Darach Miller

Email: dchmiller@gmail.com
Twitter: @darachm

Physical address: c/o Gresham lab
12 Waverly Place
New York, NY 10003

Education

PhD Biology, New York University, New York, NY, USA — February 2018
Genomics and Systems Biology track, dissertation adviser David Gresham

B.S. Genetics, University of California at Davis, Davis, CA, USA — December 2011
Minor in Quantitative Biology and Bioinformatics

Research experience

Doctoral research, Gresham lab, New York University — Summer 2013 - current

mRNA stability changes can be used to effect rapid changes in gene expression in *Saccharomyces cerevisiae* during environmental changes. I used transcript dynamics modeling to infer candidate mRNAs that are destabilized during a nitrogen upshift, and adapted 4-thiouracil labelling methods to demonstrate that the destabilization occurs using a pulse-chase qPCR experiment. I then scaled the method up to use RNAseq and made some analytical advances to demonstrate that the destabilization is more general than the Nitrogen-Catabolite-Repression regulon. To determine the *trans* genetic factors of this, I redesigned a Fluorescent In-Situ Hybridization protocol to measure mRNA FISH with flow cytometry, then redesigned barcode-sequencing protocols to more robustly handle low-input fixed cell samples with a more advanced error-correcting amplicon design, then combined these approaches with Sort-Seq modeling to estimate mRNA abundance dynamics for 3,300 mutants in a pooled library. This assay confirmed the role of previously known mRNA synthesis control, the central role of the Lsm1-7p/Pat1p complex in eukaryotic mRNA degradation, and pointed towards translation initiation events mediated by elements in the 5' UTR as contributing to the mRNA destabilization.

Summer internship, Baliga Lab, Institute for Systems Biology — Summer 2011

I worked to develop a high-throughput forward-genetic transposon-sequencing screen for *Halobacterium salinarum*. My contribution was improving the efficiency of haloarchaea transformation, so I adapted lipofection reagents from mammalian cell-culture systems to improve transformation efficiency, and characterized the efficiency of the *in-vitro* transposition reaction.

Undergraduate research, Facciotti Lab, University of California at Davis — Fall 2010 - Spring 2012

Haloarchaea express genes that facilitate competition via secreted anti-microbial compounds. I designed and carried out a 60x60 all vs. all inhibition screen via spot assays, to characterize the network of pair-wise interactions. I then used `BLAST` on their recently completed genome assemblies to identify homologs that were associated with profiles of inhibitory effects.

Training

CSHL Yeast Genetics and Genomics Course — Summer 2015

Three-week intensive course on the methods and practices of yeast genetics, instructed by Brown, Dunham, and Gartenberg.

The Art & Craft of Teaching — Fall 2015

Semester-long course on the theory and practice of university teaching, especially focused on engaging students in active learning and using assessment effectively.

Awards

NYU Departmental Kopac Teaching Award — 2013-2014
Annual teaching award, here for work on graduate-level Applied Genomics course

NYU Departmental Kopac Service Award — 2014-2015
For making a strong contribution to the department's academic environment, in organization of peer-to-peer skills development workshops

Publications

Steady-state and dynamic gene expression programs in response to variation in environmental nitrogen — 2016

Molecular Biology of the Cell, doi.org/10.1091/mbc.E14-05-1013

Edoardo Airoldi, **Darach Miller**, Rodoniki Athanasiadou, Nathan Brandt, Farah Abdul-Rahman, Benjamin Neymotin, Tatsu Hashimoto, Tayebeh Bahmani, David Gresham

We explored the transcriptome responses of budding yeast to changes in environmental nitrogen. I used mRNA dynamics modeling and 4-thiouracil pulse-chase labeling with qPCR to identify and confirm some mRNA subject to destabilization upon a re-feeding of nitrogen.

Growth Rate-Dependent Global Amplification of Gene Expression — Preprint, revising for resubmission

Pre-print on *bioRxiv*, doi.org/10.1101/044735

Niki Athanasiadou, Benjamin Neymotin, Nathan Brandt, **Darach Miller**, Daniel Tranchina, David Gresham

We explored the scaling of the yeast transcriptome with growth rate, using a novel statistical normalization method for using spike-ins with RNAseq. To confirm these results, I designed, optimized, and used a fluorescent poly-dT probe flow cytometry assay as orthogonal confirmation.

Presentations

Accelerated mRNA Degradation Contributes to Gene Expression Remodeling During a Nitrogen Upshift — August 2017
Selected talk @ 2017 International Conference of Yeast Genetics and Molecular Biology

High-throughput Genetics of mRNA Dynamics using FISH, FACS, and Sequencing — August 2017
Selected talk @ New York Area Meeting in Quantitative Biology

Genetic factors controlling accelerated mRNA degradation during a nitrogen upshift (video) — July 2016
Selected talk @ GSA's TAGC16 in Orlando

Screening and Investigating Interactions Between Haloarchaeal Species — April 2011
Talk @ UCDavis Undergraduate Research Conference

Posters

mRNA stability regulation accelerates functional reprogramming of the yeast transcriptome during a nitrogen upshift — August 2017
CSHL Eukaryotic mRNA processing meeting, ICYGMB 2017 meeting

Accelerated mRNA degradation contributes to gene expression remodeling during a nitrogen upshift — September 2015
ICYGMB annual meeting.

Teaching

Quantitative Methods in Human Genetics — Spring 2015, Spring 2016
Undergraduate-level course

Designed and taught introductory R to explore examples of relevant statistical methods

Applied Genomics: Intro. to Bioinf. & Network Modeling — Fall 2013
Graduate-level course

Designing and running practice in the analysis of genomics datasets using techniques such as network clustering and transcript dynamics modeling.

Principles of Biology — Fall 2012
Undergraduate-level course

Coordinate exercises in benchwork and data analysis of basic molecular biology and genetics.

Mentoring

Daniel Pham, Undergraduate at North Park University — Summer 2017
Mentored as part of 2017 Summer Undergraduate Research Program
Finishing undergraduate studies

Alex Ferrena, Undergraduate at New York University — Fall 2016
Former student, mentored his transition into bioinformatics
Starting MS Bioinformatics program at Columbia

Stephen Nyarko, Student at Stuyvesant High School — Fall 2015, Summer 2016
Mentored design of a yeast genetic screen for a science competition
Starting undergraduate studies at Harvard

Other experience

Social media coordinator, Yeast Course, Cold Spring Harbor Laboratory — 2017

Working to build a social media presence for the the CSHL Yeast Course. Building an alumni list and connecting alumni across years to help attendees and boost recruitment of new attendees from outside the community.

Research technician, van Winkle Lab, UC Davis — 2008 - 2009

Microscopy sample preparation (mouse dissection via microtome).

Bike mechanic/instructor, Davis Bike Collective — 2007 - 2012

Volunteer mechanic/instructor and shift supervisor at community bike shop. Lots of teaching and reconciling bicycle theory with the extensive natural variation in design and function. Never met a seatpost I couldn't extract.

Experience, skills

Budding yeast methods
- General handling, culturing in batch and chemostat, genetics, crossing and dissection
- mRNA FISH, specific (Stellaris and Affymetrix) and general (poly-A homebrew)

Molecular biology
- Nucleic acids from extraction to sequencing, primarily mRNA using a lab-homebrew RNAseq protocol
- Developed a low-input amplicon library preparation protocol
- 4-thiouracil metabolic-labeling experiments
- RT-qPCR

Flow cytometry
- Designed (poly-dT hybridization) and optimized several assays (mRNA FISH, FITC, SytoxGreen)
- Experienced with a BD Accuri C6; trained but not independently approved to solo a BD Aria

Other wet-bench
- Haloarchaea culturing and genetic manipulation
- Paraffin and araldite embedding and sectioning of mouse tissue

Scripting/programming languages
- **R** is my primary working language for analysis. Very familiar with `ggplot`, familiar with `tidyverse` packages. Modeling experience, using `lm()` and `mle()` for transcript dynamics, growth phenotypes, flow cytometry & Sort-seq
- **Python** used to develop a combination UMI-extractor and amplicon-splitter using `BioPython` and `multiprocessing` queues
- **Perl** was my first language, took an introductory computer science course in **C**.

Linux/Unix systems, bioinformatics
- Used a HPC system with PBS and SLURM scheduler to develop and run pipelines for sequencing quantification and modeling. Used *in silico* benchmarking simulations to optimize tools for RNAseq alignment, amplicon barcode calling, and for extracting and using UMIs.
- Using Linux-only as personal system since 2010: Ubuntu 10.04, then Crunchbang, then Arch for the last five years

Other computational
- LaTeX, `pandoc` (this), `git`, `Makefiles`
- Basic ImageJ batch scripting, some `EBimage`