

Chantriont-Andreas Kapourani

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Research and Professional Experience

- The University of Edinburgh 2018–Present **Cross-disciplinary research fellow, MRC Human Genetics Unit and School of Informatics.**
Advisors Dr Catalina Vallejos and Prof Neil Henderson
Project: Machine learning and statistical modelling of single-cell genomics
Analysed multi-modal single cell data, including sc/snRNA-seq, sequence- and image-based spatial transcriptomics, to decode molecular mechanisms regulating liver fibrosis and regeneration.
Applied computational methods to elucidate relationship between tissue localization and gene expression variation and understand how location and function interact to regulate the transition from healthy to pathological disease states.
Performed latent class analysis to identify transcriptional subtypes in human-derived glioblastoma stem cell lines.
- The University of Edinburgh 2015–2021 **Teaching Support, School of Informatics.**
Supervisor: Co-supervised MInf student for 2-year research project on cancer data science and epigenetics. Also supervised Erasmus student on machine learning for computational biology.
Tutor, demonstrator, marker for various courses at the School of Informatics. Created course lab contents: www.inf.ed.ac.uk/teaching/courses/inf2b/learnLabSchedule.html
- DaXtra Technologies 2013–2014 **Junior Software Developer, Edinburgh.**
Adapted company's proprietary software to client's needs: integration with 3rd party database management systems, web services and online job boards, including Indeed and LinkedIn.

Education

- The University of Edinburgh 2015–2018 **PhD in Data Science, School of Informatics.**
Under the supervision of Prof. Guido Sanguinetti
Thesis: Spatial statistical modelling of epigenomic variability.
Developed statistical machine learning methods to model (single-cell) data and capture spatial correlations of epigenetic marks that would uncover the interplay between genetic and epigenetic mechanisms in transcriptional regulation.
Analysed single-cell multi-omics data to investigate regulatory relationships during mouse embryo development.
- The University of Edinburgh 2014–2015 **MSc by Research in Data Science with Distinction, School of Informatics.**
Dissertation: Mixture modelling of high-throughput biomedical data.
Developed machine learning approach to extract higher order methylation features that were predictive of gene expression levels.
Performed integrative clustering of heterogeneous sources of biological data.
- The University of Edinburgh 2012–2013 **MSc in Artificial Intelligence with Distinction, School of Informatics.**
Dissertation: Unsupervised motif discovery from acoustic time series data.
- Harokopio University of Athens 2008–2012 **BSc in Informatics with Distinction, Department of Informatics and Telematics, Greece.**
Dissertation: Integration of external applications in the Unity academic social network environment using Google's OpenSocial API.
- Roskilde University 2010–2011 **Erasmus Placement, Department of Computer Science, Denmark.**
Project: Developed *Find Friend Location*, a distributed real-time location tracking system for Android mobiles provided by SOAP Web Services.

Computational Genomics Software

- SeuratPipe SeuratPipe enables **reproducible computational analysis** of single-cell genomics (sc/snRNA-seq and Visium) by wrapping common tasks in easy to run pipelines (andreaskapou.github.io/SeuratPipe/).
- scMET scMET shares information across cells and genomic features using a Bayesian framework to **quantify genuine biological single-cell epigenetic heterogeneity** (bioconductor.org/packages/scMET/).
- Melissa Melissa **jointly clusters and imputes** single-cells by accounting for local correlations via a generalised linear model and global similarities using a mixture model (bioconductor.org/packages/Melissa/).
- BPRMeth BPRMeth **extracts higher order methylation features** that can be used for downstream modelling efforts, such as predicting gene expression or clustering genomic regions or cells according to their methylation patterns. (bioconductor.org/packages/BPRMeth/).

Awards and Distinctions

- 2021 Nominated as **supervisor of the year** for the EUSA teaching awards at the University of Edinburgh.
- 2016 **Best paper award** at the 15th European Conference on Computational Biology (ECCB).
- 2013 Winner of **Travel App Prize** (Skyscanner) University of Edinburgh (<http://easyscn.appspot.com/>). Natural language processing system for converting natural text to flight queries.
- 2012 Bodossaki foundation **scholarship for postgraduate studies**.
- 2009–2012 Scholarship from Greek state scholarships foundation (IKY) for excellent performance, **highest ranked student** for the 1st, 2nd, 3rd and 4th academic years.
- 2010 **Erasmus placement** scholarship for international studies.

Data Science Skills

- Machine Learning/
Statistics Generalized linear models, Bayesian inference, Deep learning, Gaussian processes, Approximate inference, Optimization, Latent variable models, Graphical models, Mixture models, Neural networks, Markov chain Monte Carlo, Kernel methods, Hidden Markov models.
- Languages R, Python, Torch, Pyro, Stan, Java, C/C++, MATLAB, SQL, HTML.

Public Engagement

- Ongoing Tutorial-like blog with accompanying code on statistical machine learning and Bayesian inference: <https://andreaskapou.github.io/blog/>.
- 2020 Involved in the **IGC statistical seminar series**, teaching biomedical researchers how to use statistical and machine learning methods to answer research questions.
- 2018 Contributed to the **XD Challenge** public event: provided students with challenging biomedical problems and how they could apply computational approaches to tackle them.

List of Publications

- Under submission Matchett KP, Wilson-Kanamori J*, **Kapourani, C.A.***, Portman, JP*, Fercoq F, May S, Mackey J, Brice M, Zadje E, Beltran-Sierra M, Sutherland E, Wilson G, Wallace SJ, Kitto L, Younger NT, Dobie R, Oniscu GC Wigmore SJ, Ramachandran P, Vallejos CA, Carragher NO, Simpson KJ, Kendall TJ, Acute Liver Failure Study Group; Rule JA, Lee WM, Hoare M, Weston CJ, Marioni JC, Teichmann ST, Bird TG, Carlin L, Henderson NC (Under submission to Nature). **Multimodal decoding of human liver regeneration**.
- 2021 **Kapourani, C.A.***, Argelaguet, R*, Sanguinetti, G, Vallejos, C (2021). **scMET: Bayesian modelling of DNA methylation heterogeneity at single-cell resolution**. *Genome Biology*, 22(1), pp.1-21.
- 2021 Gangoso, E., Southgate B., Bradley L., Rus, S., Galvez-Cancino, F., McGivern, N., **Kapourani, C.A.**, Byron, A., Ferguson, K., ..., Sproul, D., Margaret Frame, M., Serrels, A. and Pollard, S. (2021). **Glioblastoma stem cells hijack myeloid-affiliated transcription factors via epigenetic immunoediting to elicit immune-evasion**, *Cell*, 184(9), pp.2454-2470.
- 2019 Argelaguet, R., Clark, S.J., Mohammed, H., Stapel, L.C., Krueger, C., **Kapourani, C.A.**, Imaz-Rosshandler, I., Lohoff, T., Xiang, Y., Hanna, C.W., Smallwood, S., Ibarra-Soria, X., Buettner, F., Sanguinetti, G., Xie, W., Krueger, F., Gottgens, B., Rugg-Gunn, P.J., Kelsey, G., Dean, W., Nichols, J., Stegle, O., Marioni J.C. and Reik, W. (2019). **Multi-omics profiling of mouse gastrulation at single-cell resolution**. *Nature*, 576(7787), 487-491.

- 2019 **Kapourani, C.A.** and Sanguinetti, G. (2019). **Melissa: Bayesian clustering and imputation of single-cell methylomes.** *Genome Biology*, 20(1), 1-15.
- 2018 Clark, S.J., Argelaguet, R., **Kapourani, C.A.**, Stubbs, T.M., Lee, H.J., Alda-Catalinas, C., Krueger, F., Sanguinetti, G., Kelsey, G., Marioni, J.C., Stegle, O. and Reik, W., (2018). **scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells.** *Nature Communications*, 9(1), p.781.
- 2018 **Kapourani, C.A.** and Sanguinetti, G. (2018). **BPRMeth: a flexible Bioconductor package for modelling methylation profiles.** *Bioinformatics*.
- 2016 **Kapourani, C.A.** and Sanguinetti, G. (2016). **Higher order methylation features for clustering and prediction in epigenomic studies.** *Bioinformatics*, 32 (17), i405-i412. **(Best Paper Award in ECCB 2016)**
- 2014 Hatzi, O., Meletakis, G., Katsivelis, P., **Kapourani, C.A.**, Nikolaidou, M. and Anagnostopoulos, D. (2014). **Extending the Social Network Interaction Model to Facilitate Collaboration through Service Provision.** In *Enterprise, Business-Process and Information Systems Modeling* (pp. 94-108). Springer Berlin Heidelberg.

List of Conference Presentations

- Nov 2020 Oral presentation at *Biology of Genomes* meeting, Cold Spring Harbor Laboratory, New York, USA. Title: scMET: Bayesian modelling of DNA methylation heterogeneity at single-cell resolution.
- May 2020 Poster presentation at *Single cell biology* conference, Wellcome Genome Campus, Cambridge, UK. Title: scMET: Bayesian modelling of DNA methylation heterogeneity at single-cell resolution.
- May 2019 Oral presentation at *Centre for Genomic & Experimental Medicine* meeting, IGC, Edinburgh, UK. Title: Single-cell RNA-seq for identifying cell sub-population specific cis-eQTLs.
- March 2018 Oral presentation at *Mathematical and Statistical Aspects of Molecular Biology (MASAMB)* workshop, St Andrews, UK. Title: Melissa: Bayesian clustering and imputation of single-cell methylomes. DOI: [10.7490/f1000research.1115317.1](https://doi.org/10.7490/f1000research.1115317.1)
- July 2017 Poster presentations at *International Society for Computational Biology (ISMB)* conference, Prague, Czech Republic. Title: Bayesian hierarchical modelling of single-cell methylation profiles
- May 2017 Poster presentations at *Statistical Challenges in Single-Cell Biology* meeting, Ascona, Switzerland. Title: Bayesian hierarchical modelling of single-cell methylation profiles
- Sept 2016 Oral presentation at *15th European Conference on Computational Biology (ECCB)*, Hague, Netherlands. Title: Higher order methylation features for clustering and prediction in epigenomic studies. DOI: [10.7490/f1000research.1113102.1](https://doi.org/10.7490/f1000research.1113102.1)
- Sept 2016 Poster presentation at *10th International Workshop on Machine Learning in Systems Biology (MLSB)*, Hague, Netherlands. Title: Bayesian integrative clustering of heterogeneous types of high-throughput sequencing data.
- Aug 2015 Oral presentation at *Statistical Modeling of Epigenomics and Gene Regulation (SMEGR)* workshop, Harvard University, USA. Title: Mixture modelling of DNA methylation profiles.

Peer Review

Reviewer for peer-reviewed journals including *Genome Biology*, *Bioinformatics*, *PLOS Computational Biology*, *Statistical Applications in Genetics and Molecular Biology* and *IEEE/ACM Transactions on Computational Biology*.

Languages

- Greek Native Language
- Albanian Native Language
- English International English Language Testing System (IELTS)

References

Available on request