Getting help

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Course forums

JOHNS HOPKINS
BLOOMBERG SCHOOL
of PUBLIC HEALTH

Statistics for Genomic Data Science
by Jeff Leek, PhD

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0 votes	**1** answer	**19** views	**Statistics of DiffBind (How bamControl files and peak scores are considered)** diffbind written 22 hours ago by yfyuzawa • 0 • updated 3 hours ago by Rory Stark • 1.0k
0 votes	**1** answer	**16** views	**R crashes when computing score on data from mzIdentML file** mzr written 7 hours ago by Diego Diez • 530 • updated 4 hours ago by Laurent Gatto ♦ 530

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Replies
- A: readGAlignments + BamVie... by Valerie Obenchain ♦♦ 4.8k
- C: Copy Number Variation in... by voksdvoks • 0
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- A: Trouble with Ideogram Plots by florian.hahne@novartis.com • 900
- A: readGAlignments + BamVie... by arne.muller • 10

Votes
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- normalised data after RUV2()
- A: Extract specific contras...
- C: Extract specific contras...
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📃 Upcoming login changes (Stage 2 now LIVE)

🗒 Feedback Requested: Code Editor and Stack Snippets

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jtleek

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Hi I'm Jeff

I work on figuring out how to go from raw data from next generation sequencing machines to results, turning public genomic data into clinically useful tools, and understanding how people use data analysis in real life.

I do statistical research, write data analysis software, curate and create data sets, write a blog about statistics, teach people here at Hopkins, teach a lot of people online, and work with amazing students who go do awesome things. If you want to, come do stuff with me

If you want to keep up with everything we are working on, follow me on Twitter @jtleek. The best way to contact me is my gmail account (I do not check my JHU email at all), or you can call me at my office **410-955-1166** (fair warning I have answered that phone ~3 times total since 2009), send me a fax **410-955-0958** (for real, fax is still a thing?!), or if you still use the pony express you could send me a letter at:

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How to ask questions

Asking R questions

- What steps will reproduce the problem?

- What is the expected output?

- What do you see instead?

- What version of the product (e.g. R, packages, etc.) are you using?

- What operating system?

Asking data analysis questions

- What is the question you are trying to answer?

- What steps/tools did you use to answer it?

- What did you expect to see?

- What do you see instead?

- What other solutions have you thought about?

Emails/posts

- **Bad**

  a. HELP! Can't fit linear model!
  b. HELP! Don't understand PCA!
- **Better**

  a. R 2.15.0 lm() function produces seg fault with large data frame, Mac OS X 10.6.3
  b. Applied principal component analysis to a matrix - what are U, D, and V^T?
- **Even better**

  a. R 2.15.0 lm() function on Mac OS X 10.6.3 -- seg fault on large data frame
  b. Using principal components to discover common variation in rows of a matrix, should I use U, D or V^T?