Barry University

MESAplot - an open-source, dynamic interface for plotting MESA (Modules for Experiments in Stellar Astrophysics) data.
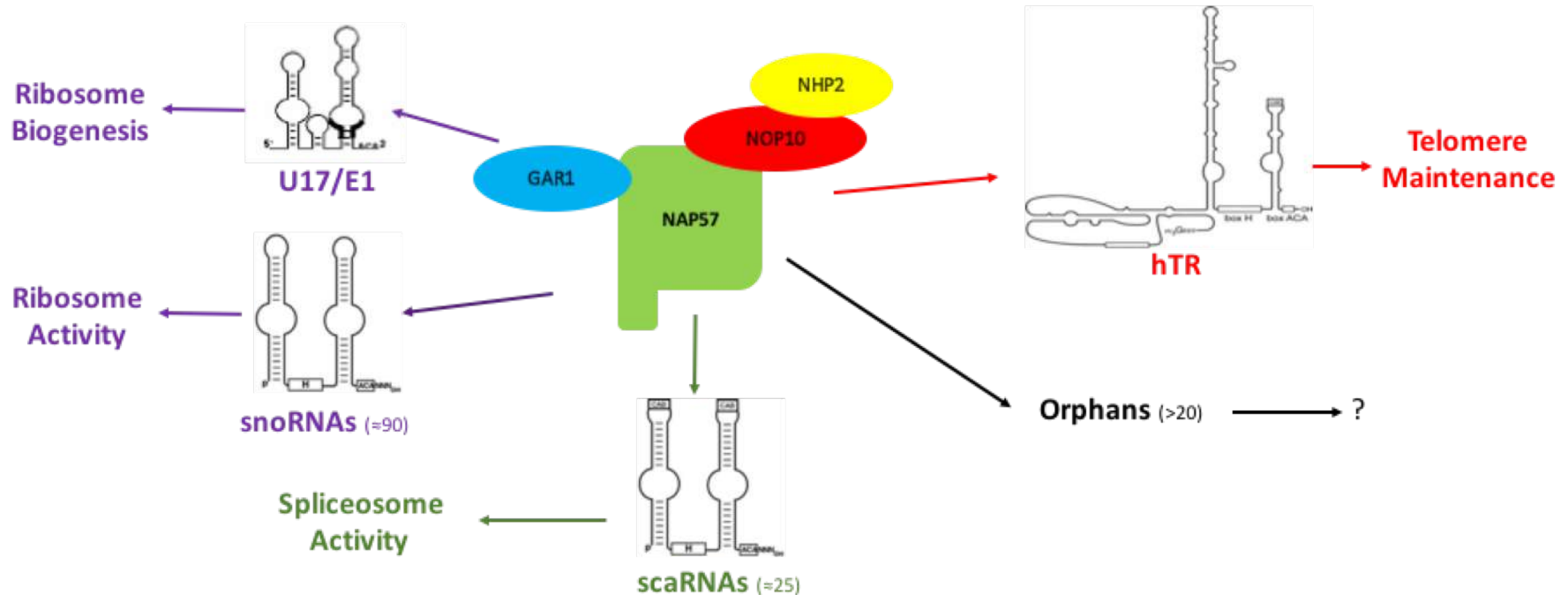

Invasive Species Population Modeling - Mathematical modeling of predator-prey populations in the Florida Everglades
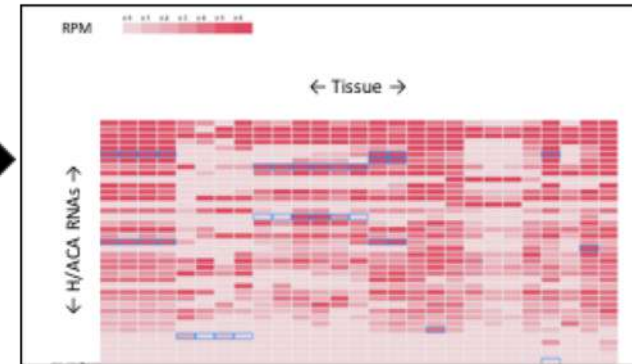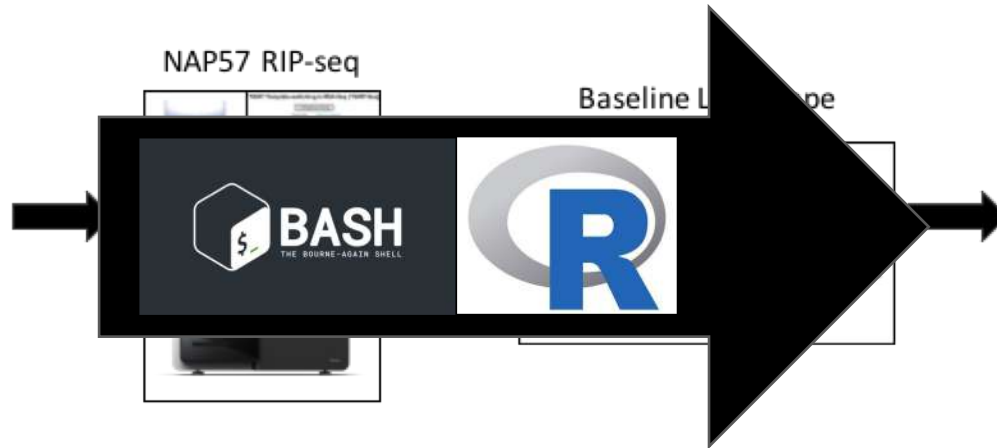
H/ACA RNA Functions

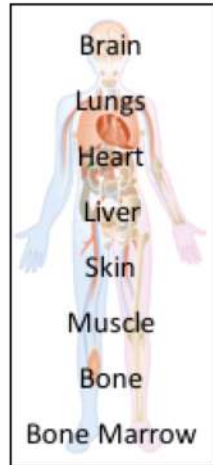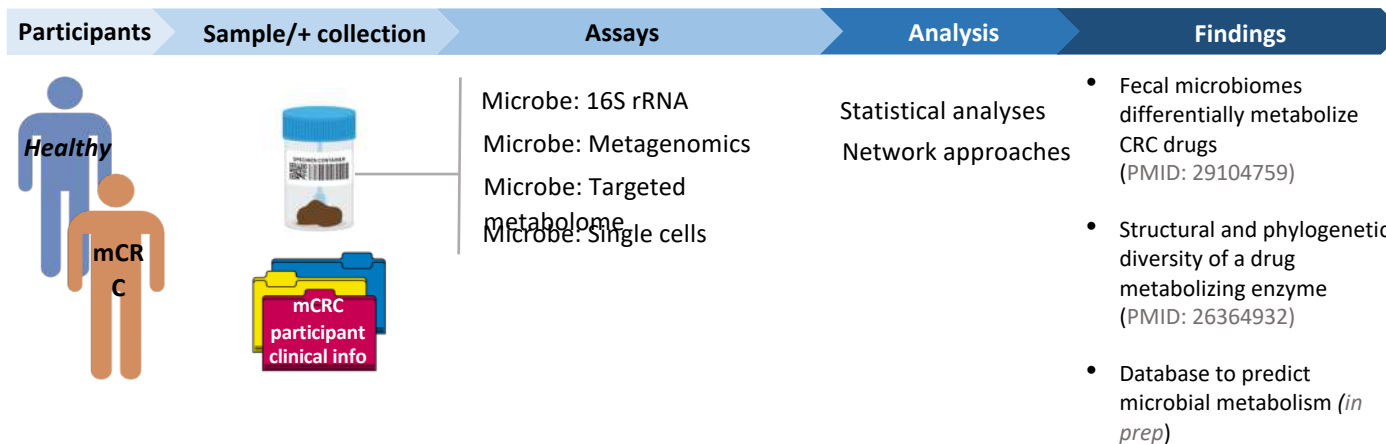Adopted from: Meier, U. Thomas. "The Many Facets of H/ACA Ribonucleoproteins." *Chromosoma*, vol. 114, no. 1, 2005, pp. 1–14.,

Exploring the H/ACA RNA Landscape in Various Healthy Human Tissues

Participants	Sample/+ collection	Assays	Analysis	Findings

Healthy

mCRC

mCRC participant clinical info

Microbe: 16S rRNA

Microbe: Metagenomics

Microbe: Targeted metabolome

Microbe: Single cells

Statistical analyses

Network approaches

- Fecal microbiomes differentially metabolize CRC drugs (PMID: 29104759)

- Structural and phylogenetic diversity of a drug metabolizing enzyme (PMID: 26364932)

- Database to predict microbial metabolism (in prep)

Metastatic colorectal cancer = mCRC

Labnotebook

Experimenta

labarchives
Chance Favors the Organized Lab

Computational

Weekly Log
Github
Markdown

leahguthrie updated notebook
5 contributor

263 lines (157 sloc) 7.5 KB

Start Entry # 8

Date Apirl 10-11, 2017

Project Aim4_Xeno_eco principles

Goals:

– Species level xenobiotic capacity analysis
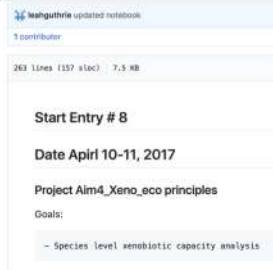
Project specific repositories
- Data
- Analysis
- Figures
- Presentations

GitHub

Online repository for sharing code managed with **git** (**Version control software**)

jupyter = R python JavaScript

docker

Network switch
Master node
Compute nodes
Users

Open source web application for creating and sharing code in your programming language of choice. Also can connect to different environments/platforms (Docker) and programs (Cytoscape).

- Graduate student in Dr. Aschner's lab (MolecPharm and Neuroscience)

  - Wet lab – *C. elegans* worm model used to investigate the neurotoxic effects of various heavy metals such as nickel, manganese and methylmercury.

  - Also interested in understanding the underlying causes of dopaminergic degeneration in Parkinson's disease with a focus on environmental toxicants.

P_{dat-1}::GFP

- Our lab is not computational at all. However, one of projects now seems like it will include some computational analysis of RNA-seq and microarray data.

- Takeaway: it's good to get your feet wet with programming now because you don't know when you might need it down the line.

Mahfuz Miah

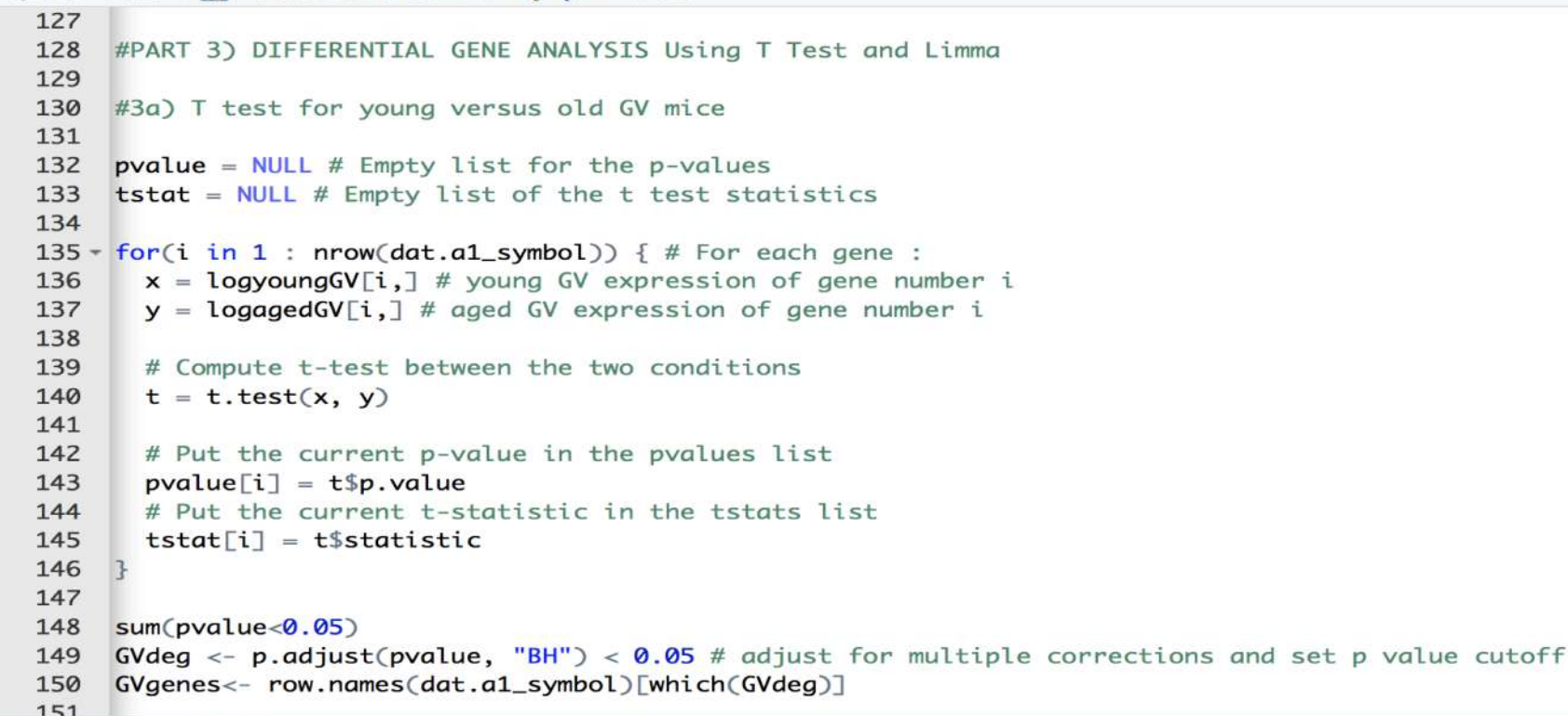|	gene expression in GV oocyte from aged mice, replicate 1	gene expression in GV oocyte from aged mice, replicate 2	gene expression in GV oocyte from aged mice, replicate 3	gene expression in GV oocyte from aged mice, replicate 4	gene expression in GV oocyte from young mice, replicate 1	gene expression in GV oocyte from young mice, replicate 2	gene expression in GV oocyte from young mice, replicate 3	gene expression in GV oocyte from young mice, replicate 4	gene expression in MII oocyte from aged mice, replicate 1	gen expr in M ooc fror mic repl
Copg1	129.24097	154.02830	152.19254	131.91518	125.32713	138.86231	122.82024	140.58685	118.78100	
Atp6v0d1	645.79100	630.28600	679.88700	711.89000	799.92800	708.61500	994.02800	906.01700	150.79900	
Golga7	2509.26000	2610.27000	2530.11000	2456.00000	2628.67000	2586.38000	2847.77000	2640.21000	2944.81000	
Psph	21.23260	30.88150	34.05110	5.73496	26.00440	43.02810	34.77710	42.70290	32.77800	
Trappc4	138.44954	133.84826	137.36144	130.71482	172.53835	206.28995	173.85260	177.03219	64.81708	
Dpm2	331.26700	297.65400	353.56500	383.76300	298.91600	366.34600	307.77500	343.10500	135.82300	
Psmb5	622.72100	565.65300	671.86200	671.81300	773.85700	834.88600	817.07000	861.41600	52.64490	
Dhrs1	152.70700	135.91200	225.14800	171.87900	162.53800	244.54200	258.89500	247.19800	421.74600	
Ppm1a	83.42978	83.18667	87.72543	98.44567	94.34183	83.11929	104.05327	91.47245	261.49045	
Psenen	4241.19000	3897.69000	4306.09000	4081.07000	4679.89000	3926.33000	3730.96000	4262.97000	3364.14000	
Anapc1	245.90187	230.33500	228.93614	222.97041	217.93367	204.74628	244.65119	226.53280	381.48383	
Mrpl43	136.37900	103.84500	110.28400	126.77400	177.19800	138.32400	154.66100	110.19500	4.74336	
Xpo7	514.78270	507.08140	588.60170	553.59154	525.20746	486.53038	534.65147	517.27637	428.48757	

Showing 1 to 13 of 22,406 entries

Console ~/Desktop/LabIII R/ ⇗

```
> rownames(dat.a1_symbol) <- unique(probe_to_symbol$SYMBOL)
> View(dat.a1_symbol)
> |
```
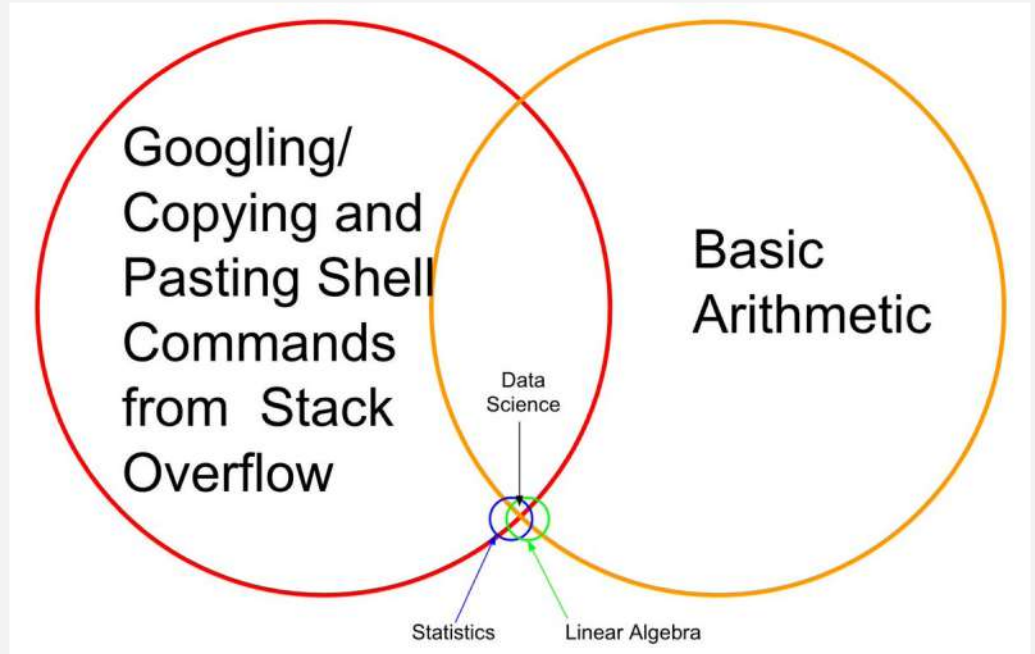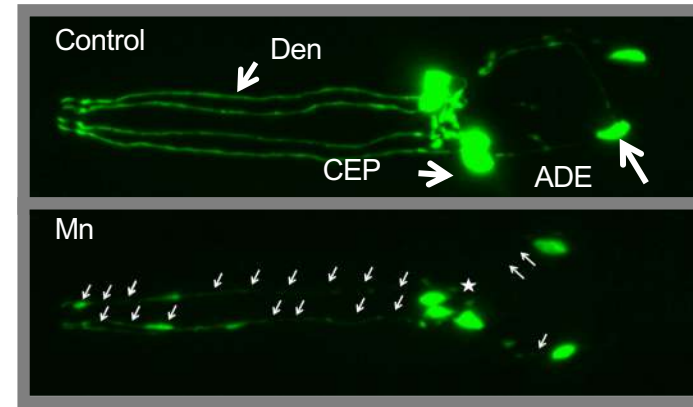
```r
127
128   #PART 3) DIFFERENTIAL GENE ANALYSIS Using T Test and Limma
129
130   #3a) T test for young versus old GV mice
131
132   pvalue = NULL # Empty list for the p-values
133   tstat = NULL # Empty list of the t test statistics
134
135 - for(i in 1 : nrow(dat.a1_symbol)) { # For each gene :
136     x = logyoungGV[i,] # young GV expression of gene number i
137     y = logagedGV[i,] # aged GV expression of gene number i
138
139     # Compute t-test between the two conditions
140     t = t.test(x, y)
141
142     # Put the current p-value in the pvalues list
143     pvalue[i] = t$p.value
144     # Put the current t-statistic in the tstats list
145     tstat[i] = t$statistic
146   }
147
148   sum(pvalue<0.05)
149   GVdeg <- p.adjust(pvalue, "BH") < 0.05 # adjust for multiple corrections and set p value cutoff
150   GVgenes<- row.names(dat.a1_symbol)[which(GVdeg)]
151
```

55:84   (Top Level) ÷

Console ~/Desktop/LabIII R/ ⇗
```
> rownames(dat.a1_symbol) <- unique(probe_to_symbol$SYMBOL)
> View(dat.a1_symbol)
>
```

Resources That I Use….

-R Studio

-GOOGLE!!!!

-datacamp.com

-Friends

- Graduate student in Dr. Aschner's lab (MolecPharm and Neuroscience)

  - Wet lab – *C. elegans* worm model used to investigate the neurotoxic effects of various heavy metals such as nickel, manganese and methylmercury.

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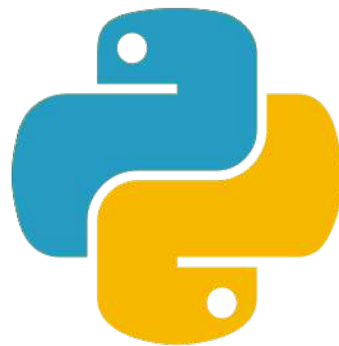

P_{dat-1}::GFP

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Mahfuz Miah

Saad Khan

Elise Ishida

3rd year PhD Student

Jacqueline Achkar's Lab

M & I / PCI

Research interests: Human antibodies and M.tuberculosis infection
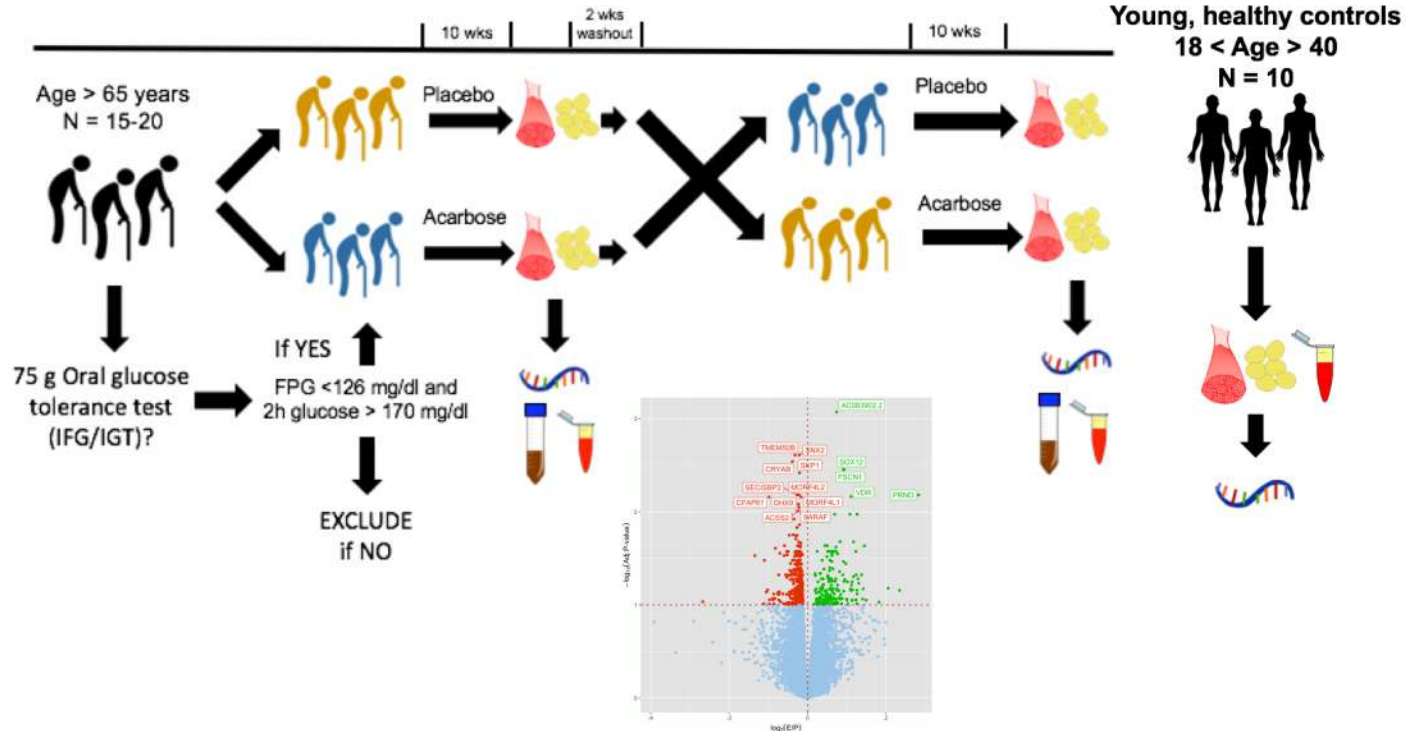
R coding level: very very basic

E-mail: eishida@mail.einstein.yu.edu

Ameya Kulkarni

4th year Ph.D. candidate - PCI track and Genetics
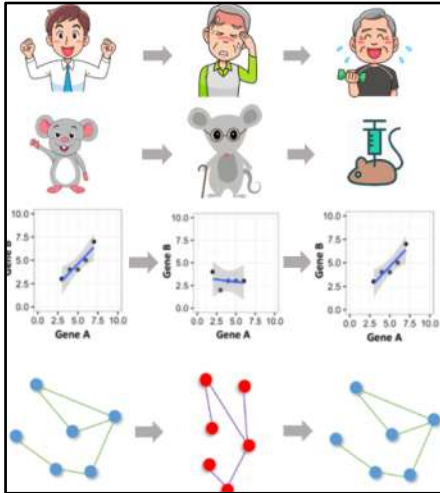Labs of Nir Barzilai, MD and Jessica Mar, Ph.D.
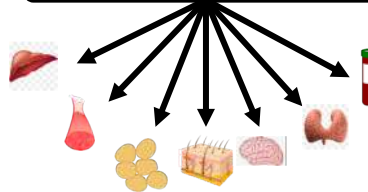
akulkarn@mail.einstein.yu.edu ; ameya225

Approaches and tools that I use/need/develop

Transcriptional Network Dynamics

		# of genes		# of samples	
GTEx / AGEMAP		**GTEx**	**AGEMAP**	**GTEx**	**AGEMAP**
		30303	8933	~200	~40

Gene expression data

Differential Gene Co-expression Analysis

1. Spearman correlation calculated
2. Fisher-transformed for normalization

$$z = \operatorname{atanh}(r) = \tfrac{1}{2} \log_e \left(\frac{1+r}{1-r} \right)$$

3. Differential correlation between age groups (Adj p < 0.05)
4. BH-corrected p-value calculated for diff correlation

Gene A   Gene B

Mitochondria

Immune system activity
and inflammation