

List of tasks for iNETgrate package

1. Drawing the **flow chart**, which will help - **Done**
2. **renaming** functions and variables, and - **In progress**
3. writing the **documentation** and - **In progress**
4. writing the **vignette**. - **In progress** -
Vignette is built successfully. Flow, functions and sample data available.
Explanation (English) needs work.
5. **Comparing** iNETgrate on AML and HCC with at least two other approaches e.g., a) Pigengene and b) similarity network [fusion](#).
6. Optionally, running iNETgrate on a third cancer, e.g., **lung cancer** on which Raheleh (cc'ed) is an expert.
7. Write a function called **prune()** that uses a greedy algorithm to reduce the number of genes in the selected module with negligible impact on the accuracy of the model (i.e. survival p-values). This would be similar to Pigengene::compact.tree() and ~/proj/dementia/code/Meghan/weed.proteins.R functions. If we do this, we've better rename the "pruned" variable in clean.RnBeads and possibly other functions to something else e.g., filtered. - Almost Done

Suggestions for renaming functions and variable names:

1. In compute.union(): newLocs -> unionLocs - **Done**.
2. In compute.eigenlocs : selectedLocs -> usefulLocs
warning("selectedLocs, which is a list of vectors, can be confused with selectedLocs
outout
of filter.low.cor.R, which is a vector. Change the name of this
variable to something else Eg. usefulLocs. Must be fixed in the 2nd
flowchart too.") - Done
3. Remove codes or functions from bitbucket, update.R, and locally that are obsolete and no more in use: **Done** - Commit ID: [d734937](#)
 - prepare.clinical.R
 - prepare.expression.R
 - createData.R
 - vignettes_script.R
4. Clean ~/proj/genetwork/code/Ghazal/Packing/data folder for all the obsolete data (Rdata files) from bitbucket as well as local machines. - Commit ID: [ee5d415](#) **Done**
 - a. Beta.RData
 - b. DeadPatientsTime.RData
 - c. cleaned.RData
 - d. clinical.RData
 - e. datalist

- f. dnamGene.RData
 - g. eigenloci.RData
 - h. exprData.RData
 - i. inputEvent.RData
 - j. inputMatrix.RData
 - k. inputTime.RData
 - l. lociPigen.RData
 - m. locus2gene.RData
 - n. sample2patient.RData
 - o. sampleInfo.RData
 - p. selectedLoci.RData
 - q. survival.RData
 - r. tokLocus2gene.RData
 - s. unionGenes.RData
5. We library packages in the following functions:
 - clean.RnBeads - library(RnBeads), library(RnBeads.hg19), require(scales)
 - Make.network - library(WGCNA)
 6. Add following functions to iNETgrate/Pigengene.
 - Prune function as explained [above](#).
 - Extract gene list from best modules identified
 - Perform pathway analysis
 7. Man files

Function Name	Assign	status
compute.union	Isha	
compute.eigenloci	Isha	
make.network	Ghazal	Done
survival.analysis	Ghazal	Done
best.inetgrator	Ghazal	Done
compute.distance.to.tss	Isha	
coxAnalysis	Ghazal	Done
accelFailAnalysis	Ghazal	In progress
find.alive.cutoff		
plotKM		
sensitivity.improvement. compute		

find.core		
compute.inetgrator		
download.data	Isha	
clean.RnBeads (replace by clean.Dnam)	Isha	
plotLoci.num	Isha	
prepare.survival	Isha	
sample.data	Ghazal	
preprocess.dnam	Isha	
filter.low.cor	Isha	
clean.Dnam	Isha	
compute.eigenLoci	Isha	

a.