

CHRIS CLARKSON

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Professional Summary

I am a PhD student in computational biology. My ambition is to apply my skills in data-science and machine learning to real-world problems. I have a range of projects under my belt (including a first author publication) and am looking to take the next step in my career. I would very grateful for the chance to work in an environment where I can further enhance my skills as a bioinformatician.

Core Qualifications

- Experienced with Next Generation Sequencing (NGS) data analysis
- Learning to use single cell data
- Programming Languages
- Advanced Python, R, Linux
- Basic Javascript (chrome extensions)
- Data Science
- PCA
- Machine learning
- Pipeline development

Experience

- PhD student in Bioinformatics** Oct 2016 to Current
- Handled Next Generation Sequencing (NGS) data
 - Developed my own pipeline (taking advantage of parallelisation, using a computer cluster) that organised large MNase-seq datasets in such a way that they could be analysed with machine learning algorithms
 - Used convolutional neural networks to study MNase-Seq data patterns
 - Developed interactive R-shiny apps to make my most commonly used analysis techniques accessible to experimentalists

Education

- PhD under supervision of Dr Vladimir Teif** 2019
University of Essex
Project: "Changes of nucleosome positioning and 3D chromatin organization in cell transitions"
- Master of Science, Bioinformatics and Theoretical Systems** 2016
Imperial College London – London
- Bachelor of Science, Biomedical Science** 2015
National University of Ireland Galway – Galway
BSc Biomedical Science
- Diploma of Higher Education, French** 2012
La Sorbonne – Paris

Accomplishments

- Talk at the conference "Chromatin and Epigenetics: From single-cells to multicellular systems", University of Essex, Colchester, 13/9/19
- EMBL Travel Award for the conference "Principles of Chromosome Structure and Function", Heidelberg, Germany, 7/9/16
- Best student poster award, School of Life Sciences, University of Essex, 2017

Publications

1. **Clarkson C.T.**, Deeks E.A., Samarista R., Mamayusupova H., Zhurkin V.B.*, Teif V.B.* (2019) CTCF-dependent chromatin boundaries formed by asymmetric nucleosome arrays with decreased linker length. *Nucleic Acids Res* **47**, 11181-11196.
 2. Wiehle L., Thorn G.J., Raddatz G., **Clarkson C.T.**, Rippe K., Lyko F., Breiling A., Teif V.B. (2019) DNA (de)methylation in embryonic stem cells controls CTCF-dependent chromatin boundaries. *Genome Research* **29**, 750-761
 3. Pavlaki I., Docquier F., Chernukhin I., Kita G., Gretton S., **Clarkson C.T.**, Teif V.B.*, Klenova E.* (2018) Poly(ADP-ribosyl)ation dependent changes in CTCF-chromatin binding and gene expression in breast cells. *Biochim Biophys Acta (BBA) - Gene Regulatory Mechanisms* **1861**, 718-730
 4. Teif V.B. and **Clarkson C.T.** (2019) Nucleosome Positioning. In Encyclopedia of Bioinformatics and Computational Biology (Ed.: S. Ranganathan, M. Gribskov, K. Nakai, and C. Schönbach), vol. 2, pp. 308-317. Oxford: Academic Press
 5. Whitton L., Cosgrove D., **Clarkson C.**, Harold D., Kendall K., Richards A., Mantripragada K., Owen M.J., O'Donovan M.C., Walters J., Hartmann A., Konte B., Rujescu D.; WTCCC, Gill M., Corvin A., Rea S., Donohoe G., Morris D.W. (2016). Cognitive analysis of schizophrenia risk genes that function as epigenetic regulators of gene expression. *Am J Med Genet B Neuropsychiatr Genet*, **171**, 1170-1179.
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Under review:

6. Teif V.B, Gould T.J., **Clarkson C.T.**, Boyd L., Ishaque N., Olins A.L. & Olins D.E. (2020). Differential exposure of linker histone variants in chromatin *in situ*.

In preparation:

7. Thorn GT, **Clarkson CT** et al. (2020). DNA sequence-dependent heterochromatin microdomain formation
 8. **Clarkson C.T.** et al. (2020). Application of convolutional neural networks to study chromatin structure
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Teaching and supervision of undergraduate students

Worked as a graduate IT lab assistant for modules “Genome Science” and “Genome Bioinformatics”;
Co-supervised undergraduate students in the Teif Lab: Emily Dellow, Ralph Samarista, Emma Deeks.

Software

NRLcalc - Shiny app- Calculation of the nucleosome repeat length for many genomic regions
<https://github.com/chrisclarkson/NRLcalc>

Paper to Audio - Text to speech conversion tailored specifically for academic papers
<https://chrome.google.com/webstore/detail/paper-to-audio/djncfliejhhejjgbhcopflpnlaeicnco?authuser=1>

Websites

Linkedin: <https://www.linkedin.com/in/christopher-clarkson-841a2195/>
Github: <https://github.com/chrisclarkson/>
TeifLab: <https://generegulation.org/chrisclarkson/>

Hobbies

I love making apps that help make my life easier e.g. see above in "Accomplishments- Paper to Audio".
I love sports- including lacrosse, wall climbing and football.
I act as co-organiser of the “Pint of Science” scientific outreach festival.