

W. Augustine Dunn, III

Technical Expertise

- expert Python, Bash, regular expressions, advanced data visualization, IPython notebooks, SGE & PBS HPC schedulers, YAML, HTML, CSS, XML, \LaTeX , pandoc, markdown, reStructuredText, Git, Python software packaging & templating, software documentation with Sphinx, Gnu Parallel
- intermediate Perl, R, JSON, vim, unit testing, Mercurial, Bazaar, Subversion
- basic MySQL, PostgreSQL, SQLite, Lua, Tcl, Apache, javascript
- Python libs pandas, scipy, numpy, statsmodels, pyMC, matplotlib/pyplot, seaborn, ggplot, rpy2, networkx, pybedtools, pysam
- miscellaneous OSX, Windows, Linux, MS Word, MS Excel, Photoshop/Gimp, Illustrator/Inkscape
- wet-lab RNA-seq, ddRAD-seq, broad range of molecular biology & protein biochemistry techniques

Authored Software

- blacktie An object oriented python pipeline that simplifies & streamlines the running of complex tophat/cufflinks-based RNA-seq experiments into a single command plus a configuration file: designed with repeatability & usability as priorities (<https://pypi.python.org/pypi/blacktie>).
 - Downloaded from <https://pypi.python.org> over 9,000 times.
- gFunc A python-based integrative analysis framework using network graphs to combine multidimensional data-types from disparate “Omics” sources for creating/exploiting functional-genomic gene sets across multiple species.
- spartan A bioinformatics package, providing the essentials to get a variety of computational jobs done quickly without flourish when that is all that is needed.

Experience

- 2014–present **Postdoctoral Associate**, Dept. of Ecology & Evolutionary Biology, Yale University, New Haven, CT.
Characterization of gene-flow and genotype/phenotype relationships in tsetse fly populations in Uganda.
Highlights:
 - Supervised month-long field expedition collecting tsetse flies in northern Uganda.
 - Maximized sensitivity while balancing specificity by implementing Bayesian filtering method to set thresholds for “interesting” SNP-pairs based on distributions of distance-binned linkage disequilibrium values in ddRAD-based population genomics results.
 - Designed & currently implementing relational database to track & curate field samples with web front-end.
 - Established & maintained a shared environment modules-based software library for the lab group on one of Yale’s super-computing clusters.
 - Substantially increased the potential user-base of pyrad (open-source RAD-seq analysis pipeline) by re-factoring to allow one-step installation with the conventional pip install pyrad form.
- 2008-2014 **Doctoral Research**, Anthony James Lab, University of California, Irvine, Irvine, CA.
Studied gene expression in midguts of four mosquito species following bloodmeal in support of designing synthetic DNA elements for engineering disease transmission-refractory phenotypes.
Highlights:
 - Applied data mining methods such as clustering, hidden Markov models, expectation maximization, and dimension reduction to large-scale multidimensional transcriptomics data.
 - Integration of multiple genome-scale data-types applied to complex phenotypes of expression profiles in species separated by 250 MY allowed generation of testable hypotheses about the underlying transcriptional control mechanisms.
 - Set up and maintained a local Galaxy-based site along with custom workflows and bespoke analysis tools to provide data-sharing and provenance for transcriptomic analyses.
 - Established numerous and productive multidisciplinary collaborative relationships which generated 11 publications from 2008-2014.

2009 **Master Consultant**, *KDH Research & Communication*, Atlanta, GA.

Reviewed & provided *pro bono* feedback & corrections on materials for “*Genetics for Kids*” modules, a supplement for communicating genetics in public school curricula.

2006–2007 **Research Laboratory Technician**, *Geomicrobiology Group*, University of Southern California, Los Angeles, CA.

Studied role of microorganisms in mediating rock, mineral, & organic matter transformations on progressively older mid-oceanic basalt samples.

Highlights:

- Set up a new lab & interfaced with construction contractors while supervisor was at sea.
- Established the lab's capacity to perform qPCR for the purpose of comparing bacterial population structures on aged basalt.

2003–2006 **Laboratory Technician II to Research Professional I**, *Dept. of Cellular Biology*, University of Georgia, Athens, GA.

Characterized the expression & annotated the gene models of cuticular protein genes in *Anopheles gambiae*.

Highlights:

- Established the lab's capacity to perform qRT-PCR.
- Trained three other labs in the theory, protocols, and analysis of qRT-PCR.
- Wrote several bespoke Perl tools to aid in primer design & a web-based primer database to manage the hundreds of primer-pairs generated by the project.

Education

2008–2014 **PhD, Biological Sciences**, *University of California, Irvine*, Irvine, CA.

topic *Comparative Transcriptomics of Blood-feeding in Midguts of Three Disease-vector Mosquito Species*

advisor Professor Anthony James (Molecular Biology & Biochemistry)

co-advisor Professor Xiaohui Xie (Department of Computer Science)

1998–2003 **BS, Biology (emphasis in molecular genetics)**, *University of Georgia*, Athens, GA.

mentor Professor Judith Willis

Selected Coursework

University of California, Irvine Representations & Algorithms for Molecular Biology, Probabilistic Modeling of Biological Data, Quantitative Methods in Biology

Honors & Awards

2011 The Pacific-Southwest Regional Center of Excellence for Biodefense & Emerging Infectious Diseases Annual Meeting Travel Award.

2010 President of UCI's IGB Biomedical Informatics Training fellows

2009-2012 Biomedical Informatics Training fellow (NIH/NLM 5T15LM007443)

Publications

M. Bonizzoni, M. Britton, O. Marinotti, W. A. Dunn, J. Fass, A. A. James. Probing functional polymorphisms in the dengue vector, *Aedes aegypti*. *BMC genomics* **2013**, 14, 739.

M. Bonizzoni, W. A. Dunn, C. L. Campbell, K. E. Olson, O. Marinotti, A. A. James. Complex Modulation of the *Aedes aegypti* Transcriptome in Response to Dengue Virus Infection. *PLoS ONE* **2012**, 7, e50512.

M. Bonizzoni, Y. Afrane, W. A. Dunn, F. K. Atieli, G. Zhou, D. Zhong, J. Li, A. Githeko, G. Yan. Comparative Transcriptome Analyses of Deltamethrin-Resistant and -Susceptible *Anopheles gambiae* Mosquitoes from Kenya by RNA-Seq. *PLoS ONE* **2012**, 7, e44607.

M. Bonizzoni, W. A. Dunn, C. L. Campbell, K. E. Olson, O. Marinotti, A. A. James. Strain variation in the transcriptome of the dengue fever vector, *Aedes aegypti*. *G3: Genes/ Genomes/ Genetics* **2012**, 2, 103–114.

M. Bonizzoni, W. A. Dunn, C. L. Campbell, K. E. Olson, M. T. Dimon, O. Marinotti, A. A. James. RNA-seq analyses of blood-induced changes in gene expression in the mosquito vector species, *Aedes aegypti*. *BMC genomics* **2011**, 12, 82.

S. N. Dissanayake, J. M. Ribeiro, M.-H. Wang, W. A. Dunn, G. Yan, A. A. James, O. Marinotti. aeGEPUCI: a database of gene expression in the dengue vector mosquito, *Aedes aegypti*. *BMC research notes* **2010**, 3, 248.

D. H. Sieglaff, W. A. Dunn, X. S. Xie, K. Megy, O. Marinotti, A. A. James. Comparative genomics allows the discovery of cis-regulatory elements in mosquitoes. *Proceedings of the National Academy of Sciences* **2009**, 106, 3053–3058.

W. Augustine Dunn, III
132 Nicoll St FL 1
New Haven CT, 06511
☎ 770-312-9544
✉ gus.dunn@yale.edu
🌐 <http://gusdunn.com>

Company Recruitment team

*Company, Inc.
123 somestreet
some city*

January 01, 1984

Dear Sir or Madam,

Lorem ipsum dolor sit amet, consectetur adipiscing elit. Duis ullamcorper neque sit amet lectus facilisis sed luctus nisl iaculis. Vivamus at neque arcu, sed tempor quam. Curabitur pharetra tincidunt tincidunt. Morbi volutpat feugiat mauris, quis tempor neque vehicula volutpat. Duis tristique justo vel massa fermentum accumsan. Mauris ante elit, feugiat vestibulum tempor eget, eleifend ac ipsum. Donec scelerisque lobortis ipsum eu vestibulum. Pellentesque vel massa at felis accumsan rhoncus.

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Albert Einstein discovered that $e = mc^2$ in 1905.

$$e = \lim_{n \rightarrow \infty} \left(1 + \frac{1}{n}\right)^n$$

Yours faithfully,

W. Augustine Dunn, III