

# Science Skills Boot Camp

- 9:00-9:15 Welcome
- 9:15-10:15 NIH and Research Culture (Phil Ryan)
- 10:15-10:30 Coffee Break
- 10:30-11:30 Reading a Scientific Paper (Barbara Fuhrman)
- 11:30 -12:30 Group Lunch
- 12:30-2:00 Communicating Science
  - Keeping a Lab Notebook (Phil Ryan)
  - Giving Group Meeting(Arjun Prasad)
  - Presenting a Poster (Ozge Gunduz Cinar)
- 2:00-2:15 Break
- 2:15-2:35 What makes a good research question? (Phil Ryan)
- 2:40-3:00 and 3:05-3:30 Concurrent sessions. Students choose 2 to attend. (NIH Postdocs)
  - Animal Models (Rocio Benabentos)
  - Biostatistics/Epidemiology (Barbara Furhman)
  - Sequence Alignment tools (Arjun)
  - Microscopy (Eilon)

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# Navigating the NIH:

## Getting the Most from Your NIH Summer Internship

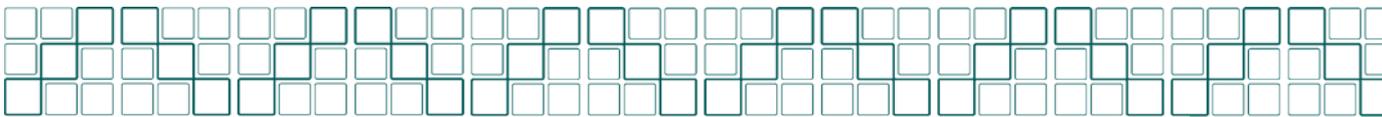
Philip Ryan, PhD  
Director of Student Services  
NIH Graduate Partnerships Program  
Office of Intramural Training and Education





# Four Sections

- Understanding the NIH
- Settling into your research group and meeting your science goals
- Using NIH resources to meet your career and professional goals
- Understanding the research culture

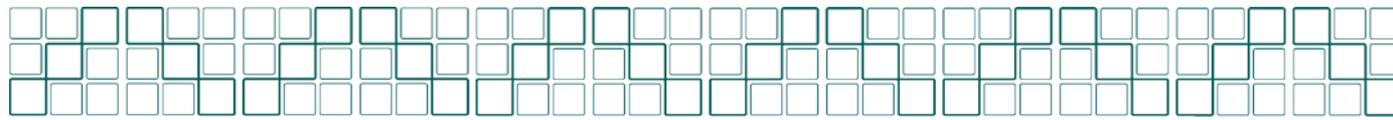


# What is the NIH?



*The Nation's Biomedical  
Research Institution*

- 27 Institutes & Centers (ICs)
- Biomedical, behavioral, and social science research at all levels - basic, translational and clinical
- Campuses in MD, NC, MT, AZ, MI and MA
- Two main divisions: **intramural** and **extramural**
- Learn more at [www.nih.gov](http://www.nih.gov)



# Bench-To-Bedside Research At NIH



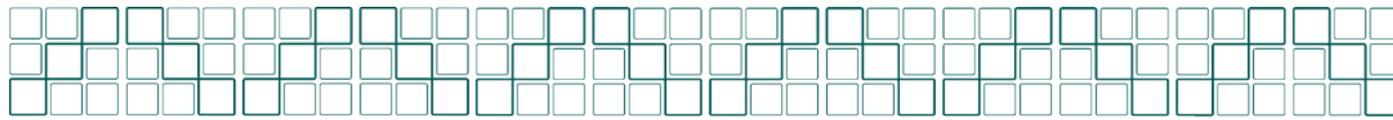
- ❑ 240 beds
- ❑ 7,000 inpatient admissions/yr
- ❑ 72,600 outpatient visits/yr
- ❑ 900 active clinical protocols

For information on clinical trials, please visit: <http://clinicaltrials.gov/>  
We seek diversity in our clinical trials!



# Researchers at NIH

- 1100 Faculty (PIs)
- 1500 Staff Scientists & Clinicians
- 3800 Postdoctoral Fellows
- 480 Clinical Fellows
- 485 Graduate Students
- 100 Medical Students
- 600 Postbacs
- YOU! ~1000 Summer interns



# People You May Meet in Your IC

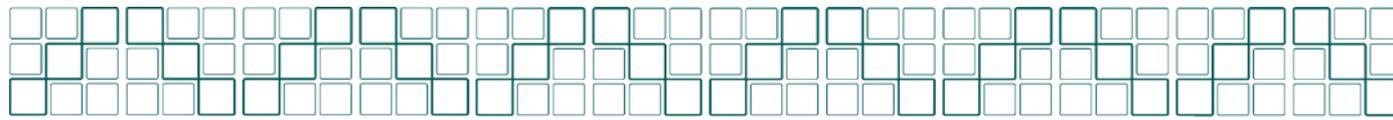
- Your Summer Coordinator, Training Director and Training Office staff
  - Be sure to attend your IC orientation
- The SD and Deputy SDs
- Your Branch or Lab Chief
- Other PIs in your Lab/Branch
- Your AO



**First --**

**Define your**

**goals**



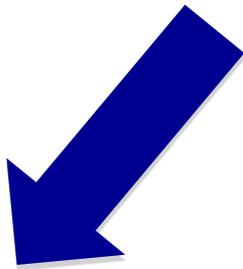
# Focus on Development In Three Areas:

- Science
- Career
- Personal



To get the most out of your summer:

## Make a plan



**Research  
goals**

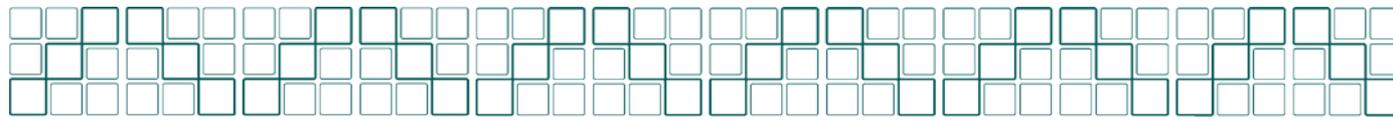


**Professional  
goals**



**Personal  
goals**

Share it with your mentor!



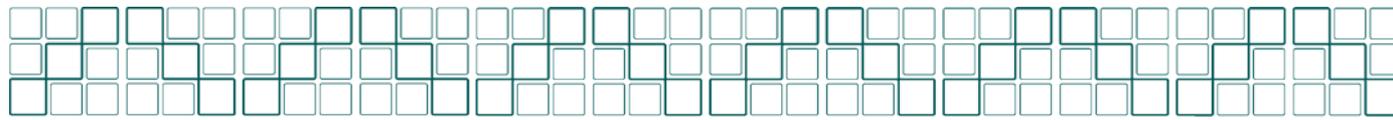
# Important Research Relationships

- Supervisor
  - Someone who directs the work of another
  - Is responsible for ensuring that someone does their job
  
- Mentor
  - Someone who passes on skills, knowledge, and wisdom to another person
  - Works to help develop someone's career by providing honest feedback, encouragement and guidance



# There is No Typical Research Experience

- Differences in lab and research groups
  - Group dynamics and atmosphere
  - Level of day-to-day engagement of the PI
  - Level of independence, at experimental level and beyond
  - Types of rules and how they are imposed
  - Type and frequency of feedback
- Work hours, work environments and expectations vary; be sure you understand expectations in your group



# Expectations Your Supervisors and Mentors Have of You

- Engagement in planning your research
- Honest communication regarding research progress
- Careful thought and regard for all elements of scientific ethics
- Energy and focus on your lab notebook
- Active participation in group activities and attention to fostering collegial relationships in your research group
- Good work ethic; balance internship and outside responsibilities effectively



# Expectations You Should Have of Your Supervisors and Mentors

- Intellectual support and guidance
- Assistance in developing a project within the framework of on-going work in the group
- Availability when needed; guidance in planning the next step
- Honest but supportive feedback
- Support for professional development activities outside of lab
- Honest feedback regarding letters of recommendation



# Mentoring Relationships Are Key To Your Success

- Successful scientists have many mentors -- in all areas
- Mentoring is a two-way relationship
- There is help to resolve issues:
  - Your IC Summer Coordinator and/or Training Director
  - Branch Chiefs and others in your research group
  - OITE staff and career counselors
  - Office of the Ombudsman, Center for Cooperative Resolution
  - NIH Employee Assistance Program (EAP)



# To Achieve Your Science Goals

- Appreciate that first impressions are key
- Meet with your supervisors - EARLY & OFTEN
- Read papers in your field; work to be sure you understand how to read a paper
- Focus on the “big picture” AND the details of your work
- Use “down-time” in lab wisely
- Actively participate in research group meetings
- Attend seminars, in and outside of your field
- Present your work at Summer Poster Day



# To Achieve Your Career Goals

- Use the online Summer Handbook and IC materials to find information on useful career development activities
- Work with your mentor to create a summer plan
- Attend the Graduate & Professional School Fair if appropriate
- Use informational interviews to explore careers



# Take Care of Your Whole Self

- Make certain you always feel your best
  - Exercise
  - Eat well
  - Stay connected to family/friends
- Get to know interns in your research group and IC
- Explore your local area



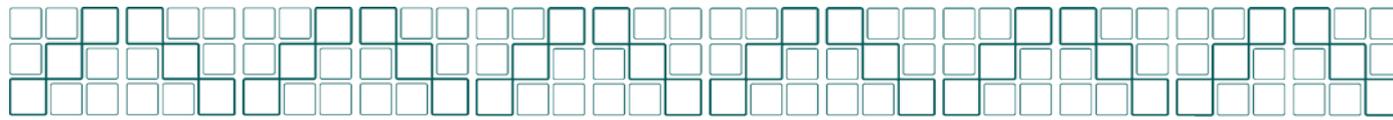
# Since you are here...

- Check out the NIH Recreation & Welfare Association (R&W)
  - Fitness centers
  - Discount tickets
- Join ClubPCRmini social listserv
- Explore Washington, DC
  - Summer Handbook has pages of things to do
  - Even if you are from area...explore it



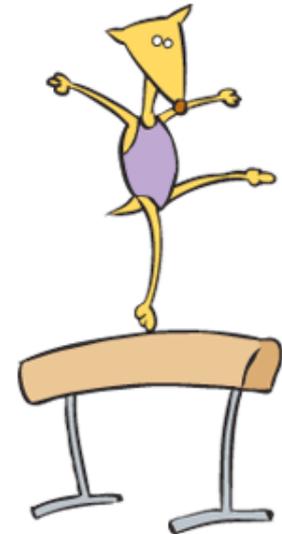
# A tale of 2 PIs

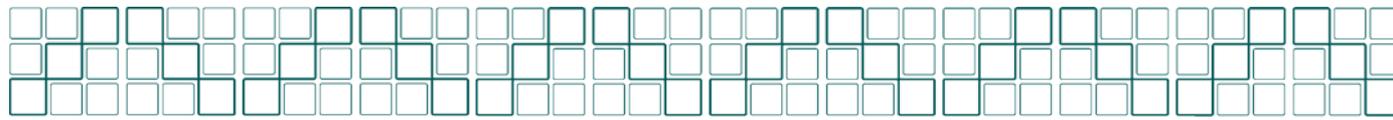
- Hands-on
- Found in the lab/office or close-by
- Talks with students and fellows all the time
- Called by his/her first name
- Hands-off
- Locked in his/her office or away at meetings
- Meets with trainees for formal meetings scheduled in advance
- Called Dr. \_\_\_\_\_



# Interacting with your mentor

- Be respectful and courteous
- Adapt to his/her mentoring style
- Accept criticism with grace
- Ask when you have questions
- Find balance between being independent and asking for help
- Address problems before they escalate





# Different research groups have their own culture

- How loud is the room?
- How clean/organized is their research space?
- What hours do people work?
- How do people dress?
- Do group members use Ipods or cell phones?
- Do group members eat lunch together?
- Do group members go to seminars together?



# Mandatory activities

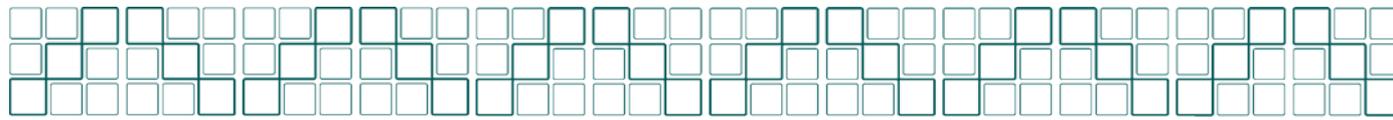
- Group meeting?
- Journal clubs?
- Seminars?





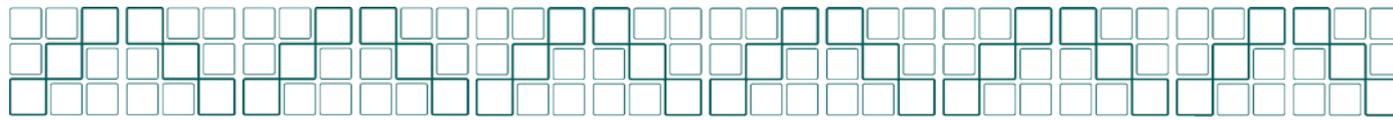
# Be a good lab citizen

- Keep common space clean
- Don't disturb other people's work
- Be extremely careful with common reagents and equipment
  - Don't contaminate!
  - Replace common reagents if they are running low
  - **Ask for help** if you don't know how to use equipment
  - Tell somebody if equipment is broken



**“Research is formalized  
curiosity. It is poking and  
prying with a purpose.”**

Zora Neale Hurston

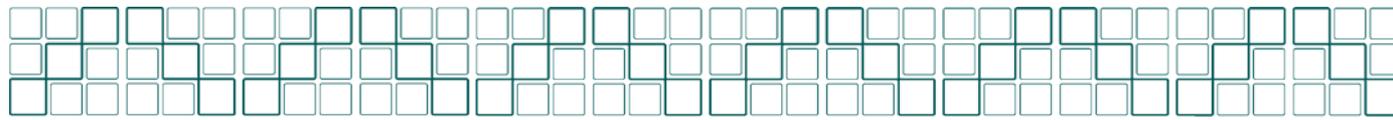


# Scientific research . . .

- Is a team effort



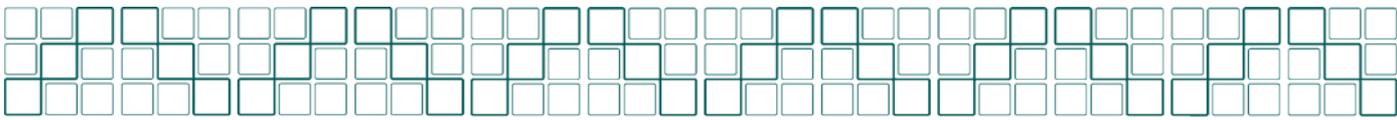
[www.barcelonafootballblog.com](http://www.barcelonafootballblog.com)



# Scientific research . . .

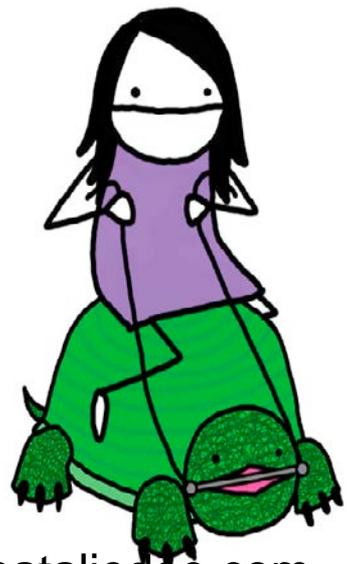
- Is a team effort
- Involves asking small, manageable questions



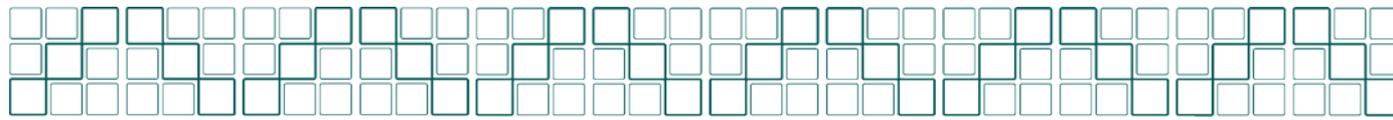


# Scientific research . . .

- Is a team effort
- Involves asking small, manageable questions
- Often moves slowly

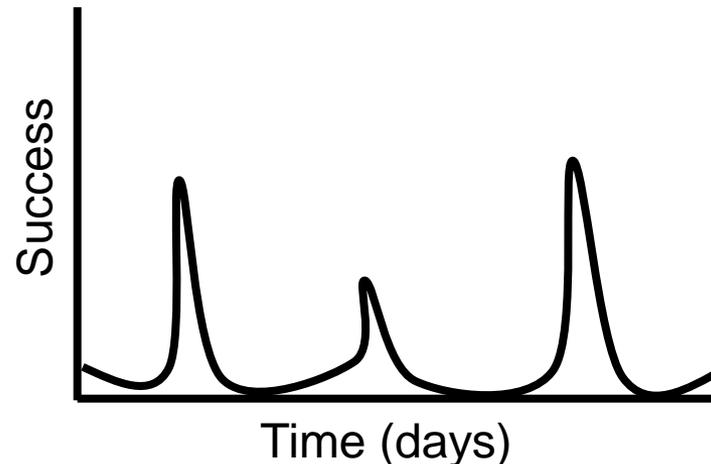


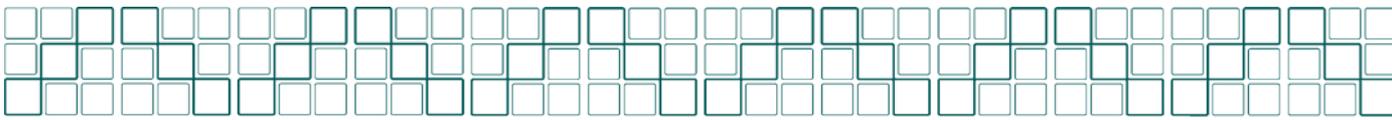
nataliedee.com



# Scientific research . . .

- Is a team effort
- Involves asking small, manageable questions
- Often moves slowly
- Contains periods of frustration between successes

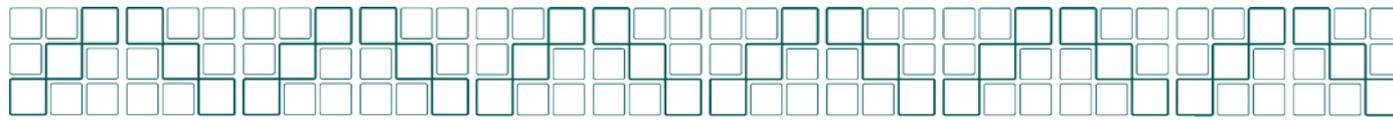




# Scientific research . . .

- Is a team effort
- Involves asking small, manageable questions
- Often moves slowly
- Contains periods of frustration between successes
- Is not a 9-5 job





# Scientific research . . .

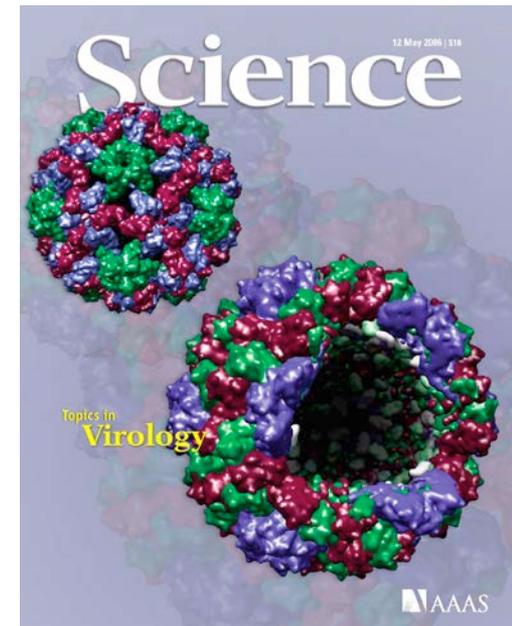
- Is a team effort
- Involves asking small, manageable questions
- Often moves slowly
- Contains periods of frustration between successes
- Is not a 9-5 job
- Must always be documented





# For data to be publishable, your work must be:

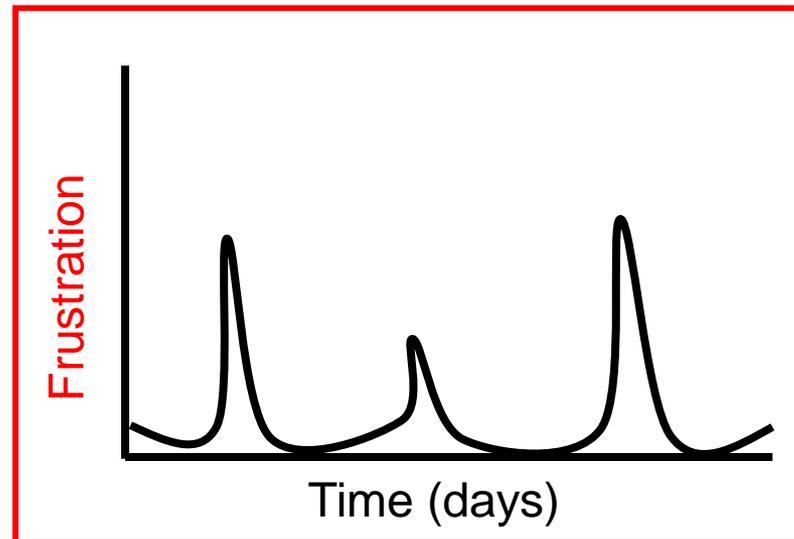
- Meticulous
- Reproducible
- Well-documented





# Science can be unpredictable

- Don't get frustrated!
- Ask for help
- Be creative
- Be flexible with your research plan

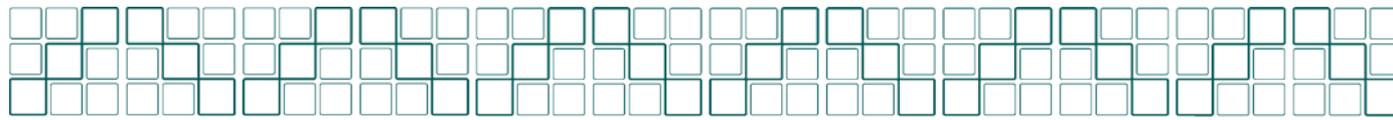




# A typical day of research

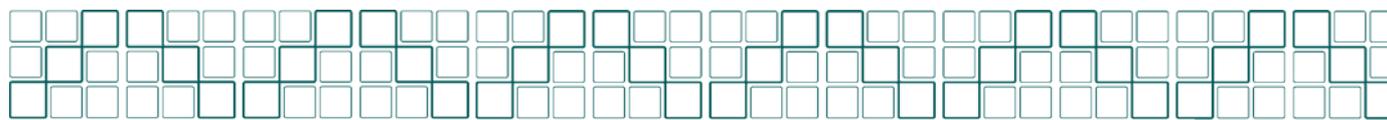
- At the bench
  - Doing experiments
  - Making reagents
- Away from the bench:
  - Planning experiment
  - Analyzing data
  - Thinking about your project
  - Reading papers





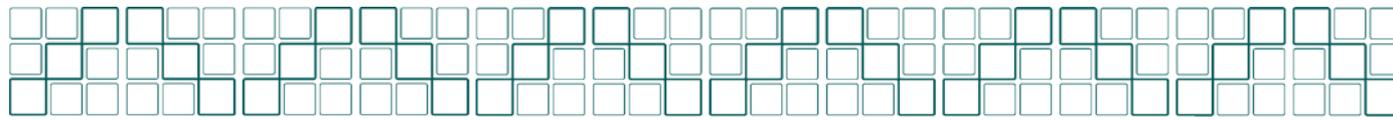
# What if you don't have any work to do?

- Read papers
- Think about your project
- Plan experiments
- Learn about other people's projects
- Volunteer to help others
- Start your poster



# To achieve your research goals

- Meet with your mentor(s) early and often!
- Be clear about expectations- yours and your supervisor's
- Read papers related to your work
- Attend the Summer Lecture Series
- Make sure you understand both the big picture and the details of your research
- Pay attention and participate during group meeting
- Volunteer to give a talk in your group meeting
- Present a poster at Summer Poster Day
- Attend a Summer Journal Club



# This is your summer job . . . But it's also a training experience!

- Attend seminars and workshops
- Take advantage of NIH resources
- Talk to other researchers
- Network
- Have fun



# **Summary:** What your research group expects of you:

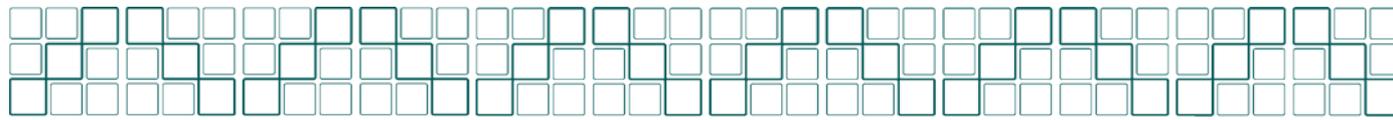
- Attention to safety
- Respect for diversity
- Respect for animal models
- Professionalism, especially when dealing with patients
- Participation in all lab/group activities
- Engagement in your research project
- Honest communication about your research



# Looking out for yourself

## **Reasonable expectations:**

- To be treated fairly and with respect
- To have some guidance from a mentor
- To have appropriate training when working with dangerous equipment or hazardous chemicals
- To have (at least a little) time to work on professional development



## If problems arise

- Be mature and rational
- Try to address the problem early, by talking calmly with the person you are conflicting with
- If necessary, talk to your PI or other mentors
- If necessary, seek help from your IC training director, OITE, or the NIH Office of the Ombudsman



# What if something really bad happens?

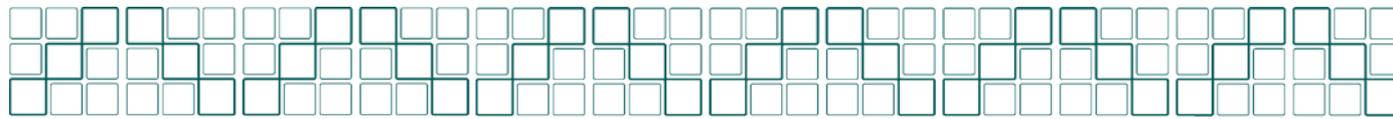
**You are not alone!**

- Your principle investigator
- Your IC training director
- Dr. Sharon Milgram, OITE Director  
[milgrams@mail.nih.gov](mailto:milgrams@mail.nih.gov)
- Dr. Pat Sokolove, Director Postbaccalaureate and Summer Intern Programming  
[sokolovp@mail.nih.gov](mailto:sokolovp@mail.nih.gov)



# Final Thoughts: ALL Summer Interns Should

- Use the online Summer Handbook
- Check that your name is on the OITE-SIP listserv
- Attend appropriate summer intern activities
- Make use of online resources from OITE
  - Follow us on twitter @NIH\_OITE
- Participate in Summer Poster Day
- E-mail me if you have questions:  
[ryanp@od.nih.gov](mailto:ryanp@od.nih.gov)



# Event

**NIH SACNAS CHAPTER: SUMMER KICK-OFF EVENT  
SPECIAL EVENT: NETWORKING OPPORTUNITIES**

**Building 40, Room 1201/1203**

**Jun 22, 2012 4:00 pm - 5:00 pm**



Research Boot Camp  
National Institutes of Health, Bethesda MD  
Barbara Fuhrman, PhD  
June 1, 2012

# READING A SCIENTIFIC PAPER

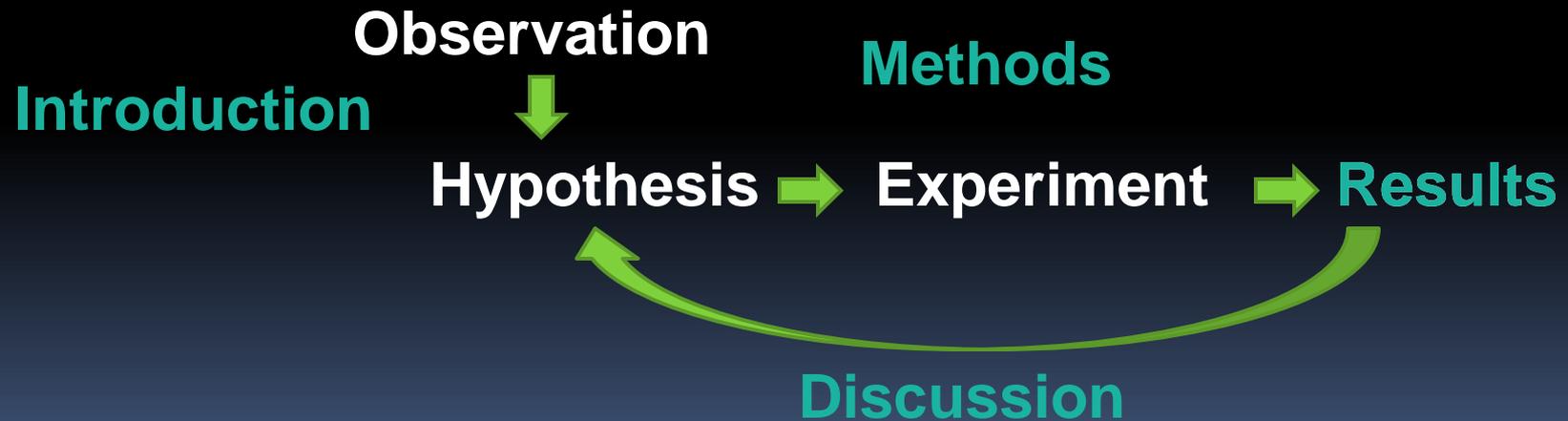


# Types of scientific articles

- Review
  - Research article
  - Methods article
  - Commentary
  - Letters
- 

# The research article

- Bread and butter
- Highly scripted
- Recapitulates the research process





# Titles

- Titles are written to
    - be brief and informative
    - attract readers
  - Titles may
    - include factors that have been measured
    - reveal the main findings
- 

# What do they measure and compare?

- **Social learning spreads knowledge about dangerous humans among American crows.** Cornell HN, Marzluff JM and S Pecoraro. *Proc. R. Soc. B* (2012) 279, 499–508.
- **Local macrophage proliferation, rather than recruitment from the blood, is a signature of TH<sub>2</sub> inflammation.** Jenkins SJ, Ruckerl D, Cook PC, Jones LH, Finkelman FD, van Rooijen N, MacDonald AS, Allen JE. *Science* (2011) 332(6035):1284-8.
- **Reproductive Technologies and the Risk of Birth Defects.** Davies MJ, Moore VM, Willson KJ, B Sc KJ, Van Essen P, Priest K, Scott H, Haan EA, Chan A. *N Engl J Med* (2012) 366:1803-13.
- **Concordance among Gene-Expression–Based Predictors for Breast Cancer.** Fan C, Oh DS, Wessels L, Weigelt B, Nuyten DSA, Nobel AB, van't Veer LJ, and CM Perou. *N Engl J Med* (2006) 355:560-569.



# Abstract

- Very succinct summary (~250 words)
- Motivation, methods
- Refers to most significant findings
- States conclusions



# Introduction

- Background
- Motivation
- Loose structure
  - Known
  - Known
  - Unknown
    - Experimental approach
- This is the authors' story

# Introduction

- Some crow groups ... habitually follow or scorn particular humans.
- Threatening people are scolded with harsh vocalizations and may be mobbed by groups ...
- Individual crows learn from a single experience when they are captured.
- We test the hypothesis that observing others



# Materials and methods

- Recipe, catalog, and narrative

- What they did
- In what order
- How they did it
- Why they did it

**Study Design**

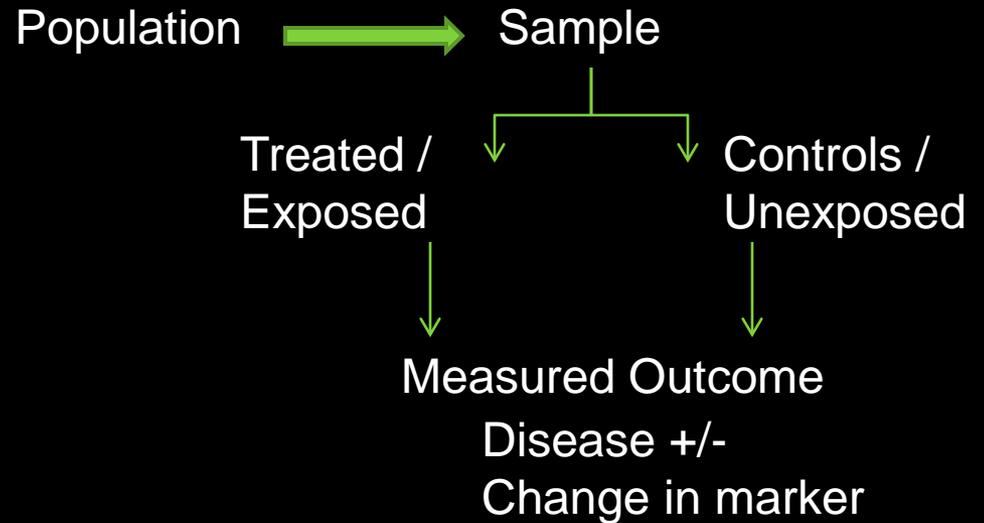
**Measurements**

**Materials used**

**Statistical Analysis**

# Research designs

- Selection
- Assignment
- Assessment
- Analysis
- Interpretation
- Extrapolation





# Results

- States results of the experiments described in methods
  - Refers to data presented in tables, figures
  - In experimental research articles, progression from one experiment to the next may be described here
- 



# Discussion

- Restates most important findings
  - Places them in context of previous research and other relevant data
  - Describes strengths and limitations
  - Discusses implications of study findings
    - Research (what next?)
    - Real world
  - This is a story about the world
- 



# Tables

- Frequencies and denominators
- Measures of central tendency, and of variation
- Statistical significance of estimates
- Structure should tell you what is being compared
- Look – what is the answer to the question posed in the introduction?
- Consider what is not included



# Figures

- Model
    - Background knowledge
    - Causal model
    - Study design
    - Sample derivation
  - Data
    - What is being measured?
    - What comparisons are being made?
- 



# Find the question

- What has been measured?
  - What is being compared?
- 



# What to look for

- Hypothesis
  - Study design
    - Experimental or observational
    - Exposure measures
    - Outcome measures
  - Experimental systems
  - Data analysis
- 



# Small group activity

- Skim the article (you have limited time)
- Draw!
  - Map the study design
  - Map the causal system
  - Make a table to capture the analytic comparison



# Be an active reader!

- Arrive at the page with a purpose
- Guess what will happen
- Draw!
  - Study design
  - Causal system
    - factors
    - relationships
    - which are under experimental control?
  - Sketch out a table



# Read against the grain

- Are they measuring what they claim to measure?
- Sources of bias?
- Could observed associations be caused by a third factor?
- Would the observed associations be meaningful to an individual? for a population?
- Are the findings consistent with what you know?
- How could it be done better?



# What to Read?

- Ask your mentor
  - Explore!
    - Pubmed.gov
    - Faculty of 1000
      - Commentary, scores
      - Labels
        - Technical advance
        - New finding
        - Novel drug target
        - Interesting hypothesis
        - Controversial
        - Refutation
- 

## **Social learning spreads knowledge about dangerous humans among American crows**

**Heather N. Cornell, John M. Marzluff\* and Shannon Pecoraro**

*School of Forest Resources, College of the Environment, University of Washington, Seattle, WA 98195, USA*

Individuals face evolutionary trade-offs between the acquisition of costly but accurate information gained firsthand and the use of inexpensive but possibly less reliable social information. American crows (*Corvus brachyrhynchos*) use both sources of information to learn the facial features of a dangerous person. We exposed wild crows to a novel ‘dangerous face’ by wearing a unique mask as we trapped, banded and released 7–15 birds at five study sites near Seattle, WA, USA. An immediate scolding response to the dangerous mask after trapping by previously captured crows demonstrates individual learning, while an immediate response by crows that were not captured probably represents conditioning to the trapping scene by the mob of birds that assembled during the capture. Later recognition of dangerous masks by lone crows that were never captured is consistent with horizontal social learning. Independent scolding by young crows, whose parents had conditioned them to scold the dangerous mask, demonstrates vertical social learning. Crows that directly experienced trapping later discriminated among dangerous and neutral masks more precisely than did crows that learned through social means. Learning enabled scolding to double in frequency and spread at least 1.2 km from the place of origin over a 5 year period at one site.

**Keywords:** American crow; *Corvus brachyrhynchos*; fear learning; mobbing; public information; social learning



<http://www.npr.org/blogs/krulwich/2009/07/27/106826971/the-crow-paradox?ps=rs>



Ask a question!

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# Keeping a Lab Notebook

## Basic Principles and Best Practices

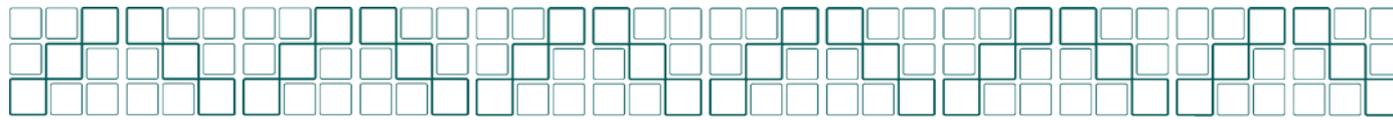
Philip Ryan, PhD

Director of Student Services

NIH Graduate Partnerships Program

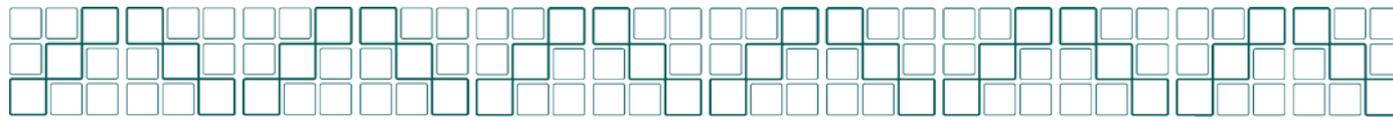
Office of Intramural Training and Education





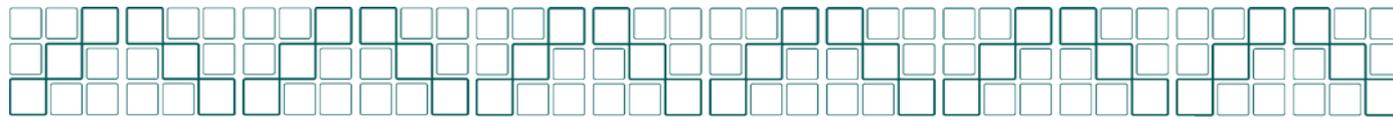
# Overview

- Introductory material
  - What is a lab notebook?
  - What are the different types of lab notebooks?
- Lab notebook do's and don'ts
  - Structure and organization
  - Lab notebook ethics
- Examples of good notebooks



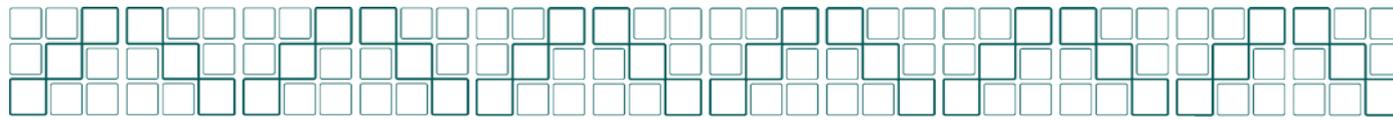
# A Lab Notebook Is...

- Complete record of procedures, reagents, data, and thoughts to pass on to other researchers
- Explanation of why experiments were initiated, how they were performed, and the results
- Legal document to prove patents and defend your data against accusations of fraud
- Scientific legacy in the lab



# A Lab Notebook Is Not...

- A journal
- A record of communications
- A place to compile lab protocols/manuals
- Yours to take home



# Different Types of Lab Notebooks

- Bound/Stitched Notebook
- Loose Leaf/Three Ring Binder Notebook
- Electronic Notebook



# Advantages/Disadvantages

<u>Type of Notebook</u>	<u>Advantages</u>	<u>Disadvantages</u>
Bound/Stitched	No lost pages, legally stronger	Difficult to copy, not logically organized, requires references to data stored elsewhere
Loose Leaf/Binder	Organized by experiment, data stored together	Sheets fall out, difficult to authenticate
Computer/Electronic	Easy to search, easy to read, digital data easy to store	Requires electronic security, corrupted files, software compatibility issues



# What Goes in the Lab Notebook

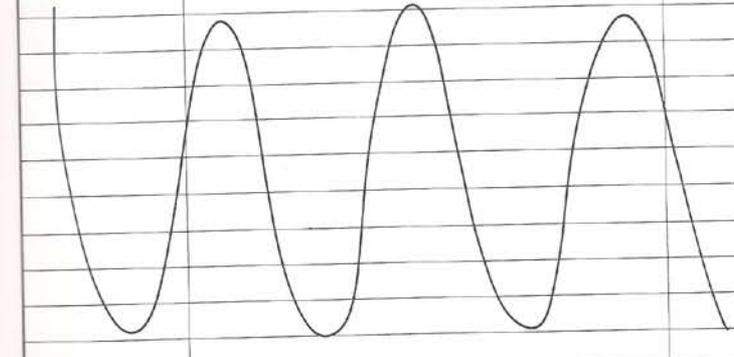
- Notebook name
- Inside cover or cover page
  - Your name and year
  - General project name
  - Lab mailing address
- Table of Contents
- Body of notebook
  - Experimental entries



# Table of Contents

- Table of Contents
  - Page number
  - Date
  - Subject/Experiment

TABLE OF CONTENTS - <i>Analyt. Chem 233-a</i>		Workbook No. <i>HMK-1</i>
Date	Subject	Page No.
9 Sept. 1984	Preface	1
(Begun 10 Sept. 84)	Table of abbreviations	2
10 Sept. 1984	Determination of chloride by gravimetry	3
17 Sept. 1984	Equivalent wt. of a solid acid	7
1 Oct. 1984	Detm'n of oxalate by $KMnO_4$ titrimetry	10
8 Oct. 1984	Fe in ore by dichromate titration	14
15 Oct. 1984	The titration curve and ionization constants of phosphoric acid	—
5 Nov. 1984	Potentiometry with quinhydrone electrode	26
12 Nov. 1984	Formation constant of $Ag-NH_3$ complex	32
19 Nov. 1984	Solubility of $Ag_2CrO_4$ by conductometry	39
4 Dec. 1984	Controlled-potential coulometry	44
10 Dec. 1984	Summary of Experimental Techniques	
	I Learned this Semester	52





# Experimental Entries

- Date
- Title
- Hypothesis or Goal: Brief statement of purpose
- Background
- How: Protocols, calculations, reagents, equipment
- Observations:
  - All that happens (planned or unplanned)
  - Raw experimental data
  - Taped in information or reference to data location
- Data analysis:
  - Processing of raw data, graphs, interpretations
- Ideas for future experiments



# The Details of “How”

- Reagents: source, product number, lot number, expiration date, how and where stored
- Solutions and how they were made
- Cells used: type, source, passage number, growth medium
- Instruments: type, name, location, serial number
- Number and volume of washes
- Centrifuge speeds and duration of spins
- Heating rates and levels of agitation
- Time between and during steps
- Gel percentages
- Type of water used



# Ethics

- All data go in to the notebook
  - Even "bad" data points or "outliers"
  - Failed experiments or contradictory experiments
- No pages come out of the notebook
  - Do not take any pages out or remove any data
  - Do not skip pages in your notebook
  - Cross out any unused parts of a page
- Correct mistakes, do not remove them
  - Cross out mistakes with a single line
  - Paste in corrections without covering anything
  - Sign and date all corrections
- Honesty is the best policy



# Example

22-206

1 Making GST tails for pull-downs

2

3 • goal: put C-terminal 10 aa's of SULT1C1 & GLUT11

4 into pGEX 5X-2

5

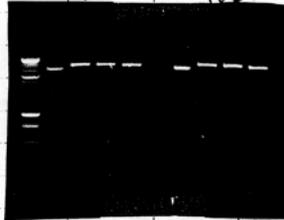
6 - procedure

7 • took pGEX 5X-2. I kept PDZ1 or PDZ4 & cut w/

8 EcoRI / NotI

9 • ran on gel & purified dbl cut PDZ4 vector (~5kb)

10

11 

12 ← vector

13 ← insert

14 • ligated 1ul vector w/

15 1ul annealed primers or

16 1ul of 1:500 dil. primers

17 in 20ul DN @ 16°C

18 • transformed DH5a & MP

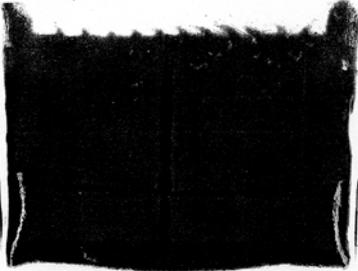
19 • confirmed sequence

20 • grew 50mL LB culture each construct

21 • induced 3hrs. w/ 0.1mM IPTG final

22 • purified fractions from the 16 TX-100 lysate

23 GST-GLUT11 GST-SULT1C1

24 

25 • combined fractions & dialyzed

26 ON against PBS

27 • BCA conc. of each ~0.2ug/ul

28

29

30

31



# Example

49

Sunday January 19, 1936.  
 1:45 PM Oxyhemoglobin against reduced hemoglobin. About 0.3 g.  
 60% active solid sodium hydrosulfite added to the oxyhemoglobin solution in A. Let stand in magnet box.

A and up. Reduced hemoglobin in A, oxyhemoglobin in B.

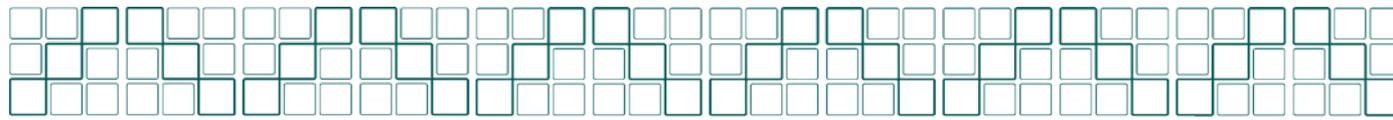
Time	Current (amps)	Reading	Averages
2:45 PM	0	210.04500	
	+10	.05600	
	+14	.05990	0 amps. 210.04490
	0	.04750	+10 210.03607
	-10	.05590	+14 210.05998
	-14	.05990	
2:50 PM	0	.04510	+56.07 +59.98
	+10	.05630	-44.90 -44.90
	+14	.06015	+11.17 mg +15.08 mg
	0	.04500	at 10 amps. at 14 amps
			+5.0% / 1.532 = +11.27 mg = ΔW <sub>14 to 10</sub>

Discussion. ΔW = +11.27 mg. ΔW<sub>corrected</sub> = +11.72 mg.  
 $\chi_{\text{water}} - \chi_{\text{air}} = -0.719 - 0.029 = -0.748 \times 10^{-6}$  ΔW<sub>air</sub> = -47.72 mg.  
 $\chi_{\text{paramagnetism hb vs. hbd}_2} = \frac{11.72}{47.72} \times 0.748 = 0.1839 \times 10^{-6}$   
 1 cc hb solution = 0.323 cc O<sub>2</sub> ST.P. =  $1.442 \times 10^{-5}$  moles O<sub>2</sub> as Fe.  
 $\chi_{\text{molel hb}} = 0.1839 \times 10^{-6} / 0.3442 \times 10^{-6} = 1.274 \times 10^{-2}$   
 $\chi T = 3.73 \quad \mu = 2.83 \chi T = \underline{5.46}$  Bohr magnetons per hb.  
 Assuming the four d-orbitals to be independent, we get  
 $\mu_{\text{obs}} = 5.46$  Bohr magnetons. This is high for four unpaired electrons: there may be some interaction tending to make them parallel in different d-orbitals.  
 See p. 113 for correction



# References

- Guidelines for Scientific Record Keeping in the Intramural Research Program at the NIH
  - <http://sourcebook.od.nih.gov/ethic-conduct/RECORDKEEPING.pdf>
- Writing the Laboratory Notebook, Howard Kanares, ACS 1985
- The Oregon State Library Special Collections
  - <http://osulibrary.orst.edu/specialcollections/rnb/index.html>



# Acknowledgements

- Charu Chaudhry, PhD
  - NICHD
  
- Garland Crawford, PhD
  - NIAMS
  
- Nicholas Fritzkee, PhD
  - NIDDK

# Lab Meetings

Arjun Prasad

Research Fellow, Genome Technology Branch,  
National Human Genome Research Institute

# Why have lab meetings?

- Update the group on your work
- Share your data and results
- Discuss problems or issues and find solutions
- Get input and ideas of where to go next
- Educate other members of lab in your field of expertise

# Styles

- Round-table update
- Casual data share
- Formal scientific presentation

# When in Rome

- Try to mimic the style of presentation that other (successful) members of the lab use
  - Better to have a talk that is too polished and formal than not enough
- Plan for discussion, don't make your presentation too long
  - < 1 slide per minute

# Round-table update

- Tips
  - Remember to prepare something to say or show
  - Try not to take up too much of the group time
  - Usually don't need to present a lot of background

# Casual data share

- Little or no PowerPoint used
- Often chalk or whiteboard use encouraged
- Prepare to show detailed data like you might find in your lab notebook, but maybe not everything (keep in mind time limitations)
- Usually using a formal lab-meeting style is ok too

# Formal presentation

- Title slide
- Introduction
- Background
- Results
- Summary
- Discussion
- Acknowledgements

# Formal presentation

- Title slide
- Introduction
- Background
- Results
- Summary
- Discussion
- Acknowledgements

# Title slides

- A descriptive title for the talk
- Your name
- Your position
- The lab you're in

# Bats

Arjun Prasad

# Some adventures in genome assembly

Arjun Prasad

Mullikin Lab

Genome Technology Branch



# ACR Molecular Biology in Clinical Oncology Workshop 2017 Bioinformatics Laboratory

Andy Baxevanis, Ph.D.

Tyra Wolfsberg, Ph.D.

Gretchen Gibney, Ph.D.

POLYMORPHISMS AND CONGENITAL HEART DEFECTS:

A CANDIDATE GENE ASSOCIATION AND  
FUNCTIONAL APPROACH TOWARD  
IDENTIFYING GENETIC SUSCEPTIBILITY

Reid Prentice

Ph.D. Proposal Presentation

National Institutes of Health - George Washington University  
Graduate Partnerships Program - Genetics

# Formal presentation

- Title slide
- Introduction
- Background
- Results
- Summary
- Discussion
- Acknowledgements

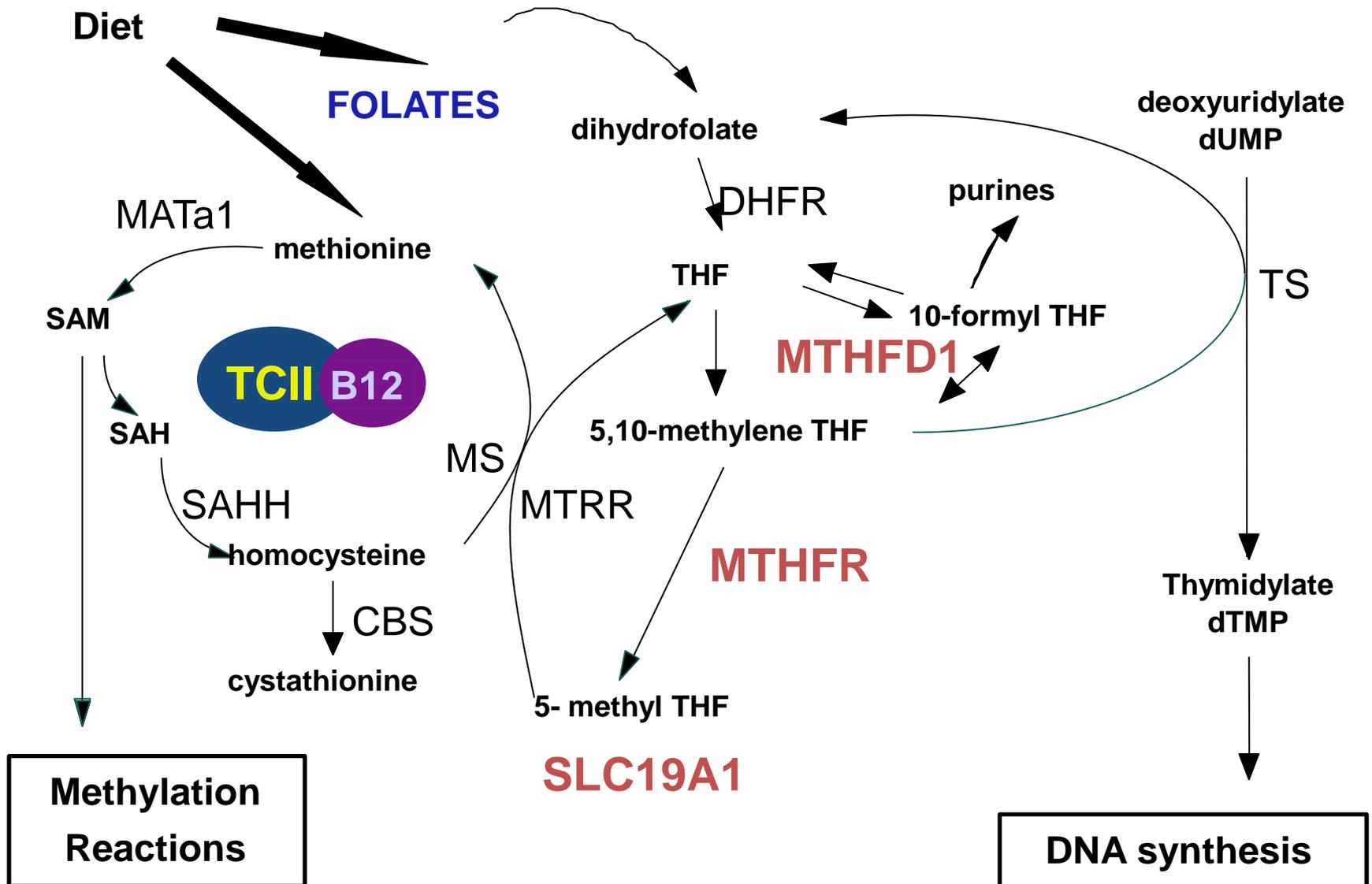
# Introduction and background

- What is the goal of the project?
- How does your project fit in with the field?
- What you need to know to understand why your work is important and what it means
- Think about your audience!

# Congenital Heart Defects

- ~1 in 100 live births
- >8% of all infant deaths
- Severe defects: >\$300,000 per patient

# Folate Metabolic Pathway



# Distance methods

Similar sequences go together



TGC



AGG



TAC



AAG



TGC



AGG



TAC



AAG

0	2	1	3
	0	3	1
		0	2
			0

# Formal presentation

- Title slide
- Introduction
- Background
- **Results**
- Summary
- Discussion
- Acknowledgements

# Results

- The experiments you performed and the results of those experiments
- Usually good to start with the goal of the experiment

# Tips

- For each data slide explain what everything on the slide means
- Explain the axes in graphs
- Zoom in on pictures so people can see what you're talking about

# Relative genome compression assessment

Experimental strategy:

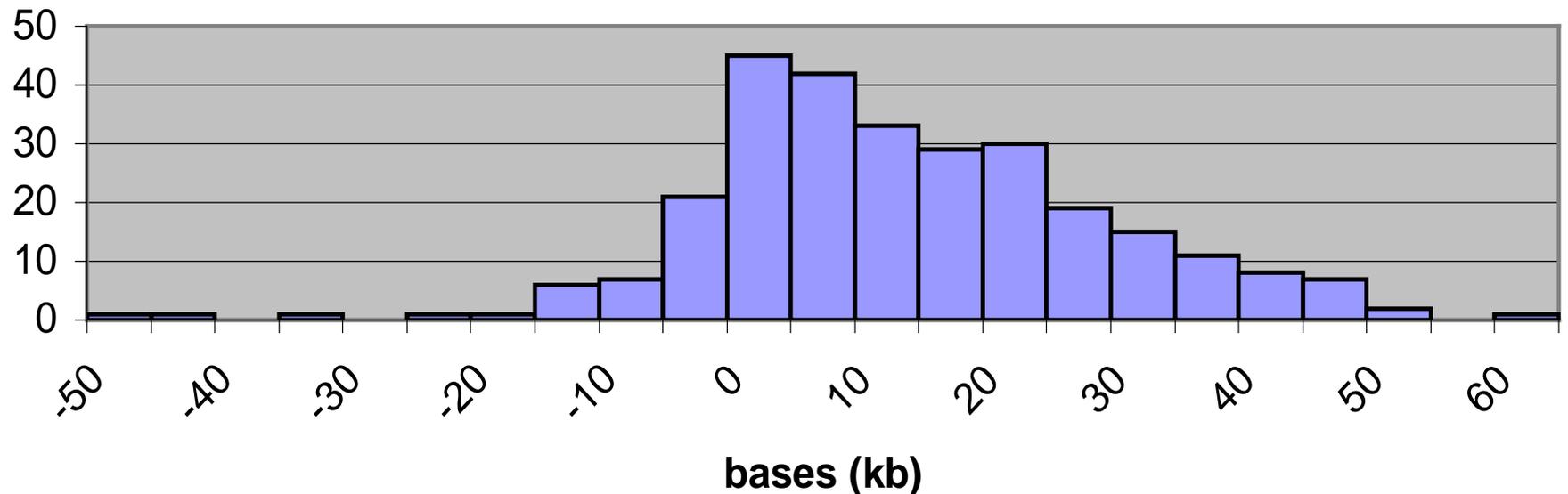
- BAC end sequence a few hundred clones
- Align BAC ends to human reference sequence
- Size BAC inserts by FPC
- Divide FPC size by coverage on the human genome to get a size ratio

# Difference between sequenced size and FPC size (Finished Clones)

Average fpc estimate ~12kb under sequenced size Std. Dev. 54kb

rflat (at 20% compression) should be ~30kb smaller than human

**FPC deviation from sequence clone length**



Lean

AK1

Morb

AK1

# Formal presentation

- Title slide
- Introduction
- Background
- Results
- **Summary**
- Discussion
- Acknowledgements

# Summary

- People will have forgotten all the experiments and results you have shown
- The conclusions that you can make from your data

# Results

- Best assemblers are different for each type of data
  - 454 – Newbler
  - Illumina – Phusion
  - 454 + Illumina – CABOG

# Formal presentation

- Title slide
- Introduction
- Background
- Results
- Summary
- Discussion
- Acknowledgements

# Discussion

- Optional, some conclusions or questions you want to remember to address
- Future directions

# Formal presentation

- Title slide
- Introduction
- Background
- Results
- Summary
- Discussion
- Acknowledgements

# Acknowledgements

Jim Mullikin

Nancy Hansen

Jamie Teer

Pedro Cruz

Praveen Cherukuri

Julie Segre

Sean Conlan

Clayton Deming

Bob Blakesley

Alice Young

Jyoti Gupta

Brian Schmidt

Richelle Legaspi

Holly Coleman

Shelise Brooks

Questions?

# Presenting a Poster

Ozge Gunduz-Cinar, PhD

Post Doctoral Fellow

National Institute on Alcohol Abuse and Alcoholism,  
National Institutes of Health

# Science Skills Boot Camp

- This lecture will provide you brief information on poster presentations
  - Information about posters
  - How to prepare a poster?
  - How to present a poster?
- You will have an excellent opportunity to practice a poster presentation at the end of your stay in NIH.

# A POSTER

- CLEAR
- WELL FOCUSED
- NOT TOO NARRATIVE
- BALANCED GRAPHS, TABLES and FIGURES

# Sections in a poster presentation

- Title
- Abstract
- Material and Methods
- Results
- Discussion
- Conclusion
- References
- Acknowledgements

# Preparing a poster in Power Point

- Check the poster dimensions allowed
- Prepare a new power point slide with the dimensions suitable to your needs (file>page set up)
- Check out how you will design your poster with the appropriate subtitles, text, graphs and tables.
- Use scale function in order to work easier on each section
- Add text boxes or insert graphs and tables into your poster
- At the end review the poster for the balanced distribution of each section.

# Things to consider *before*

- Print out on a paper and check. This will be the handout if you wish to give.
- Practice your poster don't exceed 10 min. If someone is interested in more, you may provide more information, or email him. (networking)
- Focus on the main points that you highlighted on conclusions.
- Think before for possible questions that can be asked.
- Provide your email address for people who wish to ask you some detailed questions.
- Have materials that will be useful to hang the poster-if there is no information
- If you have your research published you may bring few copies of your paper as well. This is also good for people who are interested in more details.

# *During* the poster presentation

- Make a story with background and approaches to solve the problems
- Focus on the graphs and illustrations
- Conclude and open to discussion
- Check if your audience understand why you did all that work. Make clear conclusions
- Thank for the people who are interested in. Good opportunity to network!!

# Few examples for Posters

YOU ARE WELCOME TO ASK ME ANY  
QUESTION IF YOU NEED HELP WHEN  
YOU ARE PREPARING YOUR POSTERS.

[gunduzcinaro@mail.nih.gov](mailto:gunduzcinaro@mail.nih.gov)

---

# What Makes a Good Scientific Question?

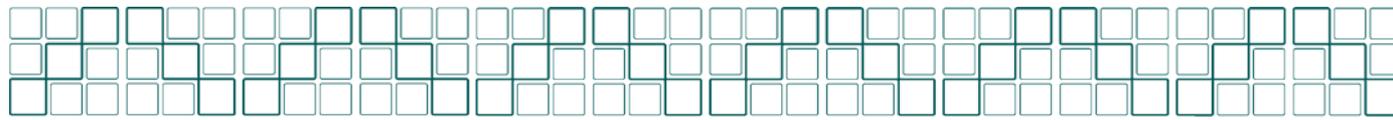
Philip Ryan, PhD  
Director of Student Services  
NIH Graduate Partnerships Program  
Office of Intramural Training and Education





# Biology

- What is the question?
  - What is Biology?
  - What's the answer?
    - The Study of Life
  
- What are the next questions?
  - What is life?
  - How do we study it?
  
- Life is defined by a set of criteria
  - Once we know that criteria, we can ask the question...
  - "Is X alive?"



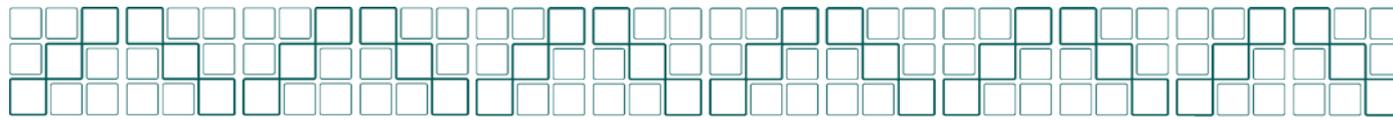
# What Makes a Good Question?

- Has not already been answered!
  - Background information is paramount
  - Literature searches, database searches
  - Reading scientific papers
  
- Can be answered
  - With the resources you have
    - Time, technology, reagents, expertise, etc.
  - Conclusively
    - While some evidence may suggest that prehistoric toads liked softer lily pads to more coarse ones....one may never know for sure.



# Relevance

- So what?
  - How does it relate to the big picture?
  - Who will be impacted?
  
- Builds on what is already known
  - That is why we publish...so others can add to it
    - Background information is important
  - If there is previous work, it is likely important to someone



# Hypothesis Driven

- There is reason to believe that the answer is X?
  - Builds on what is already known
    - Background information: notice a pattern yet?
  - Logically fits with what is understood
- Proteins Y and Z interact. Protein Z has been found in the nucleus.
  - Hypothesis: Protein Y can be found in the nucleus.
  - Question: Is Protein Y in the nucleus under the same conditions as when Protein Z is in the nucleus?



# Different Approaches

- More than one way to approach answering the question.
  - Sometimes your first approach does not give you an answer either way
  - Answering a question only one way, often is misleading
- Different approaches let you adjust the question as you go along
  - A “no” to the original question can be redirected to a related question to answer



# Further Questions

- Good scientific questions lead to more questions when they are answered
- If “no” means the end of the project...then its not a good question
  - Note: That does not mean it should not be asked and answered! Just not something to base a project on



# Answers lead to Questions

- Proteins Y and Z interact. Protein Z has been found in the nucleus and affects transcription of gene B.
  - Hypothesis: Protein Y can be found in the nucleus.
  - Question: Is Protein Y in the nucleus under the same conditions as when Protein Z is in the nucleus?
    - If yes, hypothesis two: Protein Y can affect transcription of gene B
    - Question: Does Protein Y affect transcription of gene B?
      - If yes...how?
      - If no, hypothesis three: Protein Y can affect the transcription of other genes
      - Question: Does Protein Y affect the transcription profile in cell X?



Research Boot camp  
Barbara Fuhrman, Ph.D.  
June 1, 2012



# STATISTICS FOR BEGINNERS

# A statistician's view of science

- Select a sample from the population
- Measure each individual in the sample
- Consider these measures in aggregate
  
- Estimate, Compare, or Model ...
  - Usually employing 2 kinds of information – the data, and an idea about what variation should look like
  
- And then, Infer ...

# Measurement is

- A systematic comparison of each instance with a standard scale

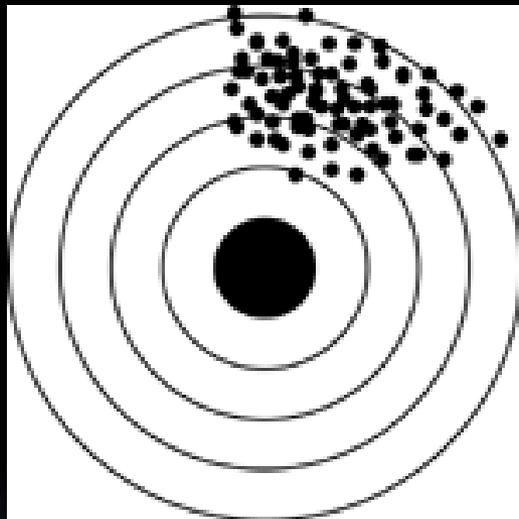
**VALIDITY**

- Two kinds of issues

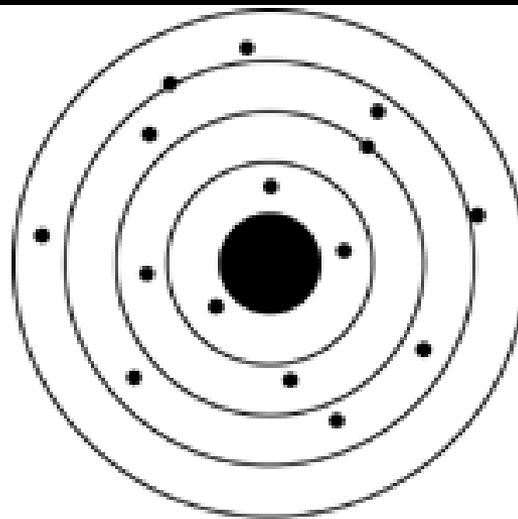
- Are we measuring what we mean to measure?
- Would repeating the measurement yield the same answer?

**RELIABILITY**

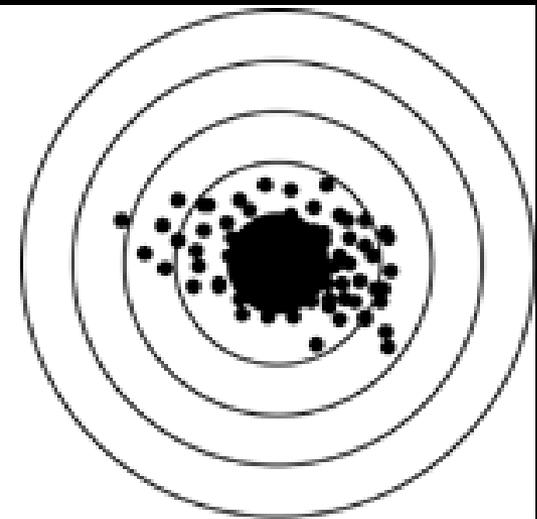
# Validity and Reliability



**Reliable but Not Valid**



**Valid but Not Reliable**



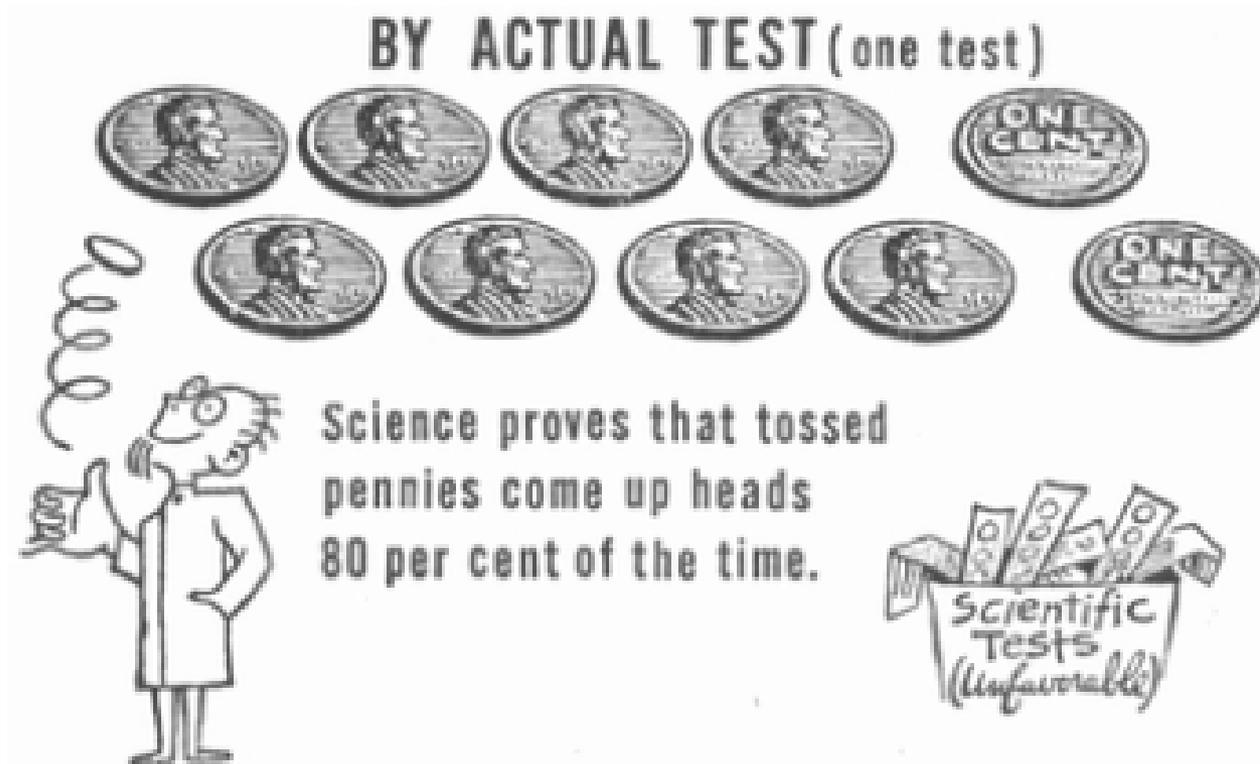
**Valid and Reliable**



# Plato vs. Darwin

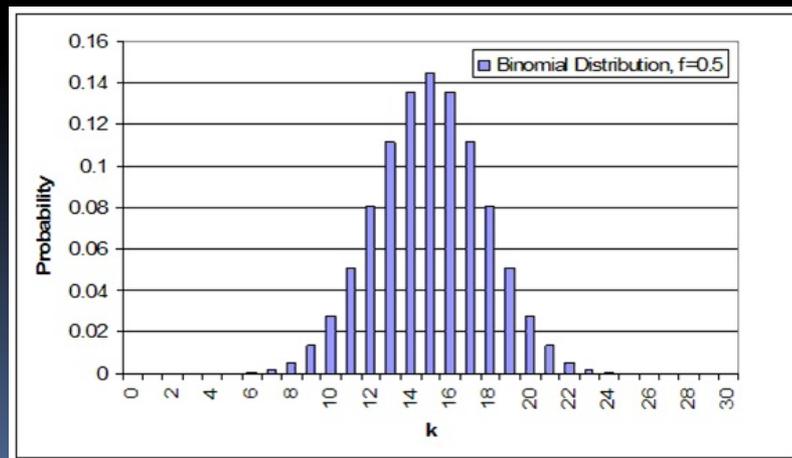
- Variation is inherent in the world (variability) and in the sampling and measurement process (error).
  - Plato observed *variations* in plant and animal populations, and explained them as imperfect manifestations of their *ideal forms*.
  - Darwin suggested that *variations* among individuals were the basis for differences in survival and reproductive success, and therefore worthy of study.
- 

# Sampling Variation



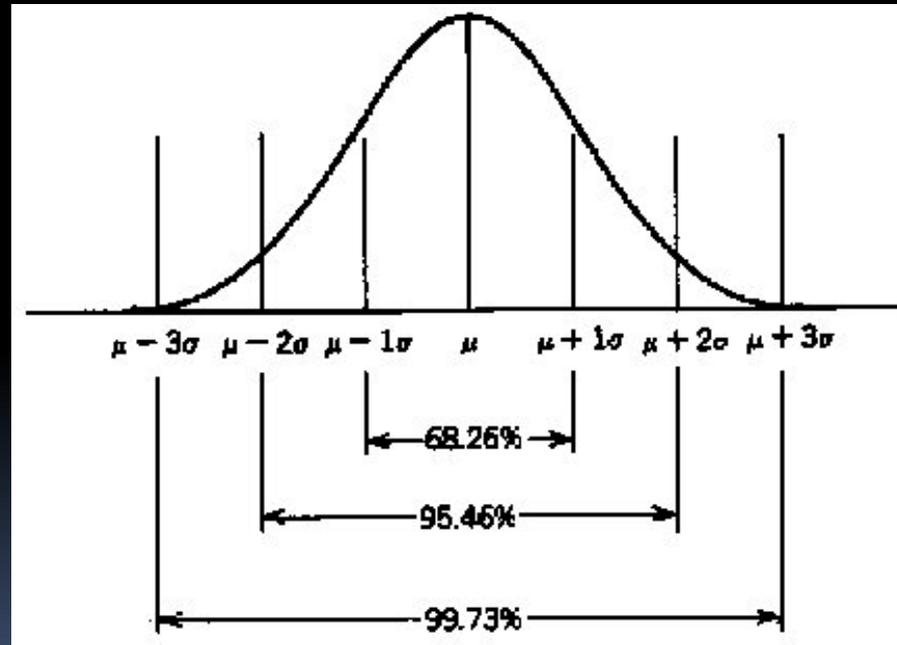
# Distributions

- An arrangement of values of a variable showing their observed or theoretical frequency of occurrence
- The binomial distribution describes the number of heads observed when  $n$  independent trials.



# A thought experiment

- How tall are we?



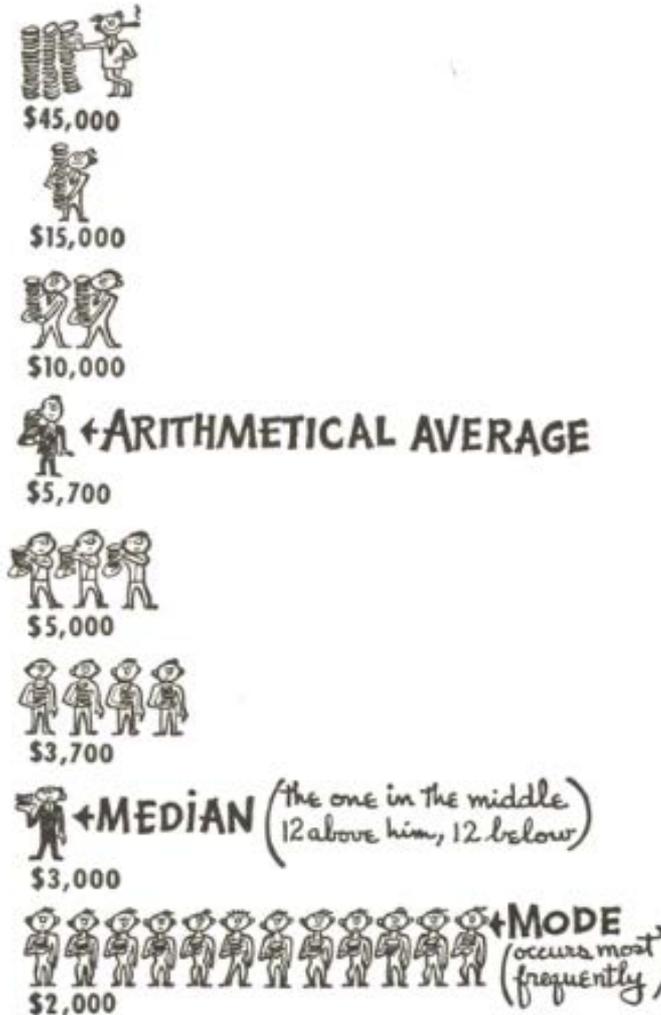
# A dataset

- Me: 5'4"
- You: 5'9"
- That guy over there: 5'11"

## Data analysis

- Consider the data in aggregate
- Visualize the data
- Describe the data
- Test hypotheses

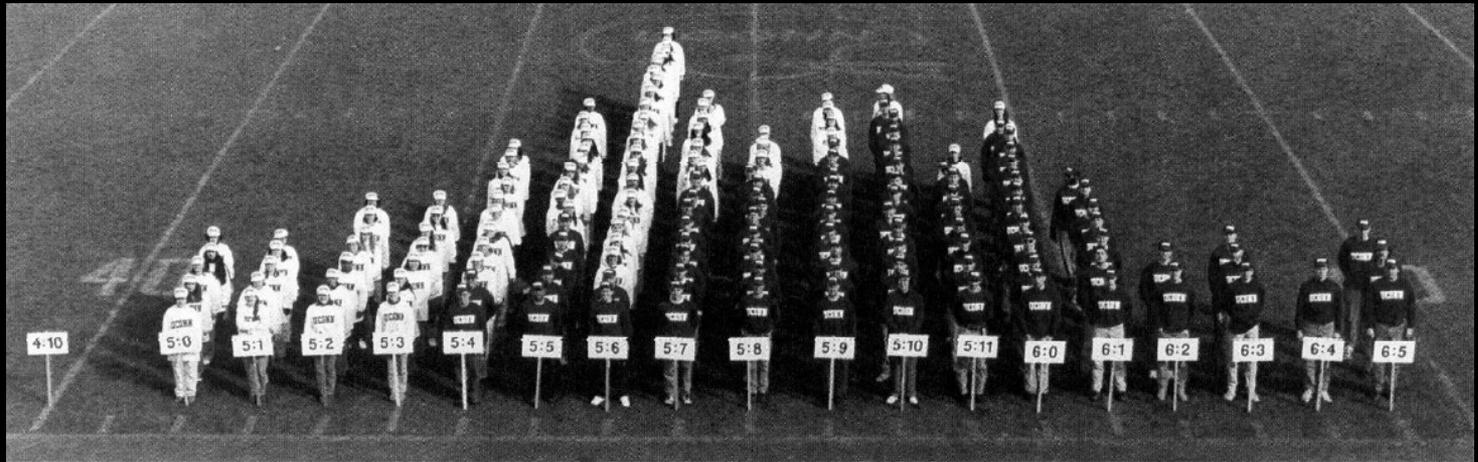
# Statistics to Describe Central Tendency





# Statistics to Describe Variation

- Range
  - Variance
  - Standard deviation
  - Standard error of the mean
  - Interquartile range
- 



- Men: 70" (s.d. 3), Women: 65 inches (s.d. 3)
- What if we used a questionnaire?
- What if I gave you a 12 inch ruler to use?
- What happens when we do the same thing next year?
- What do our measurements tell us about the height of U.S. adults aged 18-26?

# Let's meet at the hypothesis ...

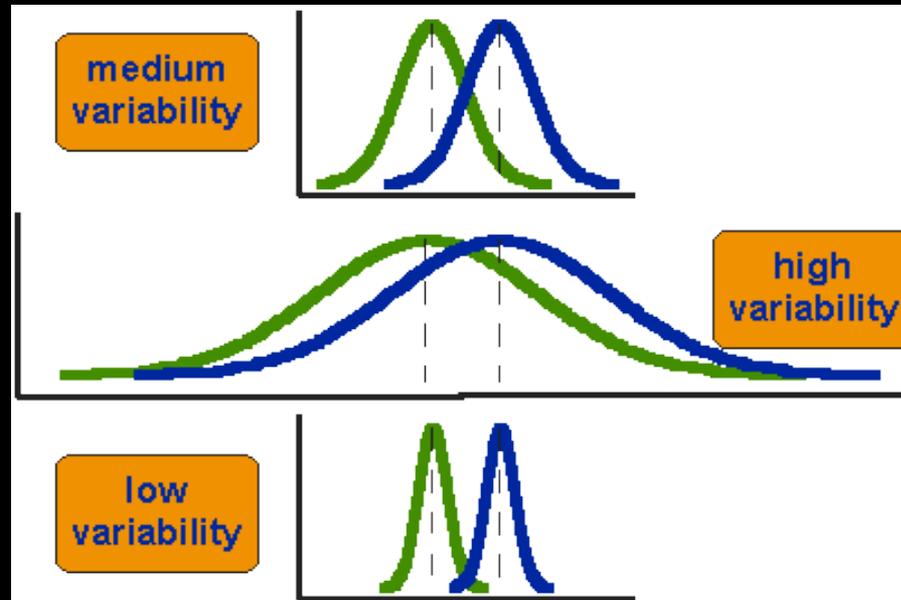
- Scientist: Maternal calorie intake during pregnancy contributes to the adult height of her offspring.
- Statistician: I bet you can't get any information about how much she ate by the height of her adult child.



# Statistics for Testing and Inference

- T-test, Analysis of Variance
  - Chi-square test
    - and many many more ...
  
  - Test the null hypothesis
  - May make assumptions about the distribution of the data
  - P value (how unlikely is that?)
  - 95% confidence limits
- 

# The t-test



- Does sex determine height?
- How do we decide if the difference we observed in our sample means anything?



# T-Test, continued

- What is the probability that the differences we observed could occur just due to sampling variation?
  - Factors
    - Group means
    - Observed Variance
    - Sample size
- 



# Scavenger Hunt

- Find a result that represents a test of statistical significance.
    - What is being compared?
    - What is the hypothesis being tested?
    - What test is being used?
- 



# Good Luck!

- Get practical experience in data management and data analysis
- Learn about the analytic tools
  - Appropriate application
  - Assumptions
- Always start by visualizing your data
- When you can, work with a statistician to plan your experiments and your data analysis!
- Take courses in statistics and programming

# Bioinformatics

Some tools you might need to use

Arjun Prasad

Research Fellow, Genome Technology Branch  
National Human Genome Research Institute

What is bioinformatics?

# What is bioinformatics?

Using computers to study biology

# A few resources

- Entrez
- PubMed
- GenBank
- OMIM
- BLAST
- UCSC Genome Browser
  - In-silico PCR

# How to find out more

- Google
- Bitesize Bio (<http://bitesizebio.com>)
  - short articles on specific laboratory technique
- OpenHelix (<http://www.openhelix.com/>)
  - Video tutorials on genomics / bioinformatics techniques (Subscription service, but some free)

# National Center for Biotechnology Information (NCBI)

- Central repository for biological information and databases for the US (and the world)
- Part of the National Library of Medicine
- Gigantic databases...
- Lots of databases...
- Entrez as entry point

Entrez cross-database search

www.ncbi.nlm.nih.gov/sites/gquery

PubMed UCSC tiki Journals Admin binfo CiteULike CiteULike2 CiteULike Lib Calendar Weather Readability Read Now Notforest ~ Other Bookmarks

  *Entrez, The Life Sciences Search Engine*

HOME SEARCH SITE MAP PubMed All Databases Human Genome GenBank Map Viewer BLAST

Search across databases    [Help](#)

### Welcome to the Entrez cross-database search page

 <b>PubMed:</b> biomedical literature citations and abstracts 	 <b>Books:</b> online books 
 <b>PubMed Central:</b> free, full text journal articles 	 <b>OMIM:</b> online Mendelian Inheritance in Man 
 <b>Site Search:</b> NCBI web and FTP sites 	

 <b>Nucleotide:</b> Core subset of nucleotide sequence records 	 <b>dbGaP:</b> genotype and phenotype 
 <b>EST:</b> Expressed Sequence Tag records 	 <b>UniGene:</b> gene-oriented clusters of transcript sequences 
 <b>GSS:</b> Genome Survey Sequence records 	 <b>CDD:</b> conserved protein domain database 
 <b>Protein:</b> sequence database 	 <b>Clone:</b> integrated data for clone resources 
 <b>Genome:</b> whole genome sequences 	 <b>UniSTS:</b> markers and mapping data 
 <b>Structure:</b> three-dimensional macromolecular structures 	 <b>PopSet:</b> population study data sets 
 <b>Taxonomy:</b> organisms in GenBank 	 <b>GEO Profiles:</b> expression and molecular abundance profiles 
 <b>SNP:</b> short genetic variations 	 <b>GEO DataSets:</b> experimental sets of GEO data 
 <b>dbVar:</b> Genomic structural variation 	 <b>Epigenomics:</b> Epigenetic maps and data sets 
 <b>Gene:</b> gene-centered information 	 <b>PubChem BioAssay:</b> bioactivity screens of chemical substances 
 <b>SRA:</b> Sequence Read Archive 	 <b>PubChem Compound:</b> unique small molecule chemical structures 
 <b>BioSystems:</b> Pathways and systems of interacting molecules 	 <b>PubChem Substance:</b> deposited chemical substance records 
 <b>HomoloGene:</b> eukaryotic homology groups 	 <b>Protein Clusters:</b> a collection of related protein sequences 
 <b>Probe:</b> sequence-specific reagents 	 <b>OMIA:</b> online Mendelian Inheritance in Animals 
 <b>BioProject:</b> aggregated biological research project data 	 <b>BioSample:</b> biological material descriptions 

 <b>NLM Catalog:</b> catalog of books, journals, and audiovisuals in the NLM collections 	 <b>MeSH:</b> detailed information about NLM's controlled vocabulary 
---	--

[Counts in XML](#) | [Entrez Utilities](#) | [Disclaimer](#) | [Privacy statement](#) | [Accessibility](#)

Search across databases

GARS

GO

Clear

Help

- Result counts displayed in gray indicate one or more terms not found

290		<b>PubMed:</b> biomedical literature citations and abstracts		66		<b>Books:</b> online books	
391		<b>PubMed Central:</b> free, full text journal articles		11		<b>OMIM:</b> online Mendelian Inheritance in Man	
none		<b>Site Search:</b> NCBI web and FTP sites					
42776		<b>Nucleotide:</b> Core subset of nucleotide sequence records		none		<b>dbGaP:</b> genotype and phenotype	
63		<b>EST:</b> Expressed Sequence Tag records		18		<b>UniGene:</b> gene-oriented clusters of transcript sequences	
12		<b>GSS:</b> Genome Survey Sequence records		1		<b>CDD:</b> conserved protein domain database	
9849		<b>Protein:</b> sequence database		1673		<b>Clone:</b> integrated data for clone resources	
17		<b>Genome:</b> whole genome sequences		16		<b>UniSTS:</b> markers and mapping data	
36		<b>Structure:</b> three-dimensional macromolecular structures		34		<b>PopSet:</b> population study data sets	
1		<b>Taxonomy:</b> organisms in GenBank		6162		<b>GEO Profiles:</b> expression and molecular abundance profiles	
2427		<b>SNP:</b> short genetic variations		1		<b>GEO DataSets:</b> experimental sets of GEO data	
95		<b>dbVar:</b> Genomic structural variation		none		<b>Epigenomics:</b> Epigenetic maps and data sets	
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9		<b>SRA:</b> Sequence Read Archive		none		<b>PubChem Compound:</b> unique small molecule chemical structures	
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231		<b>Probe:</b> sequence-specific reagents		none		<b>OMIA:</b> online Mendelian Inheritance in Animals	
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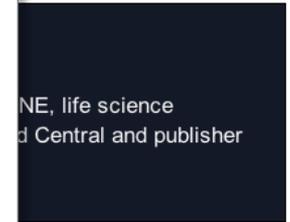
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J Neurosurg. 2010 May;112(5):1033-8. **Review.**  
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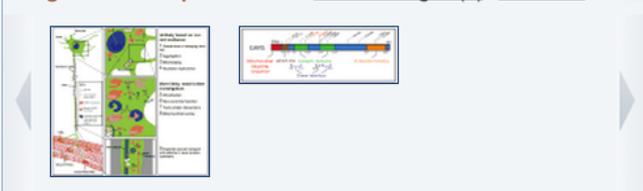
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Charcot-Marie-Tooth disease type 2D, a hereditary axonal neuropathy, is caused by mutations in glycyl-tRNA synthetase (GARS). The mutations are distributed throughout the protein in multiple functional domains. In biochemical and cell culture experiments, some mutant forms of GARS have been indistinguishable from wild-type protein, suggesting that these in vitro tests might not adequately assess the aberrant activity responsible for axonal degeneration. Recently, mouse and fly models have offered new insights into the disease mechanism. There are still gaps in our understanding of how mutations in a ubiquitously expressed component of the translation machinery result in axonal neuropathy. Here, we review recent reports, weigh the evidence for and against possible mechanisms and suggest areas of focus for future work.

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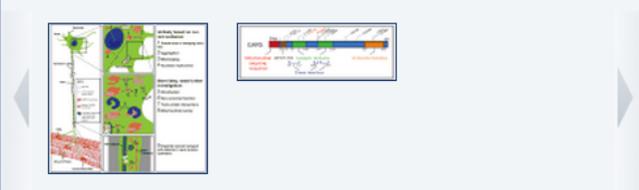
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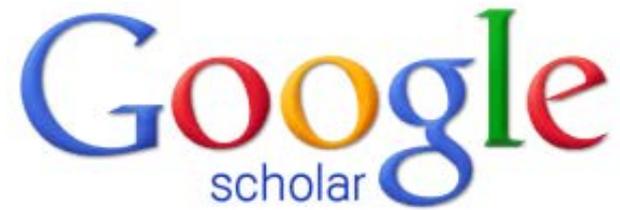
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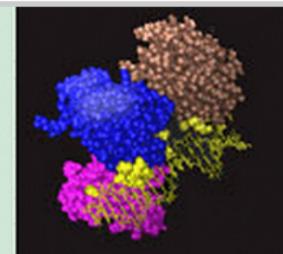
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## CHARCOT-MARIE-TOOTH DISEASE, AXONAL, TYPE 2D; CMT2D

*Alternative titles; symbols*

CHARCOT-MARIE-TOOTH DISEASE, NEURONAL, TYPE 2D  
 CHARCOT-MARIE-TOOTH NEUROPATHY, TYPE 2D

### Phenotype Gene Relationships

Location	Phenotype	Phenotype MIM number	Gene/Locus	Gene/Locus MIM number
7p14.3	Charcot-Marie-Tooth disease, type 2D	601472	GARS	600287

[Phenotypic Series](#)

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### TEXT

A number sign (#) is used with this entry because Charcot-Marie-Tooth disease type 2D can be caused by mutation in the gene encoding glycyI tRNA synthetase (GARS; [600287](#)). Distal spinal muscular atrophy type V (DSMAV; [600794](#)) is an allelic disorder with a similar phenotype.

For a phenotypic description and a discussion of genetic heterogeneity of axonal CMT type 2, see CMT2A1 ([118210](#)).

### Clinical Features

[Ionasescu et al. \(1996\)](#) reported results of clinical, electrophysiologic, and genetic linkage studies on a large pedigree with autosomal dominant Charcot-Marie-Tooth axonal neuropathy type 2, which they designated CMT2D. The pedigree consisted of 38 members, 14 of which were affected. Onset of the disease was between 16 and 30 years of age with weakness of the hands. Affected members had severe weakness and atrophy of the hands and mild to moderate weakness of the feet. Deep tendon reflexes were absent in the upper extremities and decreased in the lower extremities. There was distal hypesthesia for touch, proprioception, and vibration

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Gene ID: 2617, updated on 13-May-2012

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### Summary

**Official Symbol** GARS provided by [HGNC](#)

**Official Full Name** glycyL-tRNA synthetase provided by [HGNC](#)

**Primary source** [HGNC:4162](#)

**See related** [Ensembl:ENSG00000106105](#); [HPRD:02617](#); [MIM:600287](#); [Vega:OTTHUMG00000152769](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Homo sapiens](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

**Also known as** HMN5; CMT2D; DSMAV; GlyRS; SMAD1

**Summary** This gene encodes glycyL-tRNA synthetase, one of the aminoacyl-tRNA synthetases that charge tRNAs with their cognate amino acids. The encoded enzyme is an (alpha)<sub>2</sub> dimer which belongs to the class II family of tRNA synthetases. It has been shown to be a target of autoantibodies in the human autoimmune diseases, polymyositis or dermatomyositis. [provided by RefSeq, Jul 2008]

### Links

- [Order cDNA clone](#)
- [BioProjects](#)
- [BioSystems](#)
- [Books](#)
- [CCDS](#)

# BLAST

- Basic Local Alignment Search Tool
- Search for sequences
- Homology search (evolutionary hypothesis of relatedness)
- What sequence / sequences in the database are closely related to the sequence I'm searching with?

# BLAST example

- You get sequences for your plasmid, and they're not what you expect.
- <http://blast.ncbi.nlm.nih.gov>

```
TATTCTCATGACAGCTCGCACTGTTTATGATGATGCTGCTAGACGTGTTTGGCACTGATGAATG
TCATTACACTTGTTTACAAAGTCTACTATGGTAATGCTTTAGATCAAGCTATTTCCATGTGGGCCTT
AGTTATTTCTGTAACCTCTAACTATTCTGGTGTCGTTACGACTATCATGTTTTTAGCTAGAGCTATA
GTGTTTGTGTGTGTTGAGTATTACCCATTGTTATTTATTACTGGCAACACCTTACAGTGTATCATGC
TTGTTTATTGTTTCTTAGGCTATTGTTGCTGCTGCTACTTTGGCCTTTTCTGTTTACTCAACCGTTA
CTTCAGGCTTACTCTTGGTGTTTATGACTACTTGGTCTCTACACAAGAATTTAGGTATATGAACTC
CCAGGGGCTTTTGCCTCCTAA
```

BLAST®

Basic Local Alignment Search Tool

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[\[Sign In\]](#) [\[Register\]](#)▶ [NCBI/ BLAST Home](#)BLAST finds regions of similarity between biological sequences. [more...](#)**New** Aligning Multiple Protein Sequences? Try the [COBALT Multiple Alignment Tool](#). 

## BLAST Assembled RefSeq Genomes

Choose a species genome to search, or [list all genomic BLAST databases](#).

- [Human](#)
- [Mouse](#)
- [Rat](#)
- [Arabidopsis thaliana](#)
- [Oryza sativa](#)
- [Bos taurus](#)
- [Danio rerio](#)
- [Drosophila melanogaster](#)
- [Gallus gallus](#)
- [Pan troglodytes](#)
- [Microbes](#)
- [Apis mellifera](#)

## Basic BLAST

Choose a BLAST program to run.

**nucleotide blast**Search a **nucleotide** database using a **nucleotide** query  
*Algorithms: blastn, megablast, discontinuous megablast*[protein blast](#)Search **protein** database using a **protein** query  
*Algorithms: blastp, psi-blast, phi-blast, delta-blast*[blastx](#)Search **protein** database using a **translated nucleotide** query

## News

### [DELTA-BLAST](#)

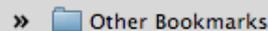
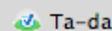
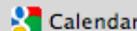
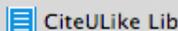
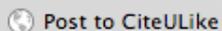
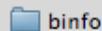
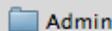
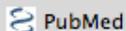
DELTA-BLAST performs more sensitive protein-protein searches.

Mon, 23 Apr 2012  
12:00:00 EST [More BLAST news...](#)

## Tip of the Day

### [Use Genomic BLAST to see the genomic context](#)

If you are interested in the evolution of a particular gene or gene family it is often interesting to examine the intron-exon structure even across species

**BLAST**<sup>®</sup>

Basic Local Alignment Search Tool

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## Standard Nucleotide BLAST

blastn

[blastp](#)[blastx](#)[tblastn](#)[tblastx](#)BLASTN programs search nucleotide databases using a nucleotide query. [more...](#)[Reset page](#)[Bookmark](#)

### Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

[Clear](#)

Query subrange

From

To

Or, upload file

[Choose File](#)

No file chosen

Job Title

Enter a descriptive title for your BLAST search

 **Align two or more sequences**

### Choose Search Set

Database

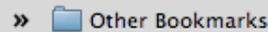
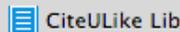
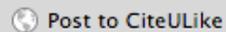
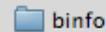
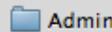
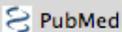
 Human genomic + transcript  Mouse genomic + transcript  Others (nr etc.):

◆ Nucleotide collection (nr/nt)

Organism  
OptionalEnter organism name or id--completions will be suggested  Exclude 

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude  
Optional Models (XM/XP)  Uncultured/environmental sample sequences



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▶ NCBI/ BLAST/ blastn suite

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blastn

blastp

blastx

tblastn

tblastx

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Enter accession number(s), gi(s), or FASTA sequence(s)

[Clear](#)

Query subrange

```
TATTCTCATGACAGCTCGCACTGTTTATGATGATGCTGCTAGACGTGTTTGGACACTGA
TGAATGTCATTACACTTGTTCACAAAGTCTACTATGGTAATGCTTTAGATCAAGCTATT
TCCATGTGGGCCTTAGTTATTTCTGTAACCTCTAACTATTCTGGTGTGTTACGACTAT
CATGTTTTTAGCTAGAGCTATAGTGTTTGTGTGTGTTGAGTATTACCCATTGTTATTTA
TTACTGGCAACACCTTACAGTGTATCATGCTTGTTTATTGTTTCTTAGGCTATTGTTGC
```

From

To

Or, upload file

[Choose File](#)

No file chosen

Job Title

Enter a descriptive title for your BLAST search

 Align two or more sequences 

## Choose Search Set

Database

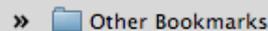
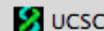
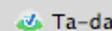
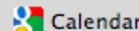
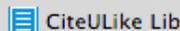
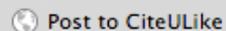
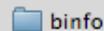
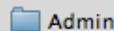
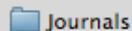
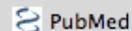
 Human genomic + transcript  Mouse genomic + transcript  Others (nr etc.):

▶ Nucleotide collection (nr/nt)

Organism  
OptionalEnter organism name or id--completions will be suggested  Exclude 

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude  
Optional Models (XM/XP)  Uncultured/environmental sample sequences



Enter a descriptive title for your BLAST search

Align two or more sequences

### Choose Search Set

#### Database

Human genomic + transcript  Mouse genomic + transcript  Others (nr etc.):

◆ Nucleotide collection (nr/nt)

#### Organism Optional

Enter organism name or id--completions will be suggested  Exclude +

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

#### Exclude Optional

Models (XM/XP)  Uncultured/environmental sample sequences

#### Entrez Query Optional

Enter an Entrez query to limit search

### Program Selection

#### Optimize for

- Highly similar sequences (megablast)  
 More dissimilar sequences (discontiguous megablast)  
 Somewhat similar sequences (blastn)

Choose a BLAST algorithm

**BLAST**

Search **database Nucleotide collection (nr/nt)** using **Megablast (Optimize for highly similar sequences)**

Show results in a new window

+ Algorithm parameters

Note: Parameter values that differ from the default are highlighted in yellow

marked with ◆ sign

NCBI/ BLAST/ blastn suite/ Formatting Results - WGRZE2NA01S

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

**Nucleotide Sequence (420 letters)**

**Query ID** |cl|12969  
**Description** None  
**Molecule type** nucleic acid  
**Query Length** 420

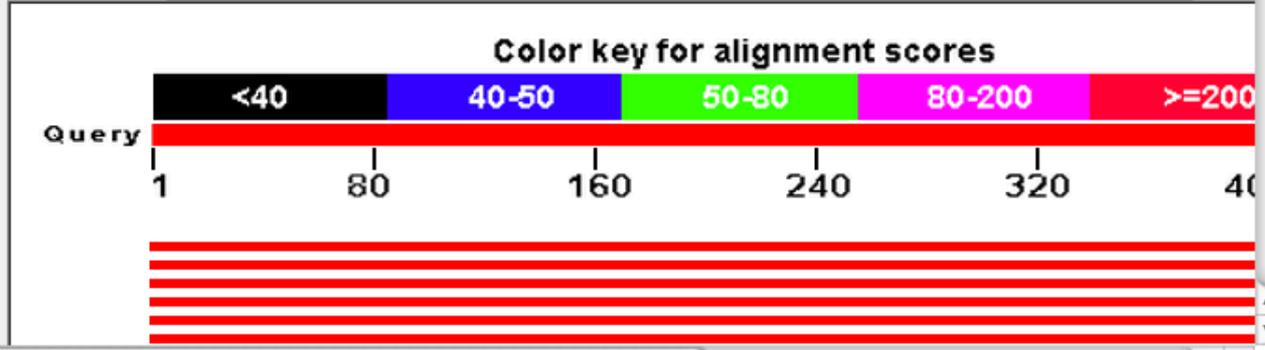
**Database Name** nr  
**Description** All GenBank+EMBL+GSS,environment  
**Program** BLASTN 2.2.26+

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

**Graphic Summary**

**Distribution of 100 Blast Hits on the Query Sequence**

Mouse over to see the define, click to show alignments



## Descriptions

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** Map Viewer **🌿** PubChem BioAssay

### Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage
<a href="#">JQ316196.1</a>	SARS coronavirus HKU-39849 isolate UOB, complete genome	<a href="#">776</a>	776	100%
<a href="#">JF292922.1</a>	SARS coronavirus ExoN1 isolate c5P1, complete genome	<a href="#">776</a>	776	100%
<a href="#">JF292915.1</a>	SARS coronavirus MA15 isolate d4ym5, complete genome	<a href="#">776</a>	776	100%
<a href="#">JF292909.1</a>	SARS coronavirus MA15 isolate d2ym4, complete genome >	<a href="#">776</a>	776	100%
<a href="#">JF292906.1</a>	SARS coronavirus MA15 ExoN1 isolate d3om5, complete gen	<a href="#">776</a>	776	100%
<a href="#">JF292903.1</a>	SARS coronavirus MA15 ExoN1 isolate d4ym5, complete gen	<a href="#">776</a>	776	100%
<a href="#">HQ890541.1</a>	SARS coronavirus MA15 isolate d2ym1, complete genome >	<a href="#">776</a>	776	100%
<a href="#">HQ890538.1</a>	SARS coronavirus MA15 ExoN1 isolate d2om5, complete gen	<a href="#">776</a>	776	100%
<a href="#">HQ890535.1</a>	SARS coronavirus MA15 ExoN1 isolate d2om2, complete gen	<a href="#">776</a>	776	100%
<a href="#">HQ890532.1</a>	SARS coronavirus MA15 ExoN1 isolate d4ym2, complete gen	<a href="#">776</a>	776	100%
<a href="#">HQ890531.1</a>	SARS coronavirus MA15 ExoN1 isolate d4ym1, complete gen	<a href="#">776</a>	776	100%
<a href="#">HQ890529.1</a>	SARS coronavirus MA15 ExoN1 isolate d2ym4, complete gen	<a href="#">776</a>	776	100%
<a href="#">HQ890526.1</a>	SARS coronavirus MA15 ExoN1 isolate d2ym1, complete gen	<a href="#">776</a>	776	100%
<a href="#">GU553365.1</a>	SARS coronavirus HKU-39849 isolate TCVSP-HARROD-00003	<a href="#">776</a>	776	100%
<a href="#">GU553364.1</a>	SARS coronavirus HKU-39849 isolate TCVSP-HARROD-00002	<a href="#">776</a>	776	100%
<a href="#">GU553363.1</a>	SARS coronavirus HKU-39849 isolate TCVSP-HARROD-00001	<a href="#">776</a>	776	100%
<a href="#">FJ882960.1</a>	SARS coronavirus ExoN1 isolate P3pp34, complete genome	<a href="#">776</a>	776	100%

## Descriptions

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [P](#) PubChem BioAssay

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Accession	Description	Max score	Total score	Query coverage
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<a href="#">GU553365.1</a>	SARS coronavirus HKU-39849 isolate TCVSP-HARROD-00003	<a href="#">776</a>	776	100%
<a href="#">GU553364.1</a>	SARS coronavirus HKU-39849 isolate TCVSP-HARROD-00002	<a href="#">776</a>	776	100%
<a href="#">GU553363.1</a>	SARS coronavirus HKU-39849 isolate TCVSP-HARROD-00001	<a href="#">776</a>	776	100%
<a href="#">FJ882960.1</a>	SARS coronavirus ExoN1 isolate P3pp34, complete genome	<a href="#">776</a>	776	100%

# BLAST

- Looks for homology
- What sequences in the database are evolutionary similar to this one?
- Can search DNA, RNA, Proteins
- Lots of tutorials and explanations on the web

# UCSC Genome browser

- Get a genomic context view of human and some other reference genomes
  - Mouse, fly, cat, dog, panda, turkey, orangutan, naked mole rat, etc.
- Annotation tracks
- What's going on at a particular locus
- <http://genome.ucsc.edu>

# UCSC Genome Bioinformatics

Genomes - Blat - Tables - Gene Sorter - PCR - VisiGene - Proteome - Session - FAQ - Help

Genome  
Browser

ENCODE

Neandertal

Blat

Table  
Browser

Gene Sorter

In Silico  
PCR

Genome  
Graphs

Galaxy

VisiGene

Proteome  
Browser

Utilities

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Release Log

Custom  
Tracks

## About the UCSC Genome Bioinformatics Site

Welcome to the UCSC Genome Browser website. This site contains the reference sequence and working draft assemblies for a large collection of genomes. It also provides portals to the [ENCODE](#) and [Neandertal](#) projects.

We encourage you to explore these sequences with our tools. The [Genome Browser](#) zooms and scrolls over chromosomes, showing the work of annotators worldwide. The [Gene Sorter](#) shows expression, homology and other information on groups of genes that can be related in many ways. [Blat](#) quickly maps your sequence to the genome. The [Table Browser](#) provides convenient access to the underlying database. [VisiGene](#) lets you browse through a large collection of *in situ* mouse and frog images to examine expression patterns. [Genome Graphs](#) allows you to upload and display genome-wide data sets.

The UCSC Genome Browser is developed and maintained by the Genome Bioinformatics Group, a cross-departmental team within the Center for Biomolecular Science and Engineering ([CBSE](#)) at the University of California Santa Cruz ([UCSC](#)). If you have feedback or questions concerning the tools or data on this website, feel free to contact us on our [public mailing list](#).

## News

News Archives ▶

To receive announcements of new genome assembly releases, new software features, updates and training seminars by email, subscribe to the [genome-announce](#) mailing list.

### 15 May 2012 - New Fugu (fr3) Assembly Now Available in the Genome Browser

We are pleased to announce the release of a Genome Browser for the October 2011 fugu, *Takifugu rubripes* (JGI v5.0, UCSC version fr3). Whole genome shotgun assembly was provided by the [International Fugu Genome Sequencing Consortium](#), led by JGI and the [Singapore Institute of Molecular and Cell Biology](#) (IMCB).

Bulk downloads of the sequence and annotation data are available via the Genome Browser [FTP server](#) or the [Downloads](#) page. These data have [specific conditions for use](#). The fugu (fr3) browser annotation tracks were generated by UCSC and collaborators worldwide. See the [Credits](#) page for a detailed list of the organizations and individuals who contributed to the success of this release.

# UCSC Genome Bioinformatics

Genomes - Blat - Tables - Gene Sorter - PCR - VisiGene - Proteome - Session - FAQ - Help

Genome  
Browser

ENCODE

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[Home](#) [Genomes](#) [Blat](#) [Tables](#) [Gene Sorter](#) [PCR](#) [Session](#) [FAQ](#) [Help](#)

## Human (*Homo sapiens*) Genome Browser Gateway

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).

Software Copyright (c) The Regents of the University of California. All rights reserved.

clade	genome	assembly	position or search term	gene	
Mammal	Human	Feb. 2009 (GRCh37/hg19)	GARS		submit

[Click here to reset](#) the browser user interface settings to their defaults.

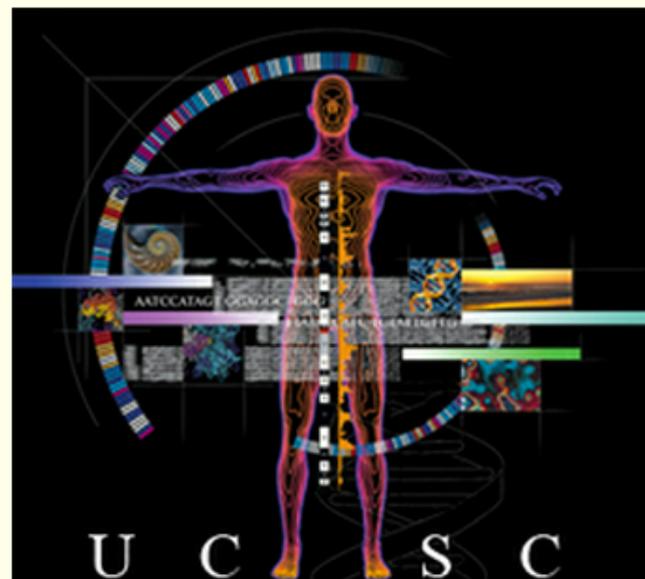
[track search](#)[add custom tracks](#)[track hubs](#)[configure tracks and display](#)[clear position](#)

### About the Human Feb. 2009 (GRCh37/hg19) assembly ([sequences](#))

The February 2009 human reference sequence (GRCh37) was produced by the [Genome Reference Consortium](#). For more information about this assembly, see [GRCh37](#) in the NCBI Assembly database.

#### Sample position queries

A genome position can be specified by the accession number of a sequenced genomic clone, an mRNA or EST or STS marker, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the human genome. See the [User's Guide](#) for more information.



## UCSC Genes

[GARS \(uc003tbm.3\) at chr7:30634181-30673648](#) - Homo sapiens glycyI-tRNA synthetase (GARS), mRNA.  
[GART \(uc010gmd.3\) at chr21:34876238-34915195](#) - Homo sapiens phosphoribosylglycinamide formyltransferase  
[GART \(uc002yrz.3\) at chr21:34876238-34915195](#) - Homo sapiens phosphoribosylglycinamide formyltransferase  
[GART \(uc002yry.3\) at chr21:34876238-34915198](#) - Homo sapiens phosphoribosylglycinamide formyltransferase  
[GART \(uc002yrx.3\) at chr21:34876238-34914464](#) - Homo sapiens phosphoribosylglycinamide formyltransferase

## RefSeq Genes

[GARS at chr7:30634181-30673648](#) - (NM\_002047) glycine--tRNA ligase precursor

## Non-Human RefSeq Genes

[gars at chr7:30638412-30672065](#) - (NM\_001093178) glycyI-tRNA synthetase  
[gars at chr7:30634682-30673476](#) - (NM\_001007491) glycyI-tRNA synthetase  
[GARS at chr7:30638412-30673476](#) - (NM\_001031510) glycine--tRNA ligase  
[GARS at chr7:30634449-30673645](#) - (NM\_001133870) glycine--tRNA ligase precursor  
[GARS at chr7:30634523-30673656](#) - (NM\_001097566) glycine--tRNA ligase  
[Gars at chr7:30634680-30673659](#) - (NM\_180678) glycine--tRNA ligase

## Basic Gene Annotation Set from ENCODE/GENCODE

[GARS at chr7:30634297-30673649](#)

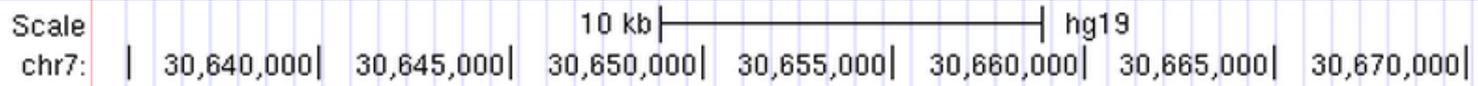
## Comprehensive Gene Annotation Set from ENCODE/GENCODE

[GARS at chr7:30634297-30673649](#)

# UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

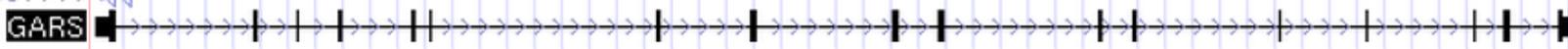
position/search chr7:30,634,181-30,673,648 gene  jump clear size 39,468 bp. configure



UCSC Genes (RefSeq, UniProt, CCDS, Rfam, tRNAs & Comparative Genomics)

LOC401320  
DJ031144

**GARS**



RefSeq Genes

RefSeq Genes



Human mRNAs

Human mRNAs from GenBank



Spliced ESTs

Human ESTs That Have Been Spliced



Layered H3K27Ac

H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE



DNase Clusters

Digital DNaseI Hypersensitivity Clusters from ENCODE



Txn Factor ChIP

Transcription Factor ChIP-seq from ENCODE



Mammal Cons

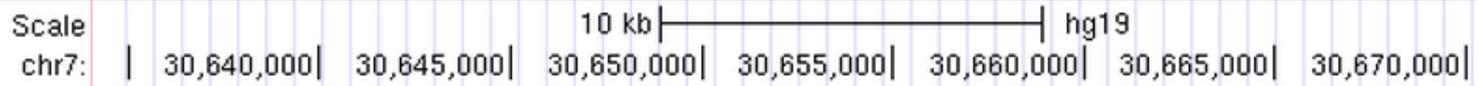
Placental Mammal Basewise Conservation by PhyloP



# UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr7:30,634,181-30,673,648 gene  jump clear size 39,468 bp. configure



UCSC Genes (RefSeq, UniProt, CCDS, Rfam, tRNAs & Comparative Genomics)

LOC401320  
DJ031144

**GARS**



RefSeq Genes

RefSeq Genes

Human mRNAs

Human mRNAs from GenBank

Spliced ESTs

Human ESTs That Have Been Spliced

Layered H3K27Ac

H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE

DNase Clusters

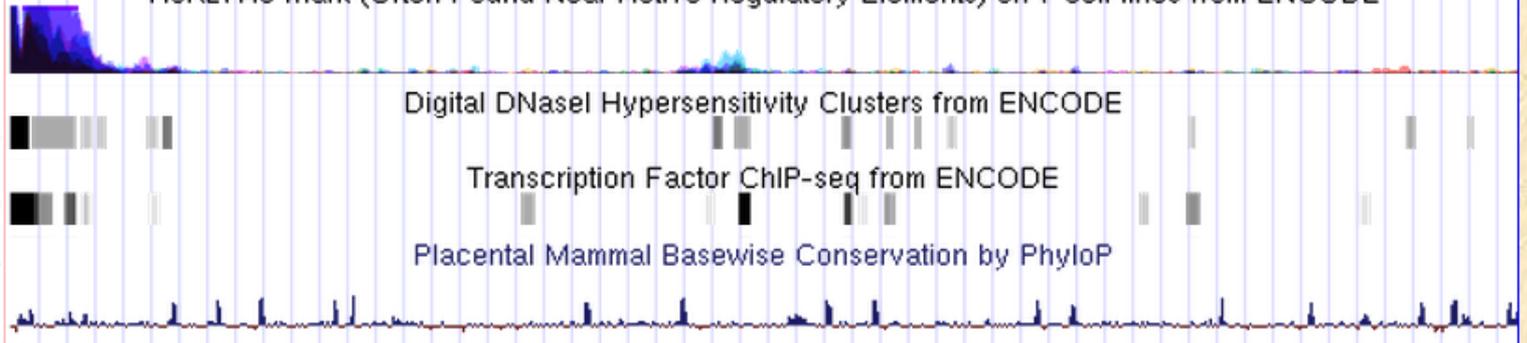
Digital DNaseI Hypersensitivity Clusters from ENCODE

Txn Factor ChIP

Transcription Factor ChIP-seq from ENCODE

Mammal Cons

Placental Mammal Basewise Conservation by PhyloP



# UCSC In-silico PCR

- Quickly check where your primers map in a genome.
- <http://genome.ucsc.edu/cgi-bin/hgPcr?db=hg19>

UCSC In-Silico PCR

genome.ucsc.edu/cgi-bin/hgPcr?db=hg19

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### UCSC In-Silico PCR

Genome:  Assembly:  Target:  Forward Primer:  Reverse Primer:

Max Product Size:  Min Perfect Match:  Min Good Match:  Flip Reverse Primer:

### About In-Silico PCR

Any Questions?

# SCIENCE SKILLS BOOT CAMP ANIMAL MODELS

---

Rocio Benabentos

[benabentosr@mail.nih.gov](mailto:benabentosr@mail.nih.gov)

# What is an animal model?

- A living organism
- Used to obtain information about other species (including humans) that are more difficult to study directly
- Possesses a biological or pathological process closely resembling the same phenomenon in man
- Widely studied because they are easy to maintain in the lab and have specific experimental advantages

# Why do we use model organisms?

- They provide insight into biological processes, through their highly developed methods of analysis
- They can be used for investigation of medical problems (even if they seemingly have little to do with them)
- They allow us to sort out biological complexity
- Allow us to understand genetic diversity and how small changes in the genome can produce different traits
- They remain in the forefront of developing new technologies

# Group Activity

- Assemble in groups of 4-5 students
- In 3 minutes, write as many examples Animal Models or Model Organisms used in biomedical research

# Nonhuman Primates

## Characteristics

- Close similarity to humans- perfect for complex physiological and behavioral phenotypes
- Close to humans in tissue structure, immune system, physiology and metabolism
- High cost
- Low availability



# Mouse (*Mus musculus*)

## Characteristics

- Mammal
- Small and relatively easy to maintain
- Generation time: 10 weeks
- Genetically identical strains routinely used
- Transgenic mouse models (knock-out or knock-in) available: good disease models



# Zebrafish (*Danio rerio*)

## Characteristics

- Vertebrate
- Small and relatively easy to maintain
- Generation time: 3 months
- High number of offspring (hundreds)
- Good number of mutants available
- Genes can be knockdown by injection
- Eggs are clear- development can be seen



# Fruit fly (*Drosophila melanogaster*)

## Characteristics

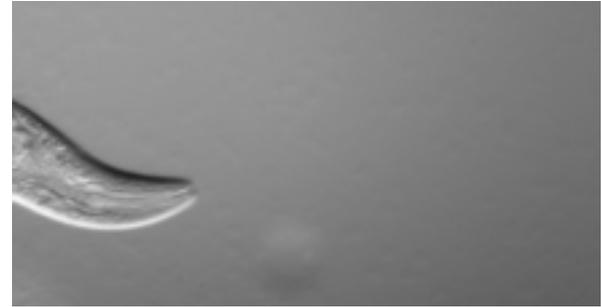
- Invertebrate
- Short generation time: 14 days
- Easy and cheap
- Large number of offspring (hundred+)
- Elegant genetics (forward and reverse)
- Large library of genetic mutants
- Foreign DNA can be introduced
- Comparative Genomics: Genomes of several *Drosophila* species known
- Can not freeze
- Homologous recombination still not easy- for targeted gene knockout



# Worms (*Caenorhabditis elegans*)

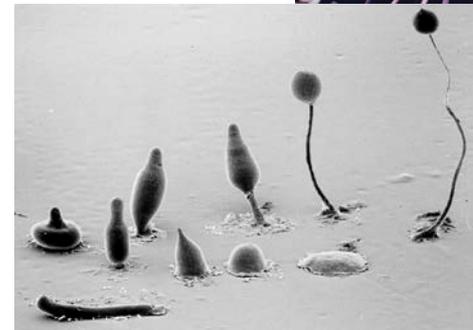
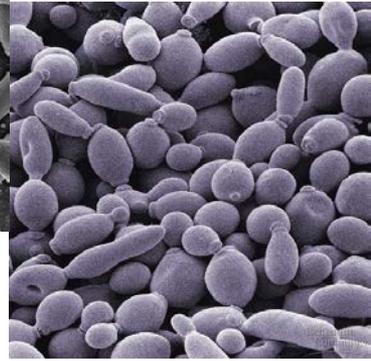
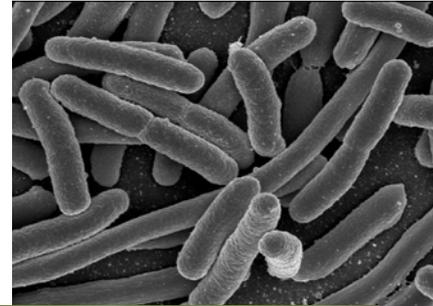
## Characteristics

- Invertebrate, small
- Short generation time: 3 days
- Easy and cheap to grow in bulk
- Can be stored as frozen stock
- 2 sexes and hermaphrodites= good for genetic mating and selfing experiments
- Large library of genetic mutants
- Foreign DNA can be introduced
- Large number of offspring (hundreds+)
- Fate of 959 cells known



# Other model organisms- great for basic biology!

- *Escherichia coli* (Prokaryotic)
  - DNA repair
  - Translation regulation
  - Transcription control
- Yeast (Eukaryotic)
  - *Saccharomyces cerevisiae*
  - *Schizosaccharomyces pombe*
  - Cell cycle regulation
  - Telomeres
  - Systems approach
- Plants (*Arabidopsis thaliana*)
  - Cellular Biology
  - Environmental studies
- Sea urchin (*Stongycentrotus purpuratus*)
  - Developmental Biology studies (gene networks)
- Social amoeba (*Dictyostelium discoideum*)
  - Cell adhesion, chemotaxis, cell-communication
  - Evolution of multicellularity



# How to choose a model organism?

- What process are we studying?
- Is this process present in this model organism?
- Is it technically advantageous to use this model organism?

# What organisms would you choose if you are studying:

- Cancer?
- Aging?
- Eye Development?
- DNA repair?
- Neurodegeneration?

# Introduction to Microscopy

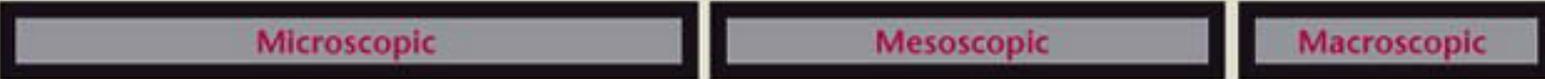


# Content

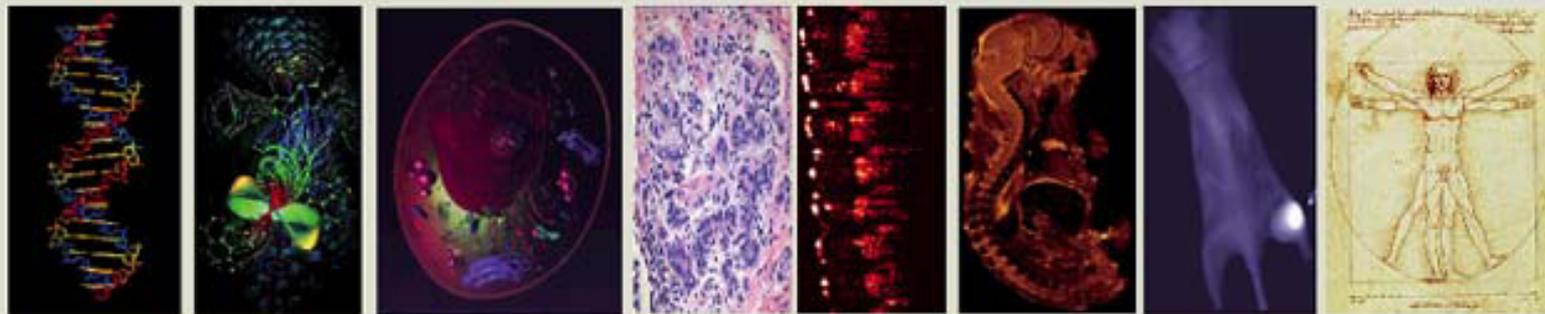
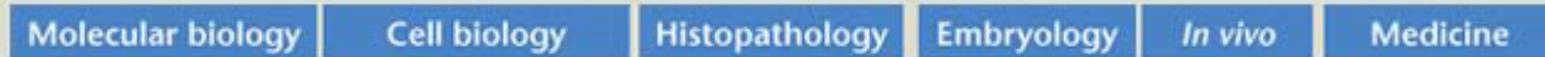
- How a light microscope works
  - Basic concepts related to light
  - The optical scheme of a light microscope
  - Fluorescence
- Examples:
  - Confocal microscopy
  - Electron microscopy
  - Super resolution microscopy

**Dimensions and complexity**

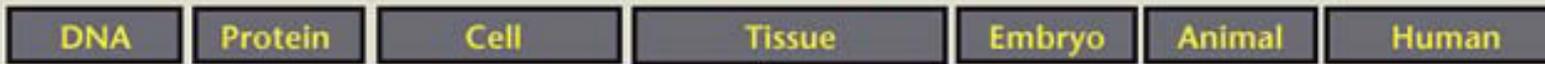
Imaging



Discipline

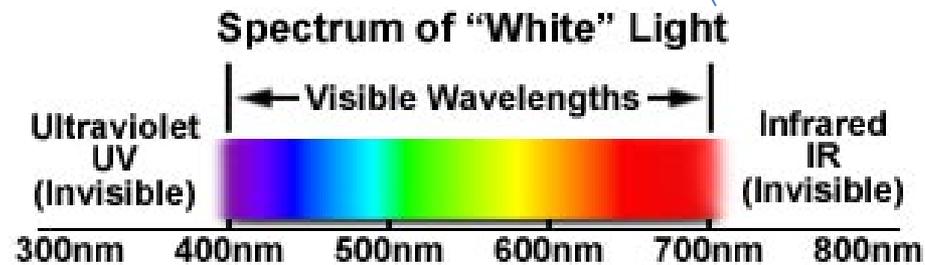
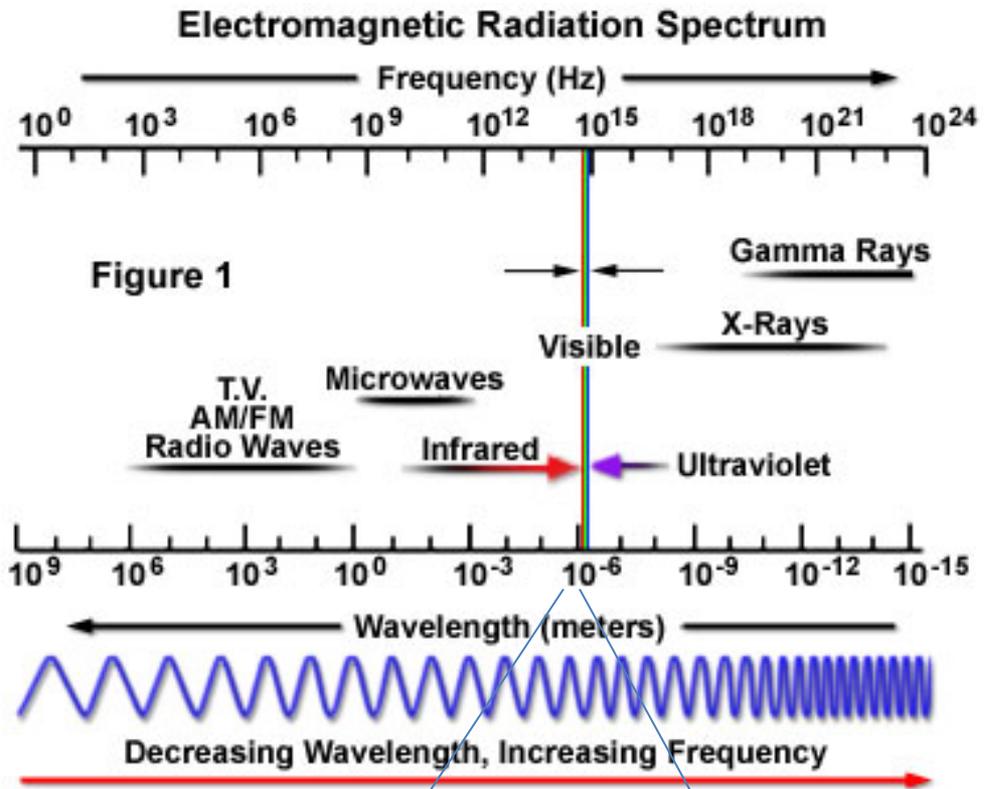


Hierarchical level



Information

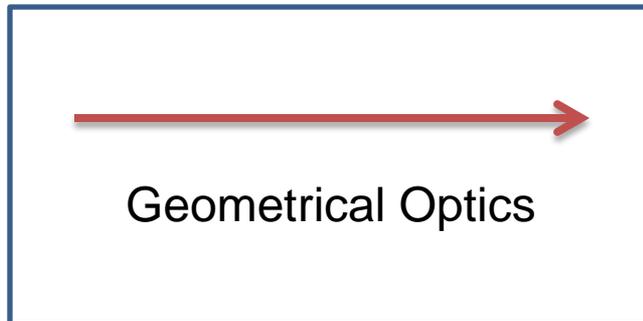
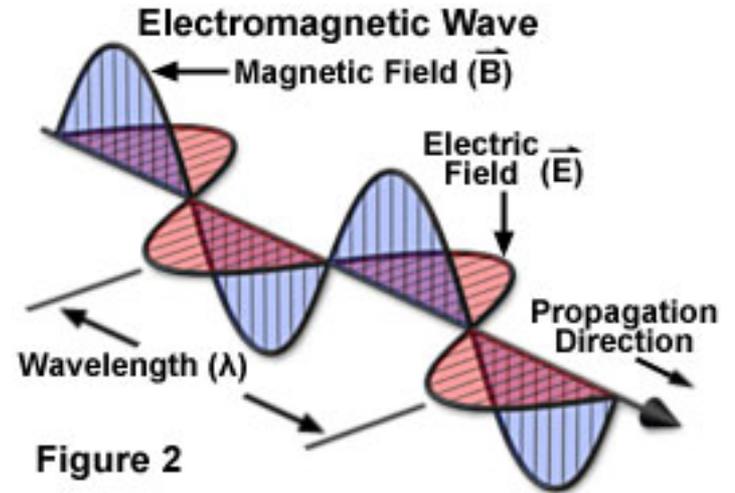
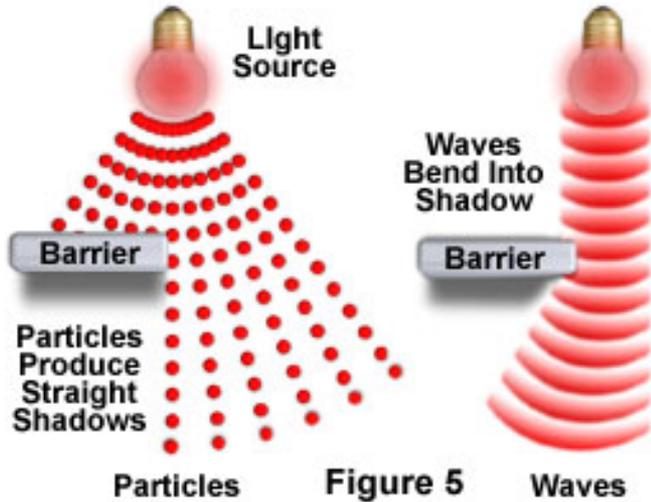




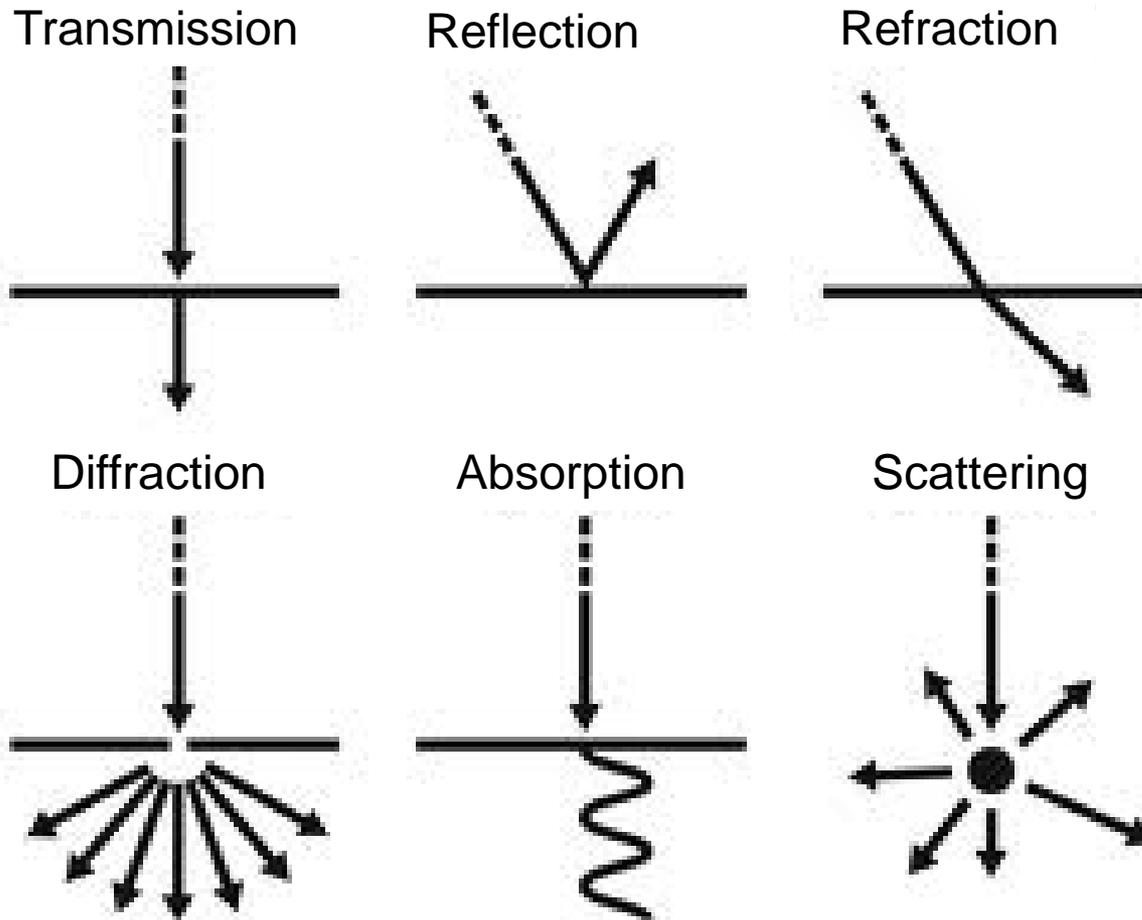
**Figure 2**

# Representation of light (EM radiation)

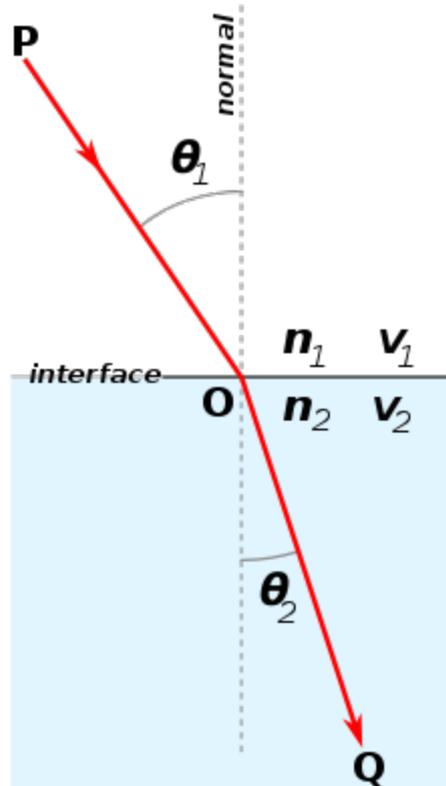
## Diffraction of Particles and Waves



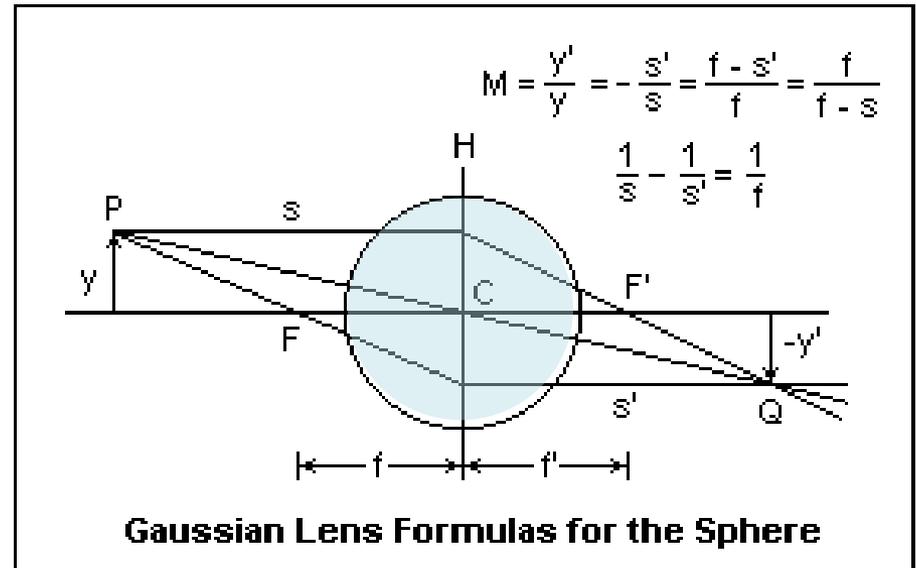
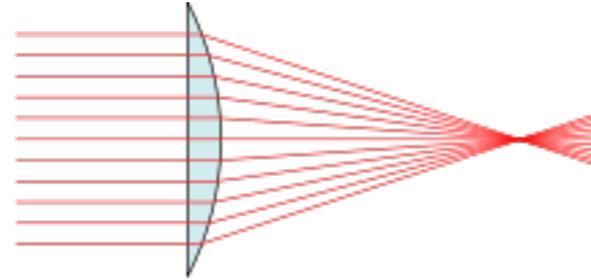
# Interaction of light and matter



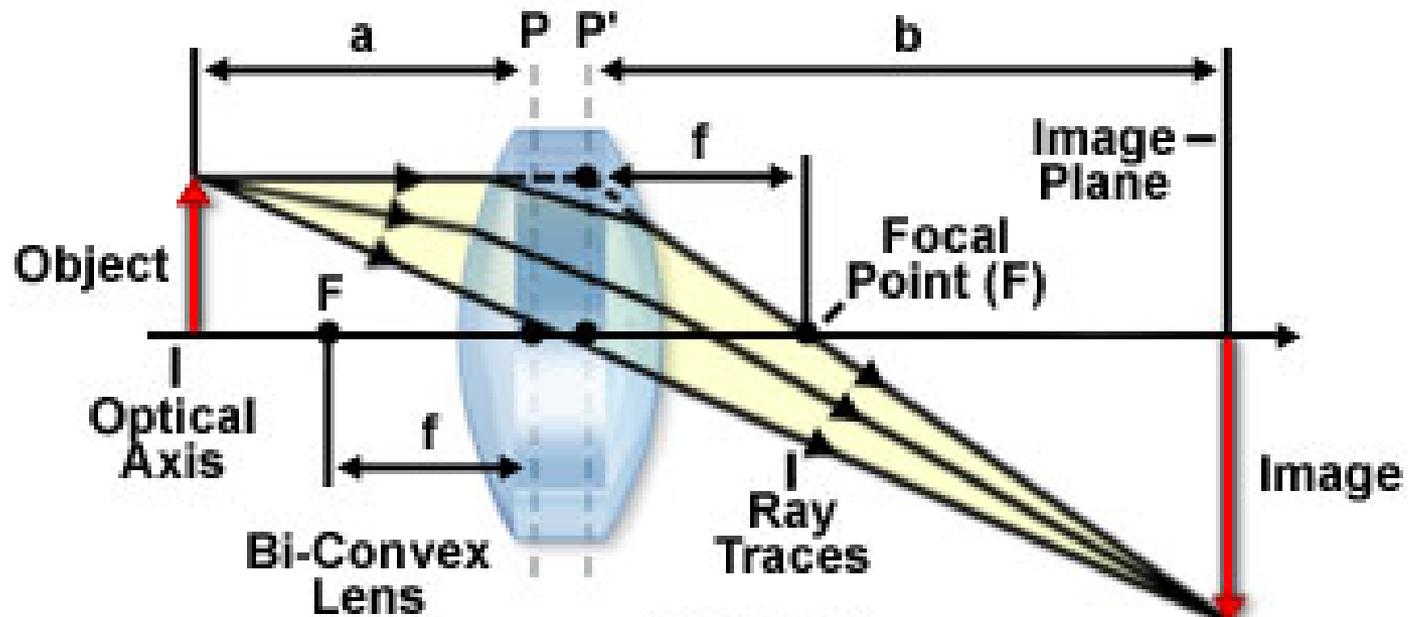
# Refraction, Snell's law and the lens



$$\frac{\sin \theta_1}{\sin \theta_2} = \frac{v_1}{v_2} = \frac{\lambda_1}{\lambda_2}$$



## Simple Thin Lens Geometrical Optics



$$M=b/a$$

## Conjugate Field Planes in the Optical Microscope

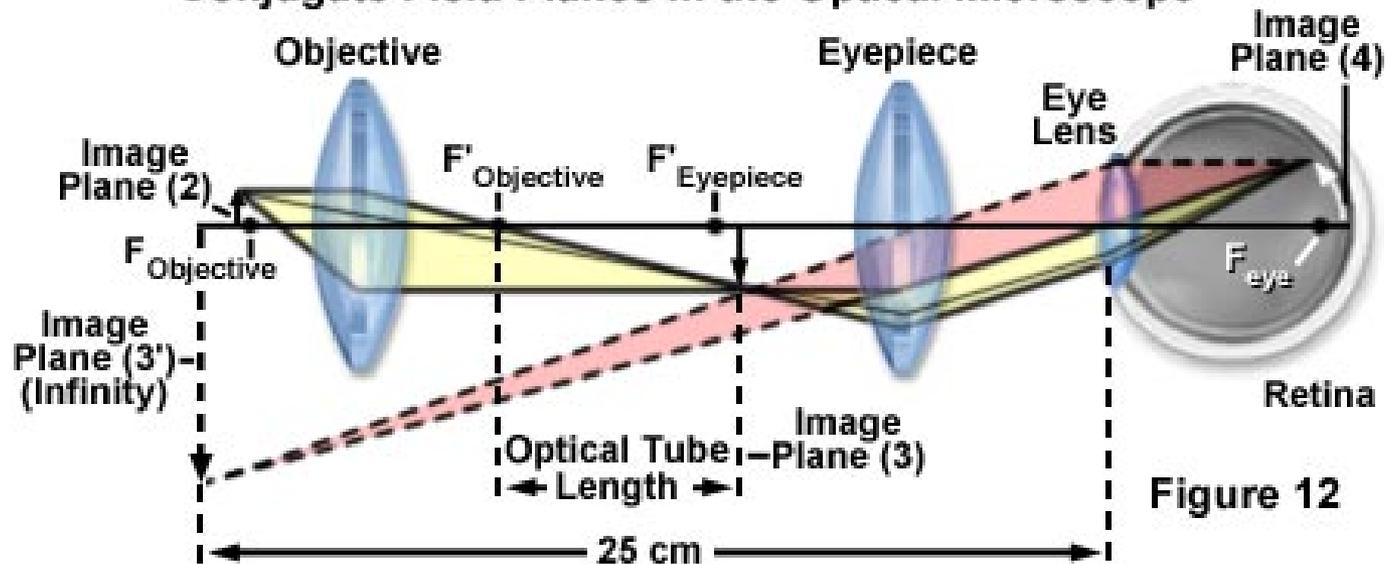


Figure 12

## Infinity-Corrected Microscope Optical Pathways

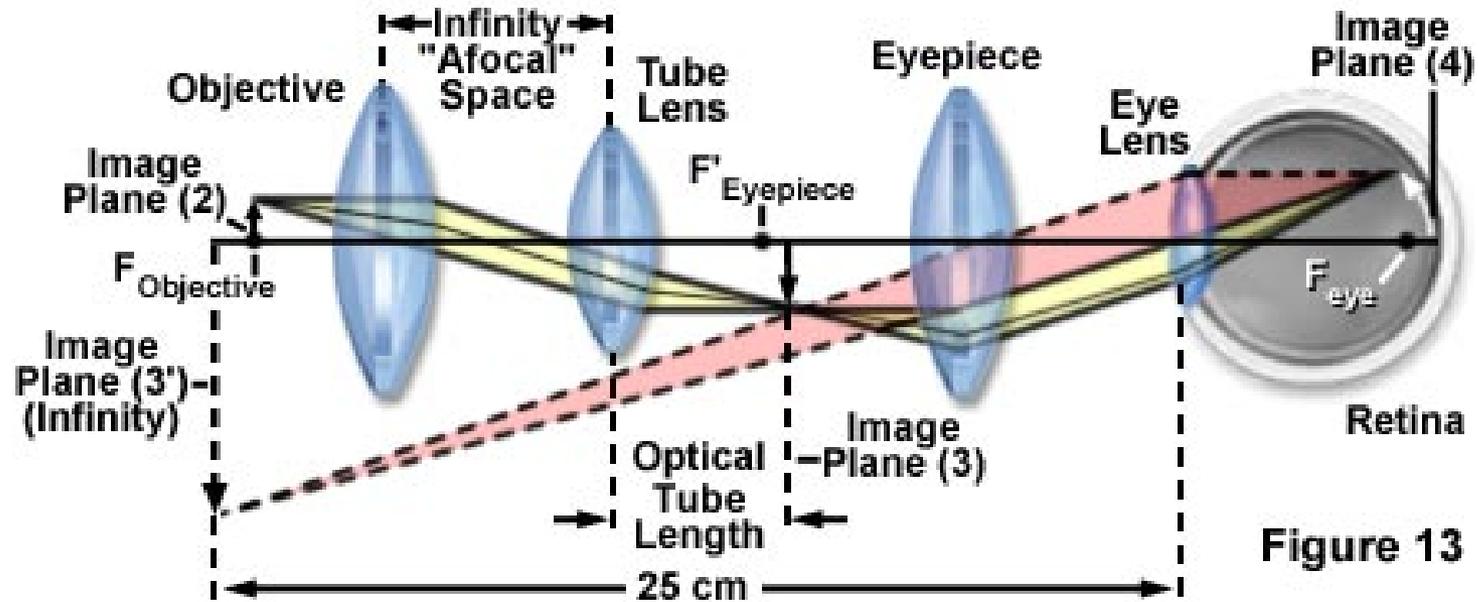


Figure 13



# Fluorescence

## Absorption and Emission of Radiation

Absorption

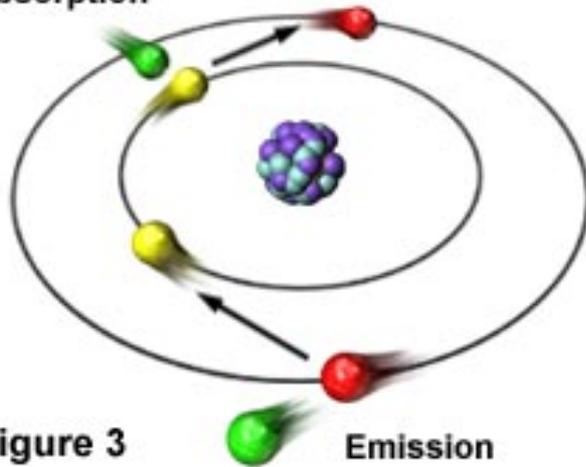
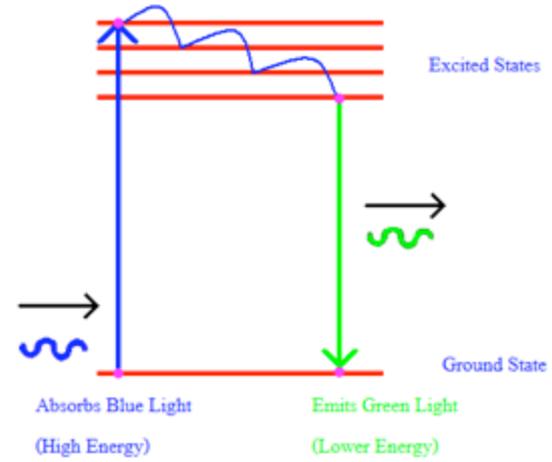
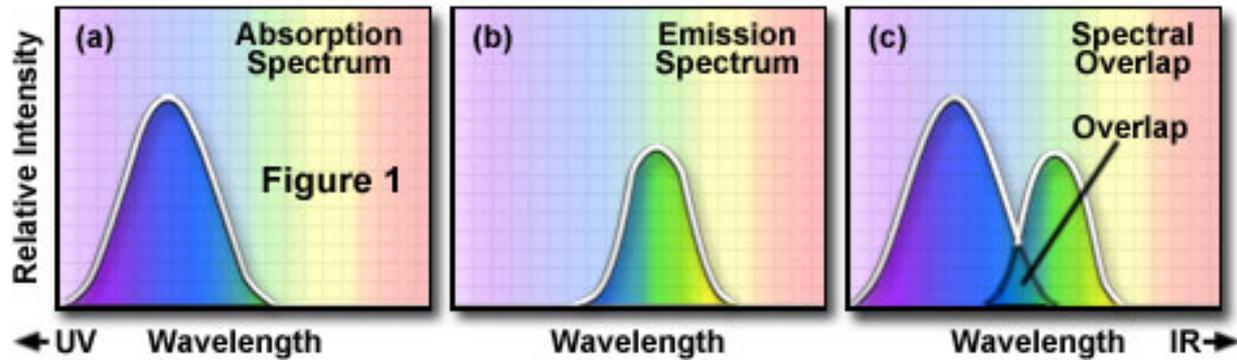


Figure 3

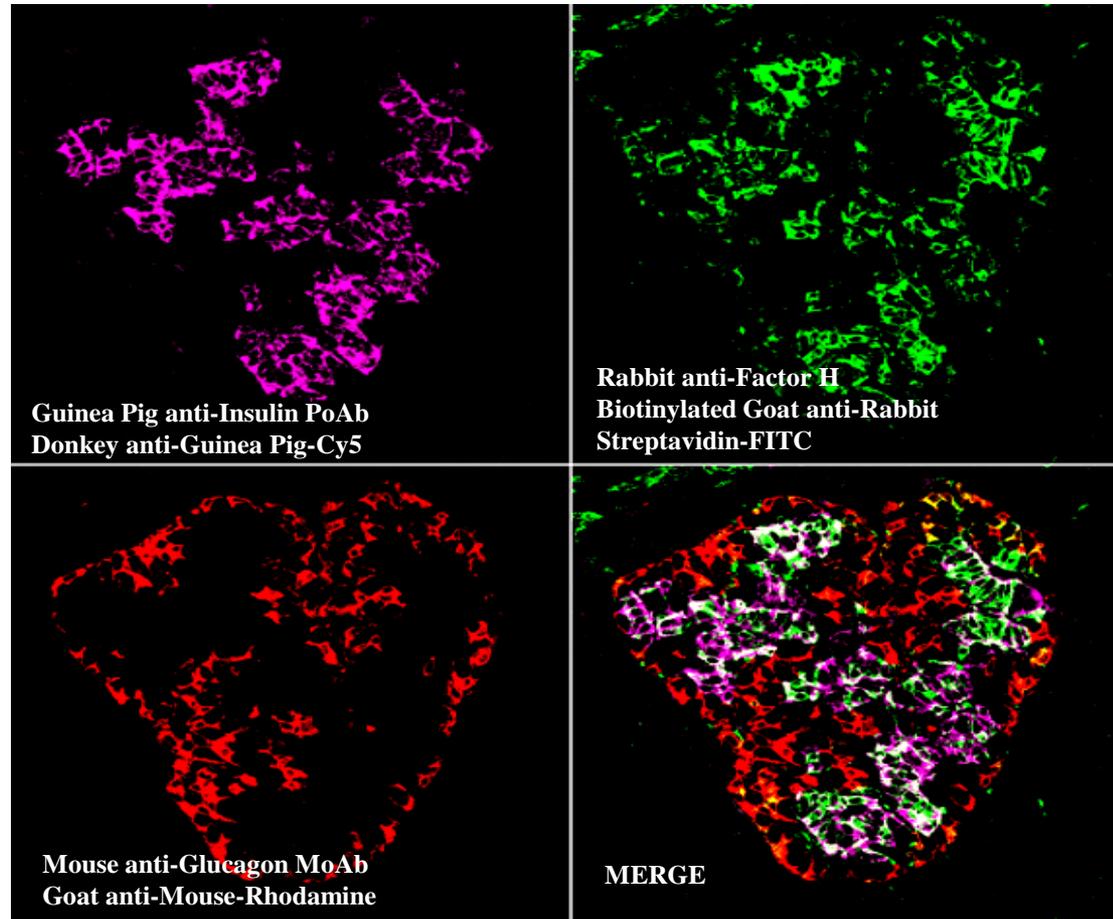
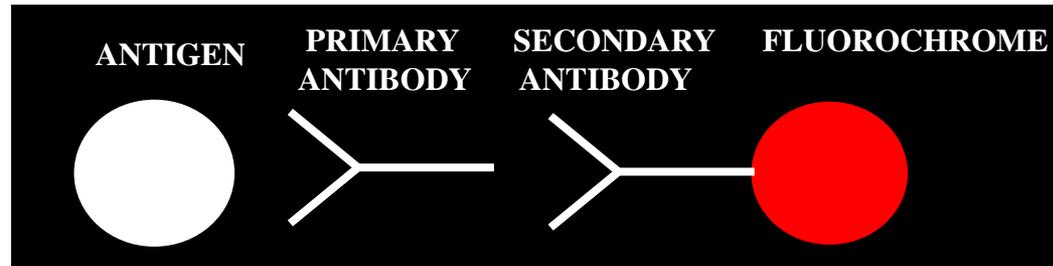
Emission



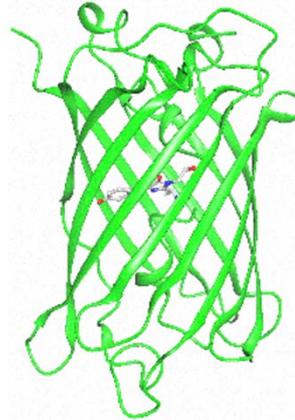
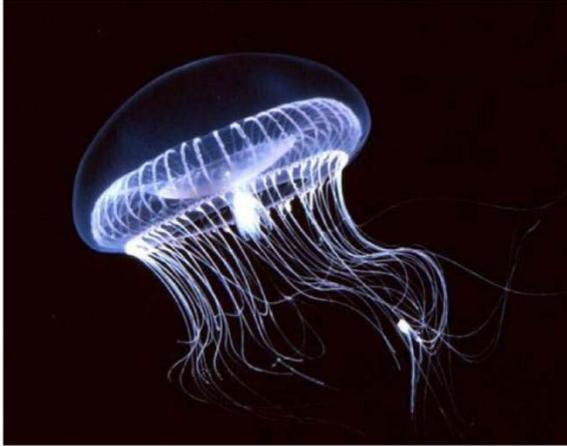
## Absorption and Emission Spectra with Overlap Profile



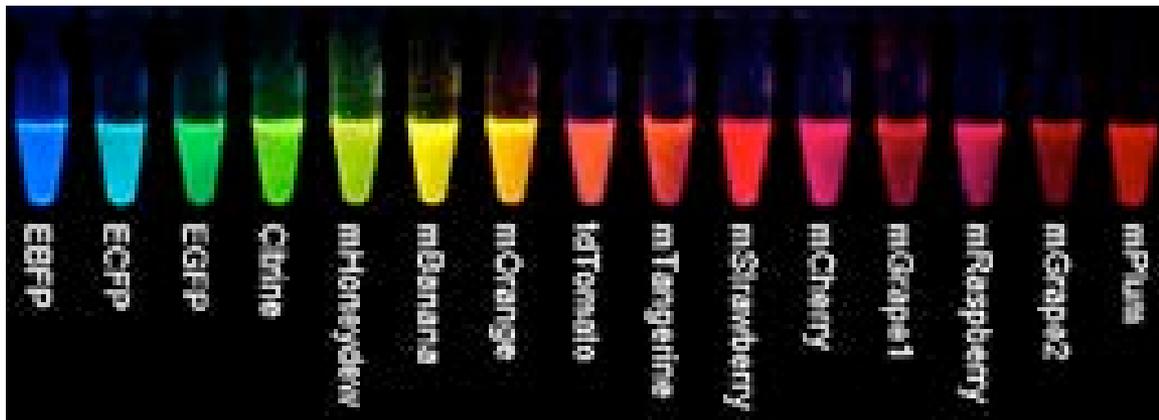
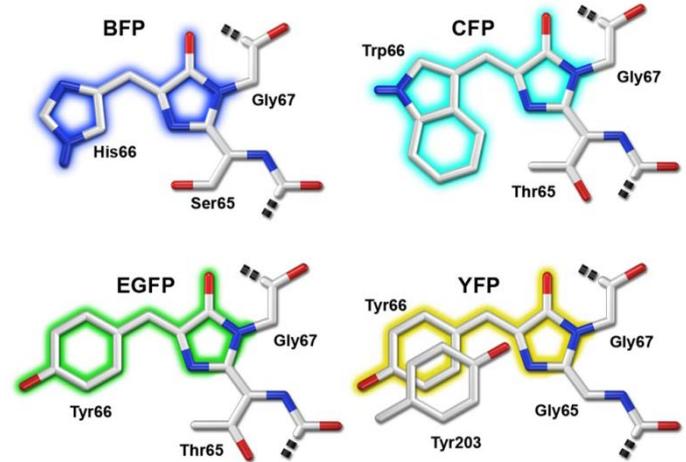
# Immuno-fluorescence



# GFP from *Aequorea victoria* (hydromedusa)

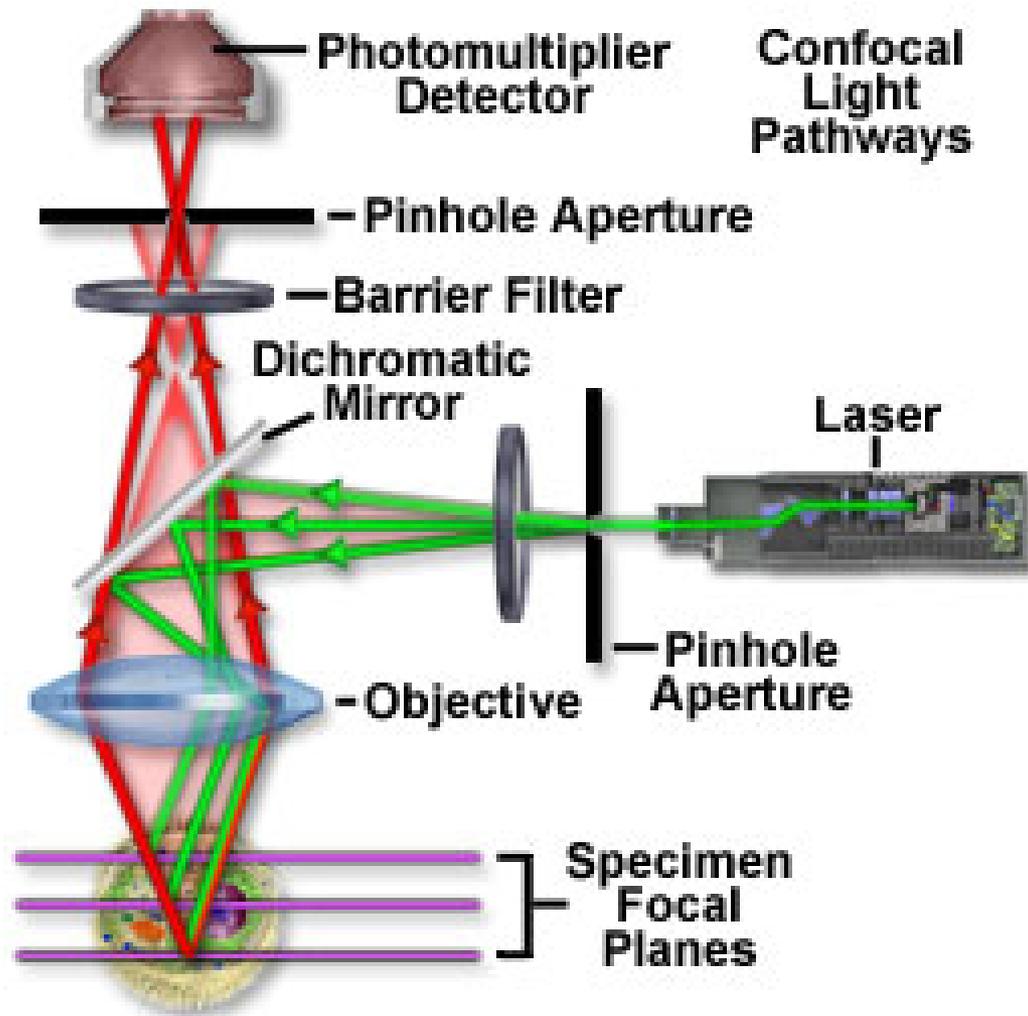


picture: Sophie Jackson, University of Cambridge



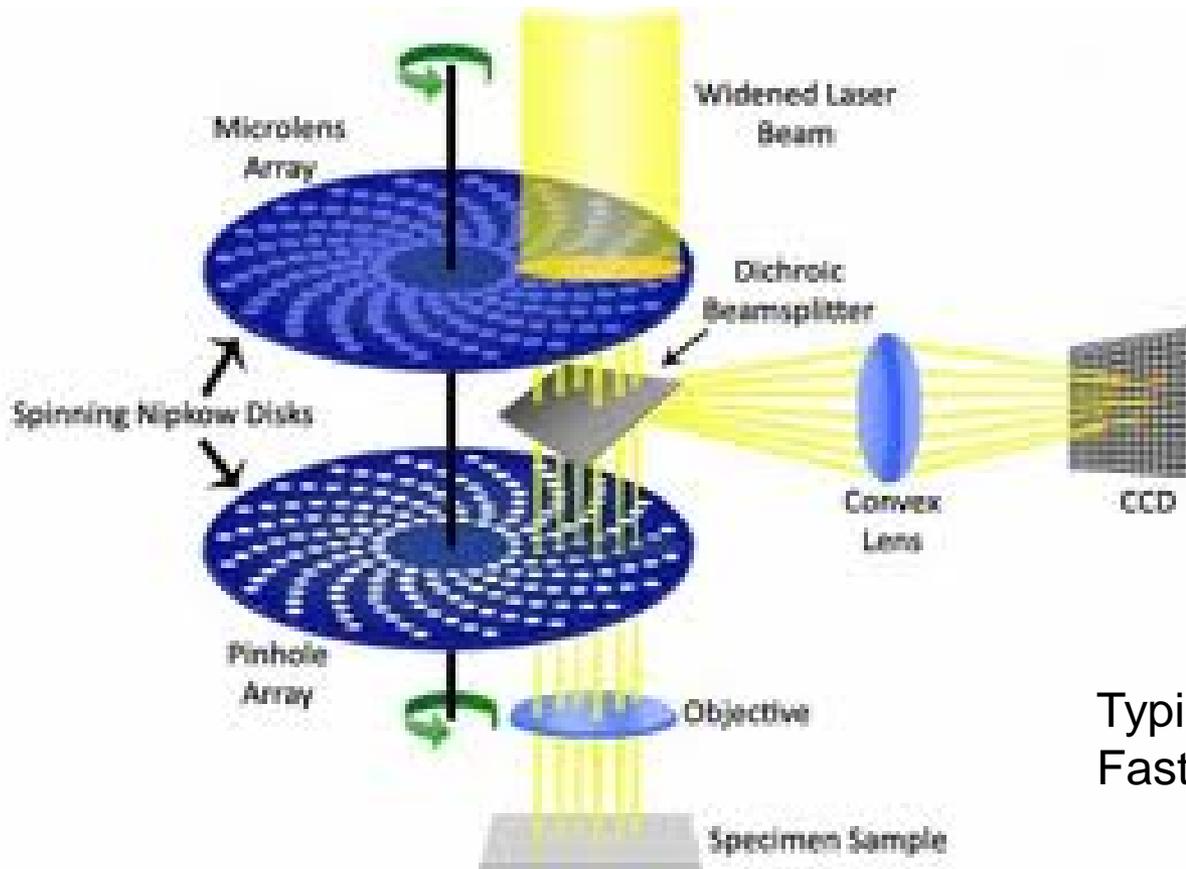
Typically used for  
Live cell imaging  
and genetic tagging

# The Confocal Microscope



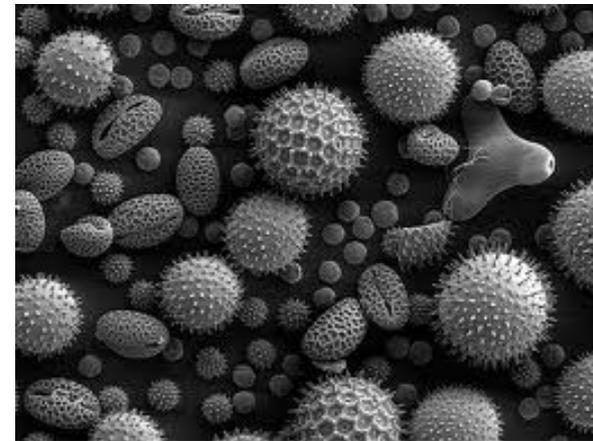
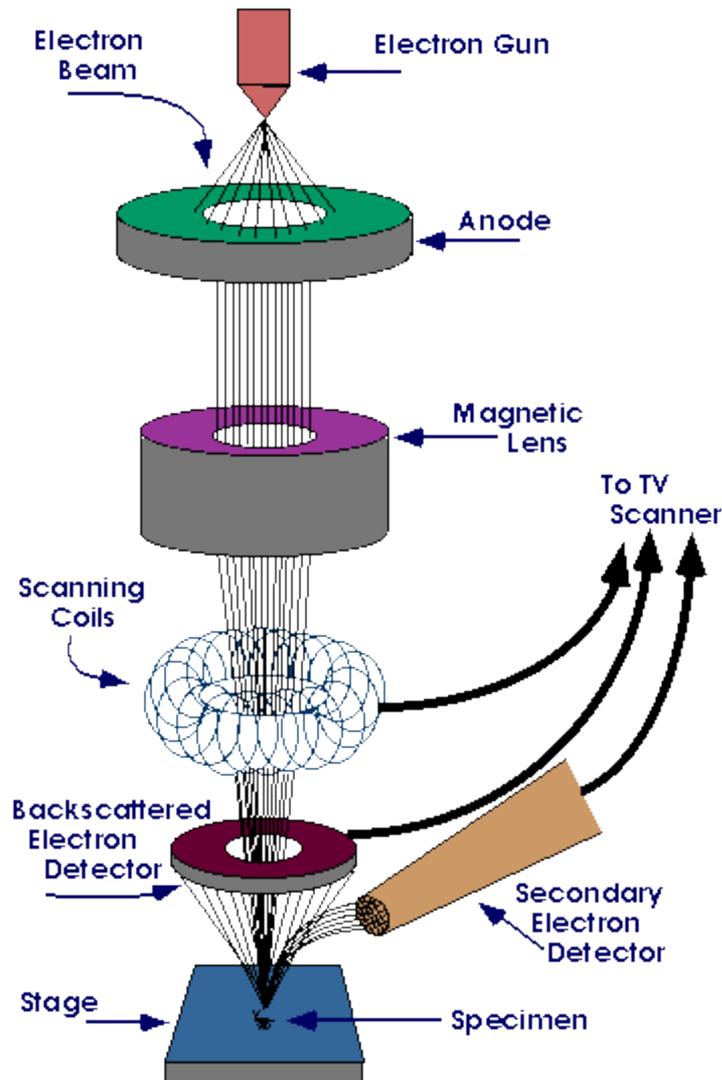
Typically used for  
Live cell imaging in 3D

# The Spinning-Disk Confocal Microscope



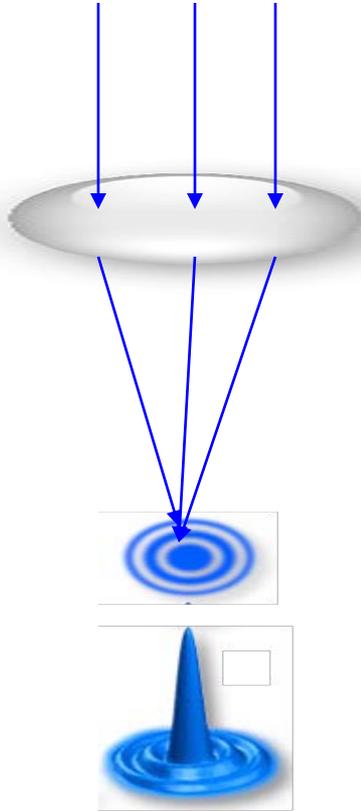
Typically used for  
Fast live cell imaging in 3D

# The Electron Microscope

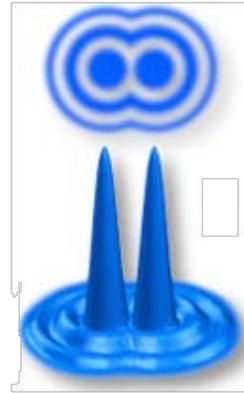


Typically used for  
Imaging fixed objects with resolution  
down to a few angstroms

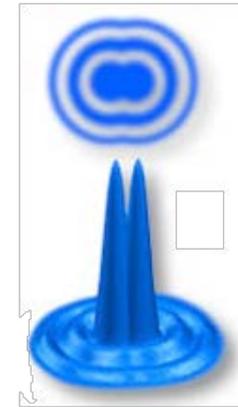
# The diffraction limit of light



The Airy Disc



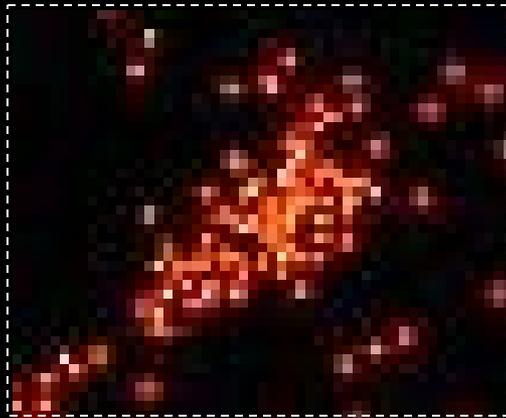
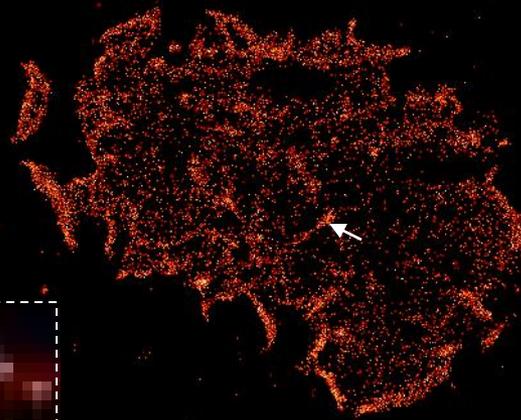
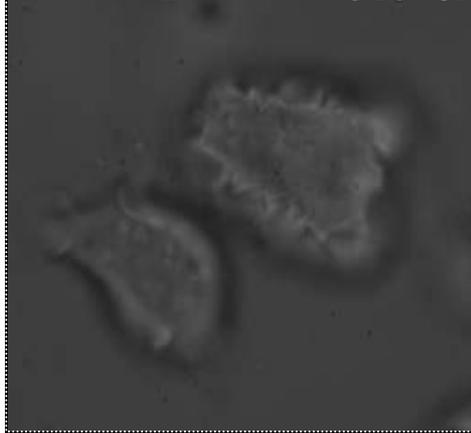
Resolved



Unresolved

$$r_o \approx \frac{0.47 \lambda}{NA} \sim 170nm$$

# PALM - Photo-activated localization microscopy

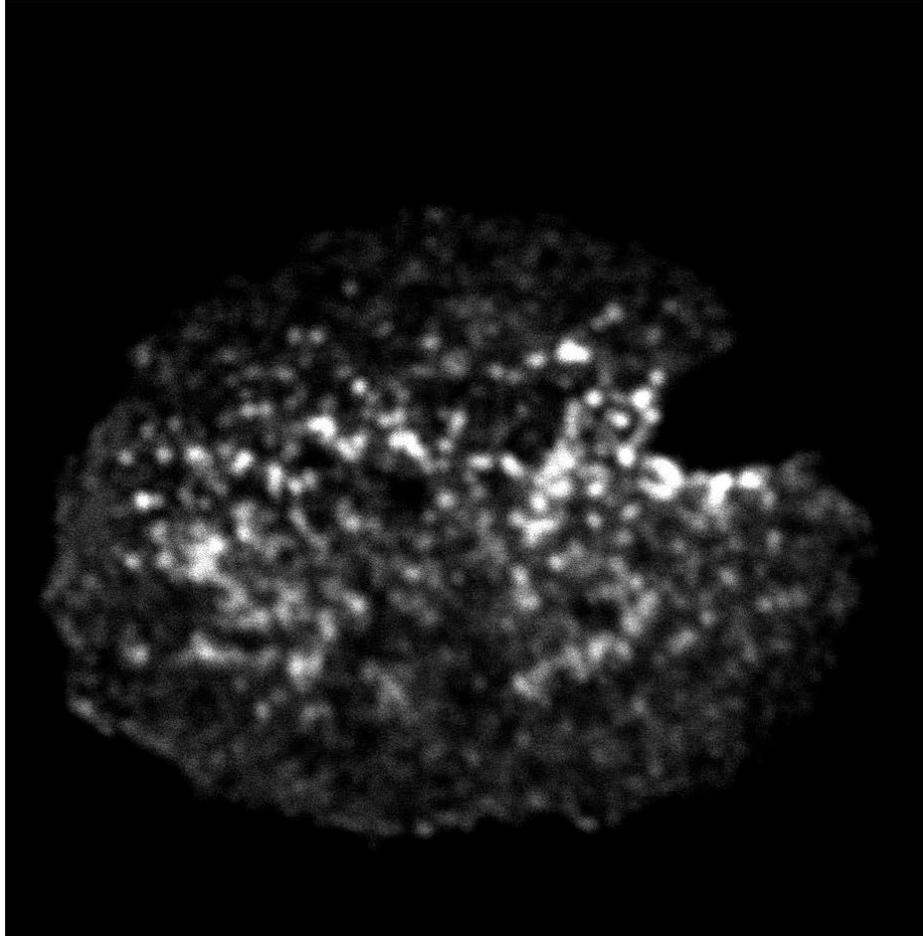


Typically used for  
Fixed cells, single molecule imaging  
Resolution down to ~20nm

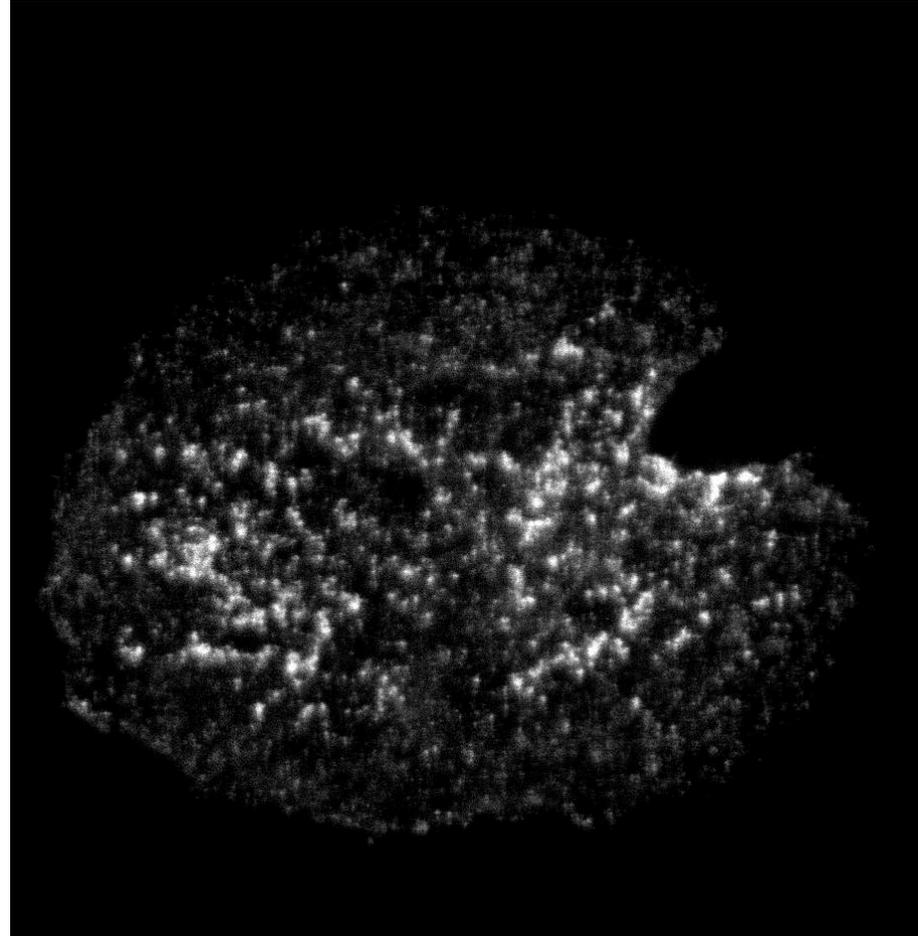
0.00000 0.00034 0.00278  
Envelope Fluor Molecule Probability /nm<sup>2</sup>

5.00 micron

Confocal



STED – Stimulated emission depletion



Typically used for  
Fixed cells, 3D imaging  
Resolution down to ~20nm

# Recommended resources

[www.olympusmicro.com](http://www.olympusmicro.com)

A great educational site with friendly primers, tutorials, and interactive tools

<http://www.invitrogen.com/site/us/en/home/support/Research-Tools/iPhone-Apps-and-Widgets.html>

Apps and tools for finding spectra of many fluorophores (**Fluorescence SpectraViewer**); requires Java

Optics. Hecht.

A basic and comprehensive book.

Principles of Fluorescence Spectroscopy. [Joseph R. Lakowicz](#)

A detailed reference book for advanced reading

Tutorial and manuals of your microscope!