

Curriculum Vitae

Name: Nathan Peter Harmston

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Current position	Assistant Professor - Computational Biology - Yale-NUS - (2019 -)
Previous positions	Senior Research Fellow - Systems Genetics / Molecular Cancer Biology - Duke-NUS - (2015 - 2019) Career Development Fellow - Computational Regulatory Genomics - MRC LMS - (2012 - 2015) Production programmer - Clinphone Ltd - Nottingham (2007) Software developer - MyCIB, University of Nottingham - (2006)
Education	PhD - Theoretical Systems Biology - Imperial College London - (2008 - 2012) Thesis title: <i>Probabilistic species-driven gene mention normalisation</i> Bioinformatics & Systems Biology MSc (Hons) - Distinction - Imperial College London (2007 - 2008) Thesis title: <i>Pathway signatures of Pediatric ependymoma clinicopathological subgroups</i> Computer Science BSc (Hons) - 2.1 - University of Nottingham (2002 - 2006)
Publications	* contributed equally, † as joint corresponding author Intrinsic mutant HTT-mediated defects in oligodendroglia cause myelination deficits and behavioral abnormalities in Huntington disease. Ferrari Bardile, C., Garcia-Miralles, M., Caron, N. S., Rayan, N. A., Langley, S. R., <u>Harmston, N.</u> , Rondelli, A. M., Teo, R. T. Y., Watzl, S., Anderson, L. M., Bae, H.-G., Jung, S., Williams, A., Prabhakar, S., Petretto, E., Hayden, M. R., and Pouladi, M. A. (2019). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 85:201818042 In Vivo Generation of Post-infarct Human Cardiac Muscle by Laminin-Promoted Cardiovascular Progenitors. Yap, L., Wang, J.-W., Moreno-Moral, A., Chong, L. Y., Sun, Y., <u>Harmston, N.</u> , Wang, X., Chong, S. Y., Öhman, M. K., Wei, H., Bunte, R., Gosh, S., Cook, S., Hovatta, O., de Kleijn, D. P. V., Petretto, E., and Tryggvason, K. (2019). <i>Cell reports</i> , 26(12):3231–3245.e9 Unbiased Profiling of Isogenic Huntington Disease hPSC-Derived CNS and Peripheral Cells Reveals Strong Cell-Type Specificity of CAG Length Effects. Ooi, J., Langley, S. R., Xu, X., Utami, K. H., Sim, B., Huang, Y., <u>Harmston, N.</u> , Tay, Y. L., Ziaei, A., Zeng, R., Low, D., Aminkeng, F., Sobota, R. M., Ginhoux, F., Petretto, E., and Pouladi, M. A. (2019). <i>Cell reports</i> , 26(9):2494–2508.e7 Systems genetics identifies a macrophage cholesterol network associated with physiological wound healing. Bagnati, M., Moreno-Moral, A., Ko, J.-H., Nicod, J., <u>Harmston, N.</u> , Imprialou, M., Game, L., Gil, J., Petretto, E., and Behmoaras, J. (2019). <i>JCI insight</i> , 4(2):71 Temporal dynamics of Wnt-dependent transcriptome reveals an oncogenic Wnt/MYC/ribosome axis. Madan*, B., <u>Harmston, N.*</u> , Nallan, G., Montoya, A., Faull, P., Petretto, E., and Virshup, D. M. (2018). <i>The Journal of clinical investigation</i> Biologically relevant laminin as chemically defined and fully human platform for human epidermal keratinocyte culture. Tjin, M. S., Chua, A. W. C., Moreno-Moral, A., Chong, L. Y., Tang, P. Y., <u>Harmston, N.</u> , Cai, Z., Petretto, E., Tan, B. K., and Tryggvason, K. (2018). <i>Nature communications</i> , 9(1):4432

Changes in macrophage transcriptome associate with systemic sclerosis and mediate GS-DMA contribution to disease risk. Moreno-Moral, A., Bagnati, M., Koturan, S., Ko, J.-H., Fonseca, C., Harmston, N., Game, L., Martin, J., Ong, V., Abraham, D. J., Denton, C. P., Behmoaras, J., and Petretto, E. (2018). *Annals of the Rheumatic Diseases*

Topologically associating domains are ancient features that coincide with Metazoan clusters of extreme noncoding conservation. Harmston, N.[†], Ing-Simmons, E., Tan, G., Perry, M., Merckenschlager, M., and Lenhard, B. (2017). *Nature Communications*, 8(1):441

An embryonic system to assess direct and indirect Wnt transcriptional targets. Suresh^{*}, J., Harmston, N.^{*}, Lim, K. K., Kaur, P., Jin, H. J., Lusk, J. B., Petretto, E., and Tolwinski, N. S. (2017). *Scientific Reports*, 7(1):11092

A Bayesian Approach for Analysis of Whole-Genome Bisulfite Sequencing Data Identifies Disease-Associated Changes in DNA Methylation. Rackham, O. J. L., Langley, S. R., Oates, T., Vradi, E., Harmston, N., Srivastava, P. K., Behmoaras, J., Dellaportas, P., Bottolo, L., and Petretto, E. (2017). *Genetics*, 205(4):1443–1458

Wnt proteins synergize to activate β -catenin signaling. Alok, A., Lei, Z., Jagannathan, N. S., Kaur, S., Harmston, N., Rozen, S. G., Tucker-Kellogg, L., and Virshup, D. M. (2017). *Journal of Cell Science*, 130(9):1532–1544

Wnt addiction of genetically defined cancers reversed by PORCN inhibition. Madan, B., Ke, Z., Harmston, N., Ho, S. Y., Frois, A. O., Alam, J., Jeyaraj, D. A., Pendharkar, V., Ghosh, K., Virshup, I. H., Manoharan, V., Ong, E. H. Q., Sangthongpitag, K., Hill, J., Petretto, E., Keller, T. H., Lee, M. A., Matter, A., and Virshup, D. M. (2015). *Oncogene*

GenomicInteractions: An R/Bioconductor package for manipulating and investigating chromatin interaction data. Harmston, N.^{*†}, Ing-Simmons^{*}, E., Perry^{*}, M., Baresic, A., and Lenhard, B. (2015). *BMC Genomics*, 16(1):963

The mystery of extreme non-coding conservation. Harmston, N.^{*}, Baresic^{*}, A., and Lenhard, B. (2013). *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 368(1632)

Chromatin and epigenetic features of long-range gene regulation. Harmston, N. and Lenhard, B. (2013). *Nucleic Acids Research*, 41(15):7185–7199

Which species is it? Species-driven gene name disambiguation using random walks over a mixture of adjacency matrices. Harmston, N., Filsell, W., and Stumpf, M. P. H. (2012). *Bioinformatics (Oxford, England)*, 28(2):254–260

What the papers say: text mining for genomics and systems biology. Harmston, N., Filsell, W., and Stumpf, M. P. H. (2010). *Human Genomics*, 5(1):17–29

Google Scholar

<https://scholar.google.com.sg/citations?user=BdHw1m4AAAAJ&hl=en>

Academic Services

Reviewer for: Scientific Reports, Journal of Clinical Investigation, Genetics, PNAS, Science

Co-organiser of London Biogeeks: a Bioinformatics seminar series held once every three months at various London Universities.

Posters

Oncogenic Wnt-Myc-ribosome axis revealed by *in vivo* transcriptome time course analysis - Babita Madan, Nathan Harmston, Gahyathiri Nallan, Alex Montoya, Peter Faull, Enrico Petretto and David M Virshup - *European Wnt Meeting* - 2018 - Heidelberg, Germany

Investigating the transcriptional differences between *in vitro*, subcutaneous and orthotopic models of pancreatic cancer - Nathan Harmston, Babita Madan, Enrico Petretto, David M. Virshup - *Lorne Genome Conference* - 2017 - Lorne, Australia

TADs are ancient features that coincide with Metazoan clusters of noncoding conservation - Nathan Harmston, Elisabeth Ing-Simmons, Ge Tan, Malcolm Perry, Mattias Merckenschlager, Boris Lenhard - *Transcription and Chromatin* - 2016 - Heidelberg, Germany

Species disambiguation using random walks over a mixture of adjacency matrices - Nathan Harmston, Wendy Filsell, Michael P H Stumpf - *MASAMB* 2011 - Vienna, Austria

Presentations	<p>Comparative genomics of multiple yeast strains - Peter Clarke, <u>Nathan Harmston</u>, Charlie Hodgman, Ed Louis - <i>Supercomputing</i> - 2006 - Nottingham, UK</p> <p>Identifying genes and proteins in text: a short review of available tools and resources - <i>London Biogeeks</i> 2011 London</p> <p>Integration of copy number, gene expression and pathways to investigate the ependymoma genome - <i>UKAffy</i> 2008 Nottingham</p>
Software	<p>GenomicInteractions - R/Bioconductor package for handling genomic interaction data http://bioconductor.org/packages/release/bioc/html/GenomicInteractions.html</p> <p>isoHD - Resource for interrogating 'omics data from a model of Huntingdon disease isohd.pouladilab.org</p> <p>ABBA - Approximate Bayesian Bisulphite Sequencing https://github.com/SystemsGeneticsSG/ABBA</p>