing maps methods to elucidate genomic signatures.

Internship: Statistical Modelling in Biology (1 first author publication) *06/2008 - 09/2008*
Imperial College, London, UK

- Performed parameter inference and sensitivity analysis in several ODE models of biological processes.

Research Assistant: Network Biology, Structural Bioinformatics **09/2007 - 05/2009**
Jacobs University, Bremen, Germany

- Two research positions in gene network robustness and force field design for RNA secondary structures.

HONOURS, AWARDS AND FUNDING

Bye Fellowship, *Murray Edwards College*, University of Cambridge **2014–2016**

Oesophageal International Cancer Genome Consortium Grant, Phase II (£6 Mil, 5 years) **2016**
 - contributed to a successfully funded grant proposal

Best Oral Presentation Award, *National Barrett's Symposium*, London - conference travel grant **2016**

Special Distinction for Excellency at postgraduate level in Europe **2013**
 -awarded by *The League of Romanian Students Abroad (LSRS)* and the Romanian Government, Bucharest

Graduate Research Fellowship, *EMBL*, Heidelberg - funding for the duration of the PhD **2009–2013**

Best Oral Presentation Award, *BeNeLux Conference on Translational Bioinformatics* **2011**

Merit-based Scholarship for the entire duration of the studies, *Jacobs University*, Bremen **2006–2009**

Member of the President's List for Academic Achievements, *Jacobs University*, Bremen **2006–2009**

TEACHING EXPERIENCE

Lecturer/ Course Organizer - Cancer Genetics, Statistical Genetics MSc module **11/2017 - present**
University College London, UK

Supervisor (Tutor) - Mathematical Biology, Part IA Natural Sciences **10/2014 - 10/2016**
Murray Edwards College, University of Cambridge, UK

Lecturer - Visualization Strategies for Biology **02/2012, 07/2012, 06/2013**
University of Luxembourg, Luxembourg

Trainer - Bioinformatics and Network Biology **10/2010, 07/2011**
European Molecular Biology Laboratory (EMBL), Heidelberg, Germany

Teaching Assistant - Computer Science, Mathematics **04/2007 - 05/2009**
Jacobs University, Bremen, Germany

ACADEMIC ACTIVITIES

Senior Editor - *Annals of Human Genetics* **2017 - present**

Review Editor - *Frontiers in Systems Biology* **2011 - present**

Additionally, reviewed papers for *Genome Research*, *Nucleic Acids Research*, *PNAS*, *Bioinformatics* etc.

Reviewer of Grant Proposals - Israel Science Foundation **09/2016**

Member of the Cambridge Cancer Centre Aerodigestive Committee **2015 - 2016**

Established bioinformatic infrastructure/expertise as one of top 3 priorities for the Cambridge Cancer Centre.

Member of the Garuda Core Alliance Consortium - Systems Biology knowledge platform **2011 - 2013**

Science Communication:

- 14 scientific presentations, 6 as invited speaker

- public outreach activities through the CRUK Catalyst Club and Science Festival (2015-2016)

- organizer of a Bioinformatics meeting series: Heidelberg Unseminars in Bioinformatics (2013)

Noble, F., .., Underwood, T.J., **OCCAMS Consortium***. Multicentre cohort study to define and validate pathological assessment of response to neoadjuvant therapy in oesophago-gastric adenocarcinoma. (s includes **Secrier M**)

Garcia, E., .., Underwood, T.J., **OCCAMS Consortium***. Authentication and characterisation of a new oesophageal adenocarcinoma cell line: MFD-1. *Sci Rep* 2016; 6:32417. (* includes **Secrier M**)

★ Noorani, A.†, Bornschein, J.†, Lynch, A.G.†, **Secrier, M.,...**, Fitzgerald, R.C. A comparative analysis of whole genome sequencing of esophageal adenocarcinoma pre- and post-chemotherapy. *Genome Res.* 2017 Jun;27(6):902-912 († joint first)

★ **Secrier, M.**†, Li, X.†, .. Fitzgerald, R.C. Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. *Nat Genetics* 2016; 48(10):1131-41 († joint first)

Contino, G., Eldridge, M., **Secrier, M.**, .., Fitzgerald, R.C. Whole-genome sequencing of nine esophageal adenocarcinoma cell lines. *F1000Res* 2016; 5:1336.

Secrier, M., Fitzgerald, R.C. Signatures of mutational processes and associated risk factors in esophageal squamous cell carcinoma: a geographically independent stratification strategy? *Gastroenterology* 2016; 150(5):1080-3.

★ De Silva, N., Schulz, L., Paterson, A., Qain, W., **Secrier, M.**, .., Fitzgerald, R.C., Ford, H. Molecular effects of Lapatinib in the treatment of HER2 overexpressing oesophago-gastric adenocarcinoma. *Br J Cancer* 2015 Nov 3;113(9):1305-12.

Ross-Innes, C.S., .., Fitzgerald, R.C., **OCCAMS Consortium***. Whole-genome sequencing provides new insights into the clonal architecture of Barrett's esophagus and esophageal adenocarcinoma. *Nat Genetics* 2015 Sep;47(9):1038-46. (* includes **Secrier M**)

Secrier, M., Schneider, R. Visualizing time-related data in biology, a review. *Brief Bioinform* 2014 Sep;15(5):771-82. *corresponding author*

Weaver, J.M., .., Fitzgerald, R.C., **OCCAMS Consortium***. Ordering of mutations in preinvasive disease stages of esophageal carcinogenesis. *Nat Genetics* 2014 Aug;46(8):837-43. (* includes **Secrier M**)

Secrier, M., Schneider, R. PhenoTimer: Software for mapping time-resolved phenotypic landscapes. *PLOS ONE* 2013 Aug 12;8(8):e72361. *corresponding author*

Fuller, J.C., .., Rajput, A.M., **HUB Participants***. Biggest challenges in bioinformatics. *EMBO Rep* 2013 Apr;14(4):302-4. (* includes **Secrier M**)

★ **Secrier, M.**, Pavlopoulos, G.A., Aerts, J., Schneider, R. Arena3D: visualizing time-driven phenotypic differences in biological systems. *BMC Bioinform* 2012 Mar 22;13:45. *highly accessed, corresponding author*

Setty, Y., Chen, C.C., **Secrier, M.**, .., Kalamatianos, D., Emmott, S. How neurons migrate: a dynamic in-silico model of neuronal migration in the developing cortex. *BMC Syst Biol* 2011 Sep 30;5:154.

Pavlopoulos, G.A., **Secrier, M.**, .., Schneider, R., Bagos, P.G. Using graph theory to analyze biological networks. *BioData Min* 2011 Apr 28;4:10. *highly accessed*

★ **Secrier, M.**†, Toni, T.†, Stumpf, M.P. The ABC of reverse engineering biological signalling systems. *Mol Biosyst* 2009 Dec;5(12):1925-35. († joint first)