Dr. Mark Dunning, PhD, FHEA

email: mark@mdbioinformatics.com
github: markdunning
orcid: 0000-0002-8853-9435

Summary

Highly accomplished and adaptable **Senior Bioinformatician** with 20 years of expertise in **genomic data analysis** and **high-throughput sequencing interpretation**. Proficient in **R, Nextflow**, and advanced **data analysis and visualization** techniques. Passionate about developing and mentoring the next generation of data-literate researchers, and committed to leveraging computational insights to directly **improve patient outcomes and experiences.**

Technical Skills

- **Programming Languages:** R, Bash/shell scripting, Python (basic)
- **Biological assay analysis:** Microarrays, Bulk RNA-seq, whole-exome sequencing, whole-genome sequencing, ChiP-seq, ATAC-seq, 10X Single-cell RNA-seq, Spatial Transcriptomics (10X Visium and Xenium)
- **Software packages (R):** DESeq2, limma, edgeR, Seurat, maftools, GenomicRanges, tidyverse, Shiny, plotly, tidymodels
- **Bioinformatics tools:** samtools, bedtools, GATK, picard, STAR, salmon, strelka, mutect2, annovar
- **Pipelines, containers and deployment:** bcbio, nextflow/nf.core, docker, singularity/apptainer, AWS
- **Operating Systems: Mac OSX,** Windows, Unix (Ubuntu), HPC

Professional Experience

March 2025 – August 2025. Bioinformatics Manager. The Faculty of Health, The University of Sheffield, Uk

- *Transition from academic to professional services career track.*
- *Developing a strategy for sustainable Bioinformatics service*
- *Ensuring that key processes are successfully delivered in accordance with university-wide ways of working*

Oct 2017 – March 2025 Bioinformatics Core Director, The Faculty of Health, University of Sheffield, Uk

- *Establishing Bioinformatics Core facility to support staff, students, clinicians across the whole campus*
- *Day-to-day support of projects involving various sequencing and high-throughput technologies; bulk and single-cell RNA-Seq, Whole-exome/whole-genome sequencing,*
- *Liaising with researchers to obtaining grant funding*
- *Run the Core's Bioinformatics training programme*

- *Line management and mentoring of junior staff*
- *Overseeing development and deployment of Bioinformatics workflows using nextflow*

Aug 2015 – Sept 2017 Bioinformatics Training Coordinator, Cancer Research Uk Cambridge Institute, University of Cambridge, Uk

- *Developing and delivering Bioinformatics training courses for staff and students; e.g. R programming, RNA-seq analysis, statistics*
- *Responsible for leading the teaching and facilitating Cancer Research Uk's Summer School in Bioinformatics*

Aug 2008 – Aug 2015 Bioinformatics Analyst / Senior Bioinformatics Analyst, Cancer Research Uk Cambridge Institute, University of Cambridge, Uk

- *Bioinformatics support and consulting for Researchers*
- *Responsible for QC, processing and preliminary analysis of high-profile studies in breast cancer (METABRIC) and prostate cancer (camcAPP)*
- *Prototyping and evaluating tools for the whole-genome analysis of Oesophageal cancer*

Educational Qualifications

Jan 2009: PhD in Oncology, The University of Cambridge, Uk. Thesis title: **Genome-wide analyses using bead-based microarrays**

Sept 2004: MSc in Data Analytics, Networks and Nonlinear Dynamics, The University of York, York, Uk

July 2003: BSc in Mathematics and Computer Science, The University of York, York, Uk

Supervision and Teaching

Secondary Supervision of two current PhD students

Third Supervisor of two current PhD students

Fellow of Higher Education Authority (FHEA)

Lecturer for MSCs in Genomic Medicine, Molecular Medicine, Genomic Approaches to Drug Discovery, Translational Oncology at University of Sheffield

Module lead for BMS3104 / BMS353 Bioinformatics for Biomedical Science at University of Sheffield

Accredited instructor for thecarpentries.org

Grants

YORKSHIRE CANCER RESEARCH, PHOENIX; Precision Healthcare in Oncology; ENabling Infrastructure and eXpertise, £1,582,625	2025-present
BREAST CANCER NOW, Development of a blood-based biomarker panel for the prediction of risk of secondary breast cancer, £383,525	2025-present
YORKSHIRE CANCER RESEARCH, FORT4RESS: translating tumour treating fields therapies for cancers of unmet need in South Yorkshire, £674,875	2025-present
YORKSHIRE CANCER RESEARCH, EVIDENT: Ex VIvo DEtermined caNcer Therapy clinical validation., £2,742,312	2024-present
Engineering and Physical Sciences Research Council, Transfer learning of pharmacogenomic information across disease types and preclinical models for drug sensitivity prediction., £346,843	2022-present
BRITISH HEART FOUNDATION, BHF: How Does Brain Microvascular Disease (MVD), Especially Pathological Changes to Capillaries, Contribute to Dementiaa, £285,520	2022-present
AMERICAN ASSOCIATION FOR CANCER RESEARCH, DNA damage response targeted combinations to enhance TTFields and overcome spatiofunctional heterogeneity, £190,840	2021-present
LONZA BIOLOGICS PLC, Centre of Excellence in Cell Engineering at Sheffield, £1,420,130	2021-present
SARCOMA UK, Identification of novel therapies for soft tissue sarcoma, £117,850	2021-present
ENGINEERING AND PHYSICAL SCIENCE RESEARCH COUNCIL, Transfer learning of pharmacogenomic information across disease types and preclinical models for drug sensitivity prediction., £350,276	2021-present
THE BRAIN TUMOUR CHARITY, Modelling glioblastoma cells left behind after surgery to tackle treatment failure, £119,936	2020-present

Full Publications

Le Maitre, C. L., Dunning, M. J., & Wilkinson, J. M. (2025). OPTIMISATION OF SPATIAL TRANSCRIPTOMICS FOR ADULT HUMAN FFPE OSTEOCHONDRAL AND INTERVERTEBRAL DISC TISSUE. *Osteoarthritis and Cartilage*, *33*, S410. doi:10.1016/j.joca.2025.02.591

Dunning, M. J., LeMaitre, C. L., & Wilkinson, J. M. (2025). Spatial transcriptomics resolves tissue-level molecular effects of denosumab therapy in a randomized clinical trial for periprosthetic osteolysis. In *Orthopaedic Proceedings* Vol. 107-B (pp. 48). Harrogate, England: British Editorial Society of Bone & Joint Surgery. doi:10.1302/1358-992x.2025.2.048

Cheng, V. W. T., Vaughn-Beaucaire, P., Shaw, G. C., Kriegs, M., Droop, A., Psakis, G., . . . Brüning-Richardson, A. (2025). ARHGAP12 and ARHGAP29 exert distinct regulatory effects on switching between two cell morphological states through GSK-3 activity. *Cell Reports*, *44*(3), 115361. doi:10.1016/j.celrep.2025.115361

Draper, B. J., Dunning, M. J., & James, D. C. (n.d.). Selecting differential splicing methods: Practical considerations. *F1000Research*, *14*, 47. doi:10.12688/f1000research.155223.1

Rominiyi, O., McGarrity-Cottrell, C., Myers, K. N., Jones, C. G., Wosnitzka, K., Williams, S. T., . . . Collis, S. J. (2024). Ex-vivo models of post-surgical residual disease in human glioblastoma [version 1; peer review: awaiting peer review]. *F1000Research*, *13*. doi:10.12688/f1000research.157013.1

Zhou, Z., Korteland, S. -A., Tardajos-Ayllon, B., Wu, J., Chambers, E., Weninck, J., . . . Evans, P. C. (2024). Shear stress is uncoupled from atheroprotective KLK10 in atherosclerotic plaques. *Atherosclerosis*, *398*, 118622. doi:10.1016/j.atherosclerosis.2024.118622

Xavier, J. M., Magno, R., Russell, R., de Almeida, B. P., Jacinta-Fernandes, A., Besouro-Duarte, A., . . . Maia, A. -T. (2024). Identification of candidate causal variants and target genes at 41 breast cancer risk loci through differential allelic expression analysis. *Scientific Reports*, *14*. doi:10.1038/s41598-024-72163-y

Pirri, D., Tian, S., Tardajos-Ayllon, B., Irving, S. E., Donati, F., Allen, S. P., . . . Evans, P. C. (2024). EPAS1 Attenuates Atherosclerosis Initiation at Disturbed Flow Sites Through Endothelial Fatty Acid Uptake. *Circulation Research*, *135*(8), 822-837. doi:10.1161/circresaha.123.324054

Arrulo, M. R., Wells, G., Dunning, M. J., English, W. R., Rantala, J. K., Danson, S., . . . Sisley, K. (2024). 1781P Multi-omics of soft tissue sarcomas with complex karyotypes: Investigating genomic and transcriptomic differences between cell lines of the same subtype. *Annals of Oncology*, *35*, S1059. doi:10.1016/j.annonc.2024.08.1872

Gelder, K. L., Carruthers, N. A., Ball, S., Dunning, M., Craggs, T. D., Twelvetrees, A. E., & Bose, D. A. (2024). Cooperation between Intrinsically Disordered Regions regulates CBP condensate behaviour. doi:10.1101/2024.06.04.597392

Wood, S. L., Lopez-Guajardo, A., Oliva, M. R., Collins, M., Pham, K., Dunning, M., . . . Brown, J. E. (2024). #28. Identification of key proteins within prostate cancer derived exosomes and their role in priming the pre-metastatic niche. *Journal of Bone Oncology*, *45*, 100566. doi:10.1016/j.jbo.2024.100566

Pirri, D., Tian, S., Tardajos-Ayllon, B., Irving, S., Donati, F., Allen, S. P., . . . Evans, P. C. (2023). EPAS1 Attenuates Atherosclerosis Initiation at Disturbed Flow Sites through Endothelial Fatty Acid Uptake. doi:10.1101/2023.12.05.570309

Payne, T., Burgess, T., Bradley, S., Roscoe, S., Sassani, M., Dunning, M. J., . . . Bandmann, O. (2023). Multimodal assessment of mitochondrial function in Parkinson's disease. *Brain*, *147*(1), 267-280. doi:10.1093/brain/awad364

McGarrity-Cottrell, C., Myers, K., Dunning, M., Bagga, V., Sinna, S., Al-Tamimi, Y., . . . Collis, S. (2023). DEfiNING SPATIAL HETEROGENEITY OF A NOVEL LIVING BIOBANK OF POST-SURGICAL RESIDUAL GLIOBLASTOMA TO DEVELOP STRATEGIES FOR TARGETED THERAPY. *Neuro-Oncology*, *25*(Supplement_3), iii14. doi:10.1093/neuonc/noad147.055

López-Guajardo, A., Zafar, A., Al Hennawi, K., Rossi, V., Alrwaili, A., Medcalf, J. D., . . . Gad, A. K. B. (2023). Regulation of cellular contractile force, shape and migration of fibroblasts by oncogenes and Histone deacetylase 6. *Frontiers in Molecular Biosciences*, *10*. doi:10.3389/fmolb.2023.1197814

Payne, T., Appleby, M., Buckley, E., van Gelder, L. M. A., Mullish, B. H., Sassani, M., . . . Bandmann, O. (2023). A double-blind, randomized, placebo-controlled trial of ursodeoxycholic acid (UDCA) in Parkinson's disease. *Movement Disorders*, *38*(8), 1493-1502. doi:10.1002/mds.29450

Keatinge, M., Gegg, M. E., Watson, L., Mortiboys, H., Li, N., Dunning, M., . . . Bandmann, O. (2023). Unexpected phenotypic and molecular changes of combined glucocerebrosidase and acid sphingomyelinase deficiency. *Disease Models & Mechanisms*, *16*(6). doi:10.1242/dmm.049954

Ashford, B. A., Appleby-Mallinder, C. S., Dawson, C., Matuszyk, M. M., Heath, P. R., Wei, W., . . . Highley, J. R. (2023). Inflammatory pathology in human motor neuron disease. In *JOURNAL OF PATHOLOGY* Vol. 261 (pp. S5). Retrieved from https://www.webofscience.com/

Barrow, R., Wilkinson, J., He, Y., Callaghan, M., Brüning-Richardson, A., Dunning, M., & Stead, L. (2022). SpheroidAnalyseR—an online platform for analyzing data from 3D spheroids or organoids grown in 96-well plates. *Journal of Biological Methods*, *9*(4). doi:10.14440/jbm.2022.388

Tonge, J. J., Notley, S. V., Dunning, M. J., López-Guajardo, A., Medcalf, J. D., Heldin, P., . . . Gad, A. K. B. (2022). Hyaluronan nanoscale clustering and Hyaluronan synthase 2 expression are linked to the invasion of child fibroblasts and infantile fibrosarcoma in vitro and in vivo. *Scientific Reports*, *12*, 1-10. doi:10.1038/s41598-022-21952-4

McGarrity - Cottrell, C., Myers, K., Wang, D., Dunning, M., Bagga, V., Al-Tamimi, Y., . . . Collis, S. (2022). STEM-02. GENERATION AND CHARACTERISATION OF A LIVING BIOBANK OF POST-SURGICAL RESIDUAL GLIOBLASTOMA TO IDENTIFY NOVEL THERAPEUTIC TARGETS. *Neuro-Oncology*, *24*(Supplement_7), vii31. doi:10.1093/neuonc/noac209.119

Souilhol, C., Tardajos Ayllon, B., Li, X., Diagbouga, M. R., Zhou, Z., Canham, L., . . . Evans, P. C. (2022). JAG1-NOTCH4 mechanosensing drives atherosclerosis. *Science Advances*, *8*(35). doi:10.1126/sciadv.abo7958

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Barrow, R., Wilkinson, J. N., He, Y., Callaghan, M., Brüning-Richardson, A., Dunning, M., & Stead, L. F. (2022). SpheroidAnalyseR – an online platform for analysing data from 3D spheroids or organoids grown in 96-well plates. doi:10.1101/2022.02.18.481039

Cottrell, C. M., Myers, K., Dunning, M., Bagga, V., Sinha, S., Al-Tamimi, Y., . . . Collis, S. (2022). Development of unique ex vivo models of post-surgical residual glioblastoma. In *WFNOS 2022 Abstract Book* (pp. S219). The Korean Brain Tumor Society; The Korean Society for Neuro-Oncology; The Korean Society for Pediatric Neuro-Oncology. doi:10.14791/btrt.2022.10.f-1136

Kariotis, S., Jammeh, E., Swietlik, E. M., Pickworth, J. A., Rhodes, C. J., Otero, P., . . . Schotte, G. (2021). Biological heterogeneity in idiopathic pulmonary arterial hypertension identified through unsupervised transcriptomic profiling of whole blood. *Nature Communications*, *12*. doi:10.1038/s41467-021-27326-0

Shah, K. M., Dunning, M. J., Gartland, A., & Wilkinson, J. M. (2021). Distinct concentration-dependent molecular pathways regulate bone cell responses to cobalt and chromium exposure from joint replacement prostheses. *International Journal of Molecular Sciences*, *22*(10). doi:10.3390/ijms22105225

Solano, B. S., Föll, M. C., Gallardo-Alba, C., Erxleben, A., Rasche, H., Hiltemann, S., . . . Grüning, B. A. (2021). Fostering accessible online education using Galaxy as an e-learning platform. *PLoS Computational Biology*, *17*(5). doi:10.1371/journal.pcbi.1008923

Serrano-Solano, B., Erxleben, A., Gallardo-Alba, C., Rasche, H., Hiltemann, S., Föll, M., . . . Grüning, B. (2020). Fostering Accessible Online Education Using Galaxy as an e-learning Platform. doi:10.20944/preprints202009.0457.v1

Rhodes, C. J., Otero-Núñez, P., Wharton, J., Swietlik, E. M., Kariotis, S., Harbaum, L., . . . Wilkins, M. R. (2020). Whole blood RNA profiles associated with pulmonary arterial hypertension and clinical outcome. *American Journal of Respiratory and Critical Care Medicine*, *202*(4), 586-594. doi:10.1164/rccm.202003-0510oc

Souilhol, C., Li, X., Canham, L., Roddie, H., Pirri, D., Ayllon, B. T., . . . Evans, P. C. (2020). JAG1-NOTCH4 Mechanosensing Drives Atherosclerosis. doi:10.1101/2020.05.15.097931

Hamilton, N., Rutherford, H. A., Isles, H. M., Petts, J. J., Weber, T., Henneke, M., . . . Renshaw, S. A. (n.d.). Failure to clear developmental apoptosis contributes to the pathology of RNASET2-deficient leukoencephalopathy. *bioRxiv*. doi:10.1101/744144

Keatinge, M., Gegg, M. E., Watson, L., Mortiboys, H., Li, N., Dunning, M., . . . Bandmann, O. (2019). Unexpected opposing biological effect of genetic risk factors for Parkinson’s disease. doi:10.1101/702340

Wood, E., Parker, M. D., Dunning, M. J., Hesketh, S., Wang, D., Pink, R., & Fratter, C. (n.d.). Clinical long-read sequencing of the human mitochondrial genome for mitochondrial disease diagnostics. *bioRxiv*. doi:10.1101/597187

Westbrook, J. A., Wood, S. L., Cairns, D. A., McMahon, K., Gahlaut, R., Thygesen, H., . . . Brown, J. (2019). Identification and validation of DOCK4 as a potential biomarker for risk of bone metastasis development in patients with early breast cancer. *The Journal of Pathology*, *247*(3), 381-391. doi:10.1002/path.5197

Bakht, M. K., Derecichei, I., Li, Y., Ferraiuolo, R. -M., Dunning, M., Oh, S. W., . . . Porter, L. A. (2019). Neuroendocrine differentiation of prostate cancer leads to PSMA suppression. *Endocrine-Related Cancer*, *26*(2), 131-146. doi:10.1530/erc-18-0226

Jurmeister, S., Ramos-Montoya, A., Sandi, C., Pértega-Gomes, N., Wadhwa, K., Lamb, A. D., . . . Neal, D. E. (2018). Identification of potential therapeutic targets in prostate cancer through a cross-species approach.. *EMBO Molecular Medicine*, *10*(3). doi:10.15252/emmm.201708274

Ross-Adams, H., Lamb, A. D., Dunning, M. J., Halim, S., Lindberg, J., Massie, C. M., . . . Neal, D. E. (2017). Corrigendum to “Integration of Copy Number and Transcriptomics Provides Risk Stratification in Prostate Cancer: A Discovery and Validation Cohort Study” [EBioMedicine 2 (9) (2015) 1133–1144]. *EBioMedicine*, *17*, 238. doi:10.1016/j.ebiom.2017.03.010

Dunning, M. J., Vowler, S. L., Lalonde, E., Ross-Adams, H., Mills, I. G., Lynch, A. G., & Lamb, A. D. (2017). Mining human prostate cancer datasets: The “camcAPP” shiny app. doi:10.1101/090589

Lalonde, E., Alkallas, R., Chua, M. L. K., Fraser, M., Haider, S., Meng, A., . . . Boutros, P. C. (2017). Translating a Prognostic DNA Genomic Classifier into the Clinic: Retrospective Validation in 563 Localized Prostate Tumors. *European Urology*, *72*(1), 22-31. doi:10.1016/j.eururo.2016.10.013

Whitington, T., Gao, P., Song, W., Ross-Adams, H., Lamb, A. D., Yang, Y., . . . Wiklund, F. (2016). Gene regulatory mechanisms underpinning prostate cancer susceptibility. *Nature Genetics*, *48*(4), 387-397. doi:10.1038/ng.3523

Shaw, G. L., Whitaker, H., Corcoran, M., Dunning, M. J., Luxton, H., Kay, J., . . . Neal, D. E. (2016). The Early Effects of Rapid Androgen Deprivation on Human Prostate Cancer. *European Urology*, *70*(2), 214-218. doi:10.1016/j.eururo.2015.10.042

Uribe-Lewis, S., Stark, R., Carroll, T., Dunning, M. J., Bachman, M., Ito, Y., . . . Murrell, A. (n.d.). 5-hydroxymethylcytosine marks promoters in colon that resist DNA hypermethylation in cancer. *Genome Biology*, *16*(1). doi:10.1186/s13059-015-0605-5

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Lalonde, E., Ishkanian, A. S., Sykes, J., Fraser, M., Ross-Adams, H., Erho, N., . . . Bristow, R. G. (2014). Tumour genomic and microenvironmental heterogeneity for integrated prediction of 5-year biochemical recurrence of prostate cancer: a retrospective cohort study. *The Lancet Oncology*, *15*(13), 1521-1532. doi:10.1016/s1470-2045(14)71021-6

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Vollan, H. K. M., Rueda, O. M., Chin, S. -F., Curtis, C., Turashvili, G., Shah, S., . . . Caldas, C. (2015). A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. *Molecular Oncology*, *9*(1), 115-127. doi:10.1016/j.molonc.2014.07.019

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Weaver, J., Ross-Innes, C., Shannon, N., Lynch, A., Murtaza, M., Forshew, T., . . . Fitzgerald, R. (2014). PTU-153 The Timing Of Oncogenic Events In The Evolution Of The Oesophageal Adenocarcinoma Genome And Implications For Clinical Diagnostics. *Gut*, *63*(Suppl 1), A105.2-A106. doi:10.1136/gutjnl-2014-307263.227

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