RR Short Course Homeworks

Keith Baggerly

Day 1

Part 1

Write a minimal toy R package

- add a README
- add a vignette
- add some data
- Can you write a minimal R package in 15 minutes or less?

Part 2

Obtain the mutation information for your favorite gene from the TumorPortal

- do the mutation patterns differ by known subtypes? Some of these include estrogen receptor (ER) status in breast cancer (BRCA), HER2 status in BRCA, tissue source site in sarcoma (SARC), and serous/endometriod status in uterine cancer (UCEC).
- Are there other features of the data you'd like clarification on?
- write up your analysis as a vignette
- include your analysis and the TumorPortal data in an R package

Part 3

(Evening) Read Potti et al (2006), our letter and the response, and Brad Perez's letter.

- What would you do? Discuss.

Day 2

Part 1

Put your toy package in a git repository

- put the repository on github

- clone your neighbor's repository
- add a new function to your neighbor's package
- submit a pull request to add your package to his github repository
- incorporate your neighbor's suggested functions into your package

Part 2

- repeat part 1 with your mutation analysis
- do the mutation patterns differ by run batch?
- post it to github
- read and comment on your neighbor's analysis
- are there sanity checks you might employ?

Part 3

(Evening) Read Petricoin et al (2002), our Bioinformatics paper, and Leek et el (2010).

- Where have you encountered batch effects?
- Are there ways in testing for batch effects?
- What sanity checks do you employ regularly?

Day 3

Structure your Tumor Analysis *as a report*, and include your report in your package as a vignette

- Include an Executive Summary
- Include a Figure
- What do positive and negative numbers mean?
- include sessionInfo()
- post it to github
- read and comment on your neighbor's report