

Cosmin Tudose *PhD student*

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📍 Systems Biology Ireland, UCD, Dublin, Ireland in cosmin-tudose

👤 Profile

I am 3rd year PhD student interested in using large omics datasets to uncover vulnerabilities in cancer. I focus my work on integrating omics outputs to unravel mechanisms underpinning disease biology. My primary interests lie in genomics data science, statistics, data visualisation, developing and implementing pipelines for omics data analysis and high-throughput screening.

🎓 Education

2020 – Present Dublin, Ireland	PhD Bioinformatics Title: Defining molecular vulnerabilities in childhood leukaemia through biological network analysis <i>Systems Biology Ireland CRT Genomics Data Science MSCA & SFI funded</i> Defining 3D chromatin architecture changes by integrating RNA-Seq, ATAC-Seq, Hi-C data obtained from cell line models harbouring epigenetic factor deletions leading to aggressive leukaemia. Using RNA-Seq, ChIP-Seq, drug screen, CRISPR screen and other publicly available data to uncover new genetic associations defining aggressive leukaemia. For my analyses I primarily use R and bash, but also implementing and adapting published pipelines that mix python, snakemake and NGS tools such as samtools and bedtools. Presented at national and international conferences. For all presentations see www.tudose.science
2016 – 2020 Nottingham, UK	MSci Genetics <i>University of Nottingham</i> Graduated with a First Class Hons degree

📁 Projects

2021/01 – Present	MAGIC-I <i>Molecular & Genomic Interrogation of Childhood Cancer in Ireland</i> Involved in a collaborative project between Systems Biology Ireland, Genuity Science and Illumina. The aim is to perform WGS+RNA-Seq on samples from every paediatric cancer patient in Ireland. Participated in meetings where the design of the bioinformatic pipelines has been discussed.
2023/06 – 2023/08	Associating transcriptomic profiles with drug screen outputs in acute myeloid leukaemia <i>Supervisor for a summer internship</i> We are employing dimensionality reduction methods to associate cell line transcriptomic profiles to patient transcriptomes and find novel associations with drug sensitivities in leukaemia.
2019/09 – 2020/05	CNV haplotype phasing using nanopore reads <i>Master's project Supervised by Prof John Armour</i> Developed a pipeline to identify copy-number variants and separate the two haplotypes based on read depth and read length from nanopore reads. Used R, bash and samtools for the analysis.

💻 Skills

Programming languages	Tools	Pipelines	Transferable skills
R, Bash, Shiny, Python, Snakemake	Samtools, Bedtools, GATK, IGV, Conda, Git, Juicer, Alignment tools	RNA-Seq, ATAC-Seq, Hi-C	Experimental design, Data viz, Presentation, Statistics

📖 Publications

Gene essentiality in cancer is better predicted by mRNA abundance than by gene regulatory network-inferred activity ✉
Tudose, Bond and Ryan - *bioRxiv*

🏆 Grants and awards

CRT data generation fund - Successfully obtained a grant to generate ATAC-Seq data on leukaemia cell line samples
Conway Festival 2021 - Best poster for my session
Systems Genomics Summit 2021 - Best poster

📚 Teaching

Demonstrator on a bioinformatics module for 3rd year Genetics students. This includes computer practicals on MSA, BLAST, UCSC Genome Browser, phylogenetics, SNP associations and protein structures.