

Mark Spensley PhD

Personal Details:

Address: 746, 73 Street SW, Calgary, Alberta. T3H 5V9
Email: maspensley@gmail.com
Telephone: +1 416 809 9405
Web: <https://markspensley.net>

Summary of Skills:

- Experienced programmer (Python; C):
 - Skilled user of image analysis libraries (scikit-image, OpenCV etc).
 - Data exploration and analysis with NumPy, Pandas, SciPy and Matplotlib.
 - Machine learning with scikit-learn, Keras and TensorFlow.
 - Experience in bioinformatics and comparative genomics.
 - Developed varied software projects from simple analysis scripts to multithreaded, event-driven applications and simple microcontroller firmware.
- Accomplished and adaptable laboratory scientist:
 - Leadership of varied research projects, developed from conception to publication.
 - Highly experienced in experimental design and data analysis.
 - Published research on both plant and animal models, on multiple biological topics.
 - Extensive experience in nematode chemical screen design.
- Instrument prototyping and development:
 - Designed and built a novel image acquisition system for *C. elegans* research.
 - Experience of specifying and integrating industrial camera and optical components.
 - Good mechanical skills and experienced in basic electronics design and construction.

Employment:

Mar 2019- Company Director
Phenalysis Inc., Canada

- Founded a company to transfer the technology I developed at the University of Toronto to a niche in commercial anti-parasitic screening.
- Contract software development for screen automation: image analysis and classification.

Nov 2012- Postdoctoral Fellow, Technology for Drug Screening in Nematodes
Feb 2019 Terrence Donnelly Centre, University of Toronto, Canada

- I developed concepts, software and experimental protocols to study the dynamics of acute drug responses in *C. elegans* in near real time:
 - My software and protocols have been adopted by several other research groups, locally and internationally.
 - This work formed the basis for four graduate student projects and two grants.

- Developed drug screens to identify compounds potentiating muscarinic signalling
- Invented a hardware platform to increase the speed of pharmacological profiling in small invertebrates one hundred-fold:
 - Identified a novel application of industrial inspection optics to biological imaging.
 - Designed and constructed prototype instrument.
 - Wrote user software and device firmware.
 - Developed software and protocols for analysis of worm movement, behaviour and morphology.

Apr 2009- Jul 2012 Postdoctoral Research Assistant, Alternative Splicing in Plants

Division of Plant Sciences, University of Dundee at James Hutton Institute , UK

- Established bioinformatic methods in the lab by developing pipelines and custom software to identify novel alternative transcripts and evolutionarily conserved "poison exons" in plant genomes.
- Designed and performed molecular biology experiments to study the role of small RNAs in the regulation of alternative mRNA splicing in *Arabidopsis thaliana*.
- Identified the need for reannotation of translational start sites the *Arabidopsis thaliana* genome database and then wrote software to accomplish this. These reannotations are included in the current official Araport genome annotation.

Education:

2003 -2007 PhD, University of Warwick, UK.

Supervisor: Isabelle Carré

Project: *Circadian and Light-Regulated Transcription of the Arabidopsis clock gene LHY*. Using a combination of biochemical approaches and *in vivo* luciferase reporter constructs, I identified a novel light-responsive element and two distinct circadian-regulated elements in the *LHY* promoter. These circadian elements responded differentially to changing dawn and dusk transitions, suggesting a mechanism by which the circadian clock can adapt to changing day length through the seasons.

2000-2003 BSc (Hons) Molecular Biology, Upper Second Class

University of Newcastle-upon-Tyne, UK

Publications:

Del Borrello S, Lautens M, Dolan K, Tan JH, Davie T, Schertzberg MR, Spensley MA, Caudy AA, Fraser AG. (2019) *Rhodoquinone biosynthesis in C.elegans requires precursors generated by the kynurenine pathway*. *Elife*. 2019 Jun 24;8

Spensley M, Del Borrello S, Pajkic D, Fraser AG (2018) *Acute effects of drugs on C. elegans movement reveal complex responses and plasticity*. *G3 Genes|Genomes|Genetics*. **8**:2941-2952.

Zhang R, Calixto CPG, Marquez Y, Venhuizen P, Tzioutziou NA, Guo W, Spensley M, Entizne JC, Lewandowska D, Ten Have S, Frei Dit Frey N, Hirt H, James AB, Nimmo HG, Barta A, Kalyna M, Brown JWS. (2017) *A high quality Arabidopsis transcriptome for accurate transcript-level analysis of alternative splicing*. *Nucleic Acids Research*. **45**:5061-5073.

Vu V, Verster AJ, Schertzberg M, Chuluunbaatar T, Spensley M, Pajkic D, Hart GT, Moffat J, Fraser AG. (2015) *Natural Variation in Gene Expression Modulates the Severity of Mutant Phenotypes*. *Cell*. **162**:391-402.

Kim SH, Spensley M, Choi SK, Calixto CP, Pendle AF, Koroleva O, Shaw PJ, Brown JW. (2010) *Plant U13 orthologues and orphan snoRNAs identified by RNomics of RNA from Arabidopsis nucleoli.* Nucleic Acids Research. **38**:3054-67.

Spensley M, Kim JY, Picot E, Reid J, Ott S, Helliwell C, Carré IA. (2009) Evolutionarily conserved regulatory motifs in the promoter of the Arabidopsis clock gene LATE ELONGATED HYPOCOTYL. Plant Cell. **21**:2606-23