Meeting minutes from the Biology Postdoc Cohort at Emory

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Date: 2019-03-04 R version: 3.5.0

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This document can be found at https://github.com/darwinanddavis/emory_postdocs

Session info

R version 3.5.0 (2018-04-23)

Platform: x86_64-apple-darwin15.6.0 (64-bit) Running under: OS X El Capitan 10.11.6

Matrix products: default

BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib

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attached base packages:

[1] stats graphics grDevices utils datasets methods base

loaded via a namespace (and not attached):

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Overview

This document contains the meeting minutes from the Biology Postdoc Cohort at Emory.

The group hosts regular meetups to learn about what the postdocs in Biology at Emory are doing, harness cool research skills and tools that everyone uses, foster research overlaps, brainstorm and troubleshoot ideas, discuss weird results that nobody knows the answer to, practise upcoming seminars, and simply build a stronger postdoc culture in Biology at Emory.

Questions and suggestions welcome at matthew.malishev@emory.edu.

TO DO list

- Add attending postdocs to OPE Emory list (Beverly)
- Come up with a cooler name for the group
- Workshop ideas
- Writing retreat
- Aim for a collaborative paper

Next meetup: March 1, 2019

March 1, 2019

Meetup on CRISPR, presented by Aileen Berasategui from the Gerardo Lab.

"CRISPR, or how a mysterious DNA sequence turned into the most important discovery of this century"

We had some stimulating conversation over the usefulness of CRISPR, its future, its contribution to modernising science, and the many ethical challenges not just academics, but also the public will face.

Aileen fielded the questions raised at the end of the presentation and has provided some more in-depth answers below.

Are the viral DNA pieces integrated in the CRISPR region random?

My instinct was to say yes, but then I have realized that certainly not. They all have a so called PAM sequence (Protospacer Adjacent Motif) at the beginning and this cannot possibly be random. For CRISPR type II, this sequence is NGG (any nucleotide, guanine, guanine). So I have read further and it has been demonstrated that the PAM sequence is essential for Cas9 recognition. (Hille and Charpentier 2016).

Have viruses evolved counteradaptations to CRISPR?

YES! I thought so but I had no specific examples. They can avoid recognition by Cas proteins by mutating their PAM sequence (very neat).

Do all spacers have the same size?

CRISPR spacers can range between 21 and 72 nucleotides long (they normally are between 32 and 38 nucleotides). Something I did not mention yesterday is that a bacterial (or achaeal) cell can have more than one CRISPR locus. The length of the spacers remain constant within one locus, but can vary between locus within the same genome, and of course between cells.

Where does genome editing by CRISPR take place?

In bacteria and archaea it takes place in the cytosol (no nucleus present). In eukaryotes, the editing happens in the nucleus. But the complete mechanism depends on how you deliver the CRISPR-Cas complex to cells. In any case, translation of the Cas9 RNA to protein has to happen in the cytosol where it will also binds to the guideRNA. Together they go back to the nucleus to edit their target host DNA.

Can CRISPR be horizontally transmitted?

There is evidence suggesting as much. However, I have dug a little bit deeper and I have found that actually (and it makes total sense), CRISPR tends to prevent HGT. That is because CRISPR recognizes foreign DNA floating in the cytosol and at some point the genes being transferred will be floating around before being integrated into the genome. So, perhaps the answer is yes, but rarely? Apparently, it depends on the method for HGT (transduction vs. transformation vs. conjugation). (Watson et al. 2018, mBio).

February 8, 2019

In this meeting we created our own research impact statements to practice distilling our specialised research areas into lay terms.

The general recipe to follow:

- What you did
- Who was helped
- In what way are they better off (different people have different perspectives on importance of the order of these points)

Molly Gallagher

Our models show that for viral infections, treating patients with defective viral particles that interfere with normal viral replication can reduce the severity of symptoms, and may reduce the chance of transmitting the infection to others.

Matt Malishev

I'm interested in how diseases spread in nature. I investigate how environmental change changes the energetics of parasite populations transmitting schistosomiasis. I apply metabolic theory to simulate human infection probability and exposure risk in space and time to inform useful biocontrol strategies.

Rohan Mehta

I develop new theoretical tools to help biologists study how the distribution and movement of populations affects their ability to adapt to environments that vary in space.

Lewis Bartlett

I study how different beekeeping practices affect the ways bee diseases spread and how deadly they become. I use laboratory studies, field tests, computer simulations, and maths to predict and test which actions beekeepers should take to prevent infectious diseases.

Scott Villa

My research focuses on understanding how and why there are so many different species. I am interested in how natural selection influences traits critical for mating. Specifically, I experimentally evolve parasites on new hosts to explore how new species form under varying environmental, genetic, and demographic scenarios.

Laramie Lemon

I use yeast to investigate how genes are activated. I focus on how the physical structure of DNA affects the ways it's read, copied, and translated to produce proteins by different mechanisms.

Venkat Talla

I study how populations become different species by measuring the genetic differences and how their genomes change with time. I use genomic data of Monarch butterflies to answer questions about species divergence, natural selection and conservation.



Effective communication: Language matters

Terms that have different meanings for scientists and the public			
Scientific term	Public meaning	Better choice	
enhance	improve	intensify, increase	
aerosol	spray can	tiny atmospheric particle	
positive trend	good trend	upward trend	
positive feedback	good response, praise	vicious cycle, self-reinforcing cycle	
theory	hunch, speculation	scientific understanding	
uncertainty	ignorance	range	
error	mistake, wrong, incorrect	difference from exact true number	
bias	distortion, political motive	offset from an observation	
sign	indication, astrological sign	plus or minus sign	
values	ethics, monetary value	numbers, quantity	
manipulation	illicit tampering	scientific data processing	
scheme	devious plot	systematic plan	
anomaly	abnormal occurrence	change from long-term average	

Source: Somerville and Hassol, Communicating the science of climate change, Physics Today, October 2011

Figure 1: Language matters

January 11, 2019

IMPACT statement workshop

- Come up with a Impact Statment (3 line summary of your research) for next meeting.

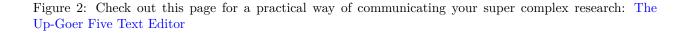
XKCD inspired page for communicating your ideas using just the ten hundred most commonly-used words: The Up-Goer Five Text Editor

HINTS TOP LATEST LIBRARY RANDOM



THE UP-GOER FIVE TEXT EDITOR

CAN YOU EXPLAIN A HARD IDEA USING ONLY THE $\underline{\text{TEN HUNDRED}}$ MOST USED WORDS? IT'S NOT VERY EASY. TYPE IN THE BOX TO TRY IT OUT.



Some writing guides from the masses

The Elements of Style by Strunk and White

Revising Prose by Richard Lanham

Idead into Words by Elise Hancock Matt's personal favourite

December 14, 2018

Biosketch of postdocs

Matt Malishev

Civitello lab

Bioenergetics and individual-based modelling of host-parasite dynamics of human schistosome populations; spatial simulation modelling; metabolic theory

Molly Gallagher

Koelle lab

Disease ecology; differential equation models; current work focuses on modeling defective interfering particles in influenza

Aileen Berasategui Lopez

Gerardo lab

The genomic and chemical basis of host-fidelity

Caitlin Conn

Gerardo lab

Host range and its genetic basis in a mycoparasite

Jeremy Harris

Koelle lab

Current IAV modeling: Passage study modeling, estimating bottleneck sizes

Mary Bushman

Rustom lab

Linking within- and between-host dynamics of infectious diseases (modeling)

David Nicholson

Prinz lab

"Lifelong Learning Machines" – continual machine learning algorithms

Julien Catanese

Jaeger lab

Derrick Morton

Corbett lab

Studying how defects in RNA processing lead to neurodegenerative disesase

Scott Villa

Gerardo lab

Role of endysymbionts in driving host reproductive isolation and adaptive radiation

Rohan Mehta

Weissman Lab

Evolution in spatially-structured populations

Workshop ideas

IMPACT workshop

- Impact of science + advancement in research

Contact: Derrick

November 30, 2018

Outcomes for postdoc group

Meetings every second and fourth week

Talk therapy among working class postdocs

Intro talks from postdocs to group

- Lightning, 2-min talk for group
- New postdocs give a brief intro talk for their first meeting

Postdoc mentorship group for assisting grad students during qualifying exams

- Online directory of postdocs showcasing background and expertise. Include non-science background stuff, such as applying for international universities.

 The journal peer review system and open access science
- Using bioarXiv and pre-prints
- Open access science
- Writing a paper on the science peer review system from postdoc perspective

November 1, 2018

Ideas for things people want

Collaborate on overlapping research Brainstorm ideas Present new results Practise conference talks Writing retreats Regular coding/math club

Bigger ideas

Combine other labs/departments

- other biology floor levels
- math/env sciences

Links and ideas