

Fels Bioinformatics Meetup

What's a meetup? /
What's changing with meetups?

Last year's meetup

The original idea for the meetups was to have a kind of office hours every other week where anyone in Fels could ask questions and get help on computational analysis, but ended up switching to more formal lectures divided between two groups.

Problems:

- can't ask questions about what you don't know
- changes from one style to the other were made on the fly
- people were only coming once a month
- If you don't use it you lose it

Meetups going forward

- weekly
- short lecture
- focus on R
- homework for practice
- All materials will be hosted on a [Fels Bioinformatics Github repository](#)

Why should you learn programming and why R?

Programming data analysis for yourself gives you far more control, flexibility, and reproducibility than clicking in a graphical interface.

R is:

- Easy to learn
- Great community
- Only programming language intended from the beginning for data analysis

Getting Set Up with R

Need to Install

Instructions were in the email about today's meetup (and on the meetup GitHub [here](#)), but if you haven't already you need to install:

1. R
2. RStudio
3. tidyverse

Install R <https://www.r-project.org/>



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R Foundation

The R Project for Statistical Computing

Getting Started

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Install RStudio <https://www.rstudio.com/>



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RStudio

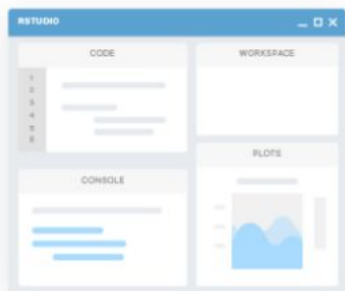
Open source and enterprise-ready professional software for R

[Download RStudio](#)

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RStudio

RStudio makes R easier to use. It



Shiny

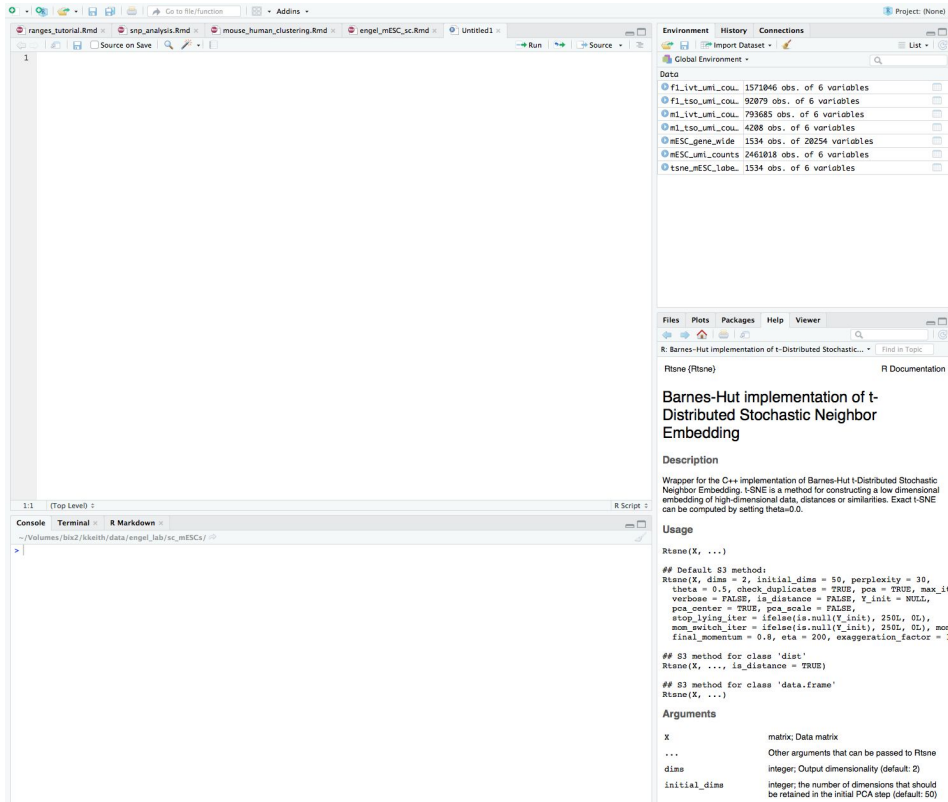
Shiny helps you make interactive web



R Packages

Our developers create popular packages

Install the tidyverse



The screenshot shows the RStudio interface. The Environment pane on the right lists several data objects: 'Data', 'fl_lvt_umi_cou.' (1571046 obs. of 6 variables), 'fl_tso_umi_cou.' (92079 obs. of 6 variables), 'ml_lvt_umi_cou.' (793685 obs. of 6 variables), 'ml_tso_umi_cou.' (4208 obs. of 6 variables), 'mESC_gene_wide' (1534 obs. of 28254 variables), 'mESC_umi_counts' (2461018 obs. of 6 variables), and 'tsne_mESC_labe.' (1534 obs. of 6 variables). The console at the bottom shows the command `install.packages('tidyverse')` being executed. The R Documentation pane on the right shows the documentation for the 'Rtsne' package, including a description and usage instructions.

1. Open RStudio
2. In the console, type the follow line:

```
install.packages('tidyverse')
```

3. And hit Enter
4. If it installs successfully, you'll a message saying:

The downloaded source packages are in
'some_folder/downloaded_packages'

Introduction to Rmarkdown

Why use markdown?

Bioinformatics analysis is mostly run on a Linux computer using the command line terminal. The rest of the universe uses Macs or PCs.

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This Causes Problems:

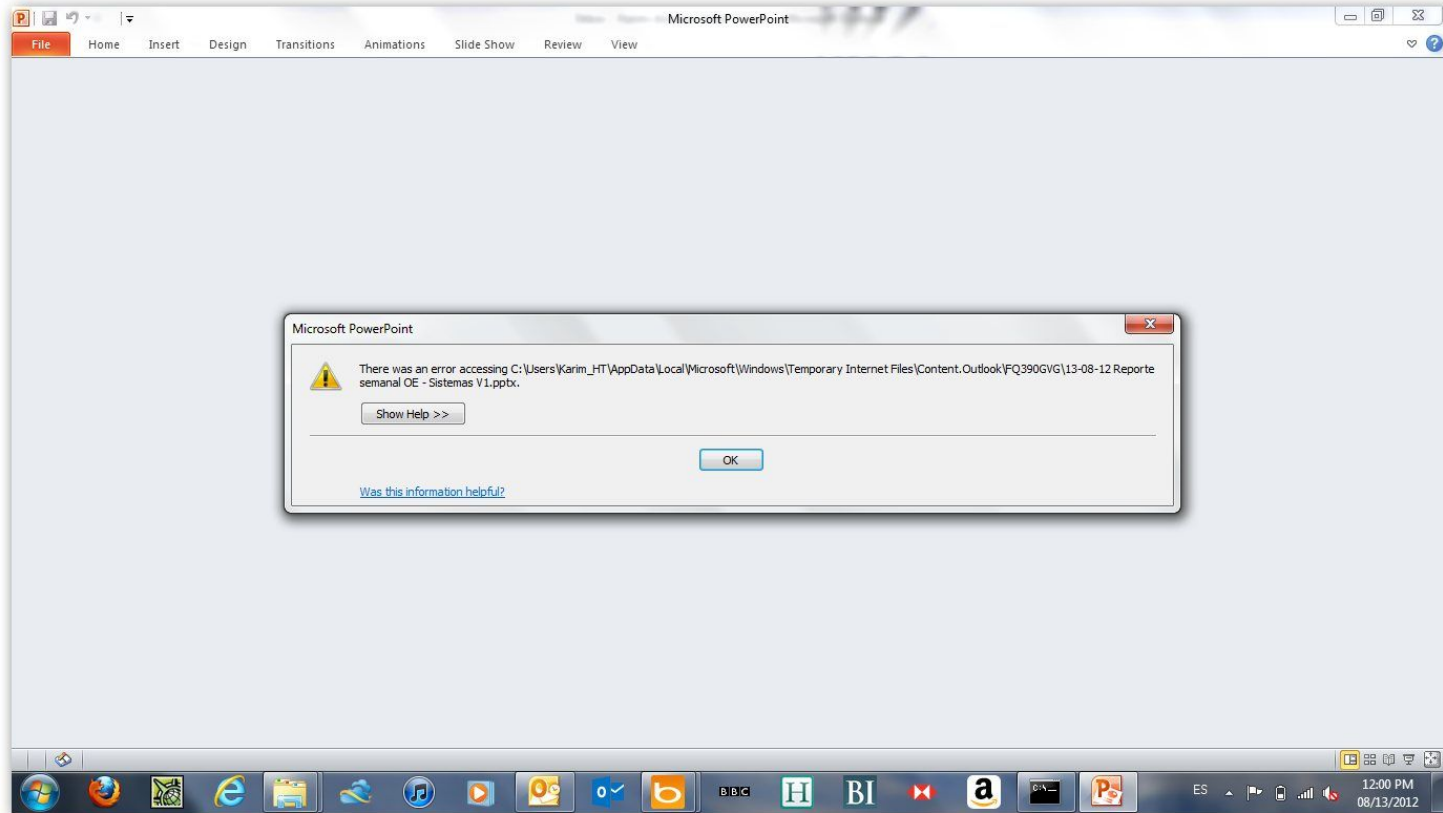
- operating systems don't like talk to each other

Why use markdown?

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This Causes Problems:

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- files are in proprietary formats

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Bioinformatics is mostly on a Linux machine using the command line terminal. The rest of the universe uses Macs or PCs.

This Causes Problems:

- operating systems don't talk to each other
- files are in proprietary formats
- files are not readable in plain text (and terminal needs them to be!)

Why use markdown?

Bioinformatics is the universe used

the rest of

This Cause

- operating s
- files are in |
- files are no

```
<?xml version="1.0" encoding="UTF-8" standalone="yes"?>
<w:document xmlns:wpc="http://schemas.microsoft.com/office/word/2010/wordprocessingCanvas"
xmlns:mc="http://schemas.openxmlformats.org/markup-compatibility/2006"
xmlns:o="urn:schemas-microsoft-com:office:office"
xmlns:r="http://schemas.openxmlformats.org/officeDocument/2006/relationships"
xmlns:m="http://schemas.openxmlformats.org/officeDocument/2006/math" xmlns:v="urn:schemas-microsoft-com:vml"
xmlns:wp14="http://schemas.microsoft.com/office/word/2010/wordprocessingDrawing"
xmlns:wp="http://schemas.openxmlformats.org/drawingml/2006/wordprocessingDrawing"
xmlns:w10="urn:schemas-microsoft-com:office:word"
xmlns:w="http://schemas.openxmlformats.org/wordprocessingml/2006/main"
xmlns:w14="http://schemas.microsoft.com/office/word/2010/wordml"
xmlns:w15="http://schemas.microsoft.com/office/word/2012/wordml"
xmlns:wpg="http://schemas.microsoft.com/office/word/2010/wordprocessingGroup"
xmlns:wpi="http://schemas.microsoft.com/office/word/2010/wordprocessingInk"
xmlns:wne="http://schemas.microsoft.com/office/word/2006/wordml"
xmlns:wps="http://schemas.microsoft.com/office/word/2010/wordprocessingShape" mc:Ignorable="w14 w15
wp14">
<w:body>
<w:p w:rsidR="00BA6BAF" w:rsidDefault="002D552B">
<w:t>TS0 protocol
for</w:t>
<w:r w:proofErr.w:type="spellStart">
<w:t>inDrop</w:t>
<w:r w:proofErr.w:type="spellEnd"/>
<w:t> library prep</w:t>
<w:r w:p.w:rsidR="002D552B"
w:rsidDefault="002D552B">
<w:t>Add T50 to the RT premix.</w:t>
<w:r w:p.w:rsidR="002D552B"
w:rsidDefault="002D552B">
<w:p w:rsidR="002D552B" w:rsidDefault="002D552B" w:rsidP="002D552B">
<w:t>
Template Switching Oligo (TS0):</w:t>
<w:r w:p.w:rsidR="002D552B"
w:rsidDefault="002D552B" w:rsidP="002D552B">
<w:t>TS0 5'- Biotin-</w:t>
<w:r w:proofErr.w:type="spellStart">
<w:t>AAGCAGTGGTATCAACGCAGAGTACATrGrGrG</w:t>
<w:r w:proofErr.w:type="spellEnd"/>
<w:t>-3'</w:t>
<w:r w:p.w:rsidR="002D552B"
w:rsidDefault="002D552B" w:rsidP="002D552B">
<w:t>Added to RT 1.3x premix. Final 1.
</w:t>
<w:r w:proofErr.w:type="spellStart">
<w:t>UM</w:t>
<w:r w:proofErr.w:type="spellEnd"/>
<w:r w:p.w:rsidR="002D552B" w:rsidDefault="002D552B"
w:rsidP="002D552B">
<w:p w:rsidR="002D552B" w:rsidDefault="002D552B" w:rsidP="002D552B">
<w:t>
Perform RT, inactivate, aliquot 2000 cells ~70</w:t>
<w:r w:proofErr.w:type="spellStart">
<w:t>Break the emulsion.
Save in -80C.</w:t>
<w:r w:p.w:rsidR="002D552B" w:rsidDefault="002D552B" w:rsidP="002D552B">
<w:p w:rsidR="002D552B" w:rsidDefault="002D552B" w:rsidP="002D552B">
<w:t>Thaw. Perform
enzymatic digestion as described by</w:t>
<w:r w:proofErr.w:type="spellStart">
<w:t>inDrop</w:t>
<w:r w:proofErr.w:type="spellEnd"/>
<w:t>
protocol.</w:t>
<w:r w:p.w:rsidR="002D552B" w:rsidDefault="002D552B"
w:rsidP="002D552B">
<w:t>Purify with</w:t>
<w:r w:proofErr.w:type="spellStart">
<w:t>AMPure</w:t>
<w:r w:proofErr.w:type="spellEnd"/>
<w:t>
1.2x.</w:t>
<w:r w:p.w:rsidR="002D552B" w:rsidDefault="002D552B"
w:rsidP="002D552B">
<w:t>Recover in 50</w:t>
<w:r w:proofErr.w:type="spellStart">
<w:t>ul</w:t>
<w:r w:proofErr.w:type="spellEnd"/>
<w:t>
LTET.</w:t>
<w:r w:p.w:rsidR="002D552B" w:rsidDefault="002D552B" w:rsidP="002D552B">
<w:p w:rsidR="002D552B" w:rsidDefault="002D552B" w:rsidP="002D552B">
<w:t>Set up PCR:</w:t>
<w:r w:p.w:rsidR="002D552B" w:rsidDefault="002D552B" w:rsidP="002D552B">
<w:p w:rsidR="002D552B" w:rsidDefault="002D552B" w:rsidP="002D552B">
<w:t>Kapa 2x premix.
50</w:t>
<w:r w:proofErr.w:type="spellStart">
<w:t>ul</w:t>
<w:r w:proofErr.w:type="spellEnd"/>
<w:t>
pPr</w:t>
<w:r w:pPr.w:pStyle.w:val="NormalWeb">
<w:pPr.w:proofErr.w:type="gramStart">
<w:t>cDNA</w:t>
<w:r w:proofErr.w:type="gramEnd"/>
<w:t>
amplification primers</w:t>
<w:r w:t.xml:space="preserve">
1</w:t>
<w:r w:proofErr.w:type="spellStart">
<w:t>ul</w:t>
<w:r w:proofErr.w:type="spellEnd"/>
<w:t>
each of 10</w:t>
<w:r w:proofErr.w:type="spellStart">
<w:t>ul</w:t>
<w:r w:proofErr.w:type="spellEnd"/>
<w:t>
pPr</w:t>
<w:r w:pPr.w:pStyle.w:val="NormalWeb">
<w:pPr.w:proofErr.w:type="gramStart">
<w:t>final</w:t>
<w:r w:proofErr.w:type="gramEnd"/>
<w:t>
100</w:t>
<w:r w:proofErr.</pre>
```

Why use markdown?

Markdown Solves Problems:

- simple
- readable by every machine AND humans
- allows some simple formatting to increase human readability

What is markdown?

Just text, with a few optional symbols that allow an interpreter to make it look good. Goal is to have something that still is human readable even without the interpreter.

What is markdown?

Fels Bioinformatics Meetup

Getting Started

Download R

Click on the link to go to R's homepage. <https://www.r-project.org/>

```
! [R project home] (r_homepage_screenshot.png)
```

To download R:

1. Click the **download R** link under Getting Started.
2. Select your CRAN mirror. Click one of the links at the top under 0-Cloud.
3. Click on the link that says "Download R for [Your Operating System]"
4. What to Pick
 - For Mac, select the latest release
 - For Windows, select base
5. R should be downloaded to your computer and you should follow the normal steps to install

Download RStudio

Click on the link to go to R's homepage. <https://www.rstudio.com/>

```
! [RStudio homepage] (rstudio_homepage_screenshot.png)
```

To download RStudio:

1. Click the Download link underneath the RStudio cartoon.
2. Click the **Download** button for the FREE RStudio Desktop.
3. Select your operating system from the list.
4. The file should download to your computer and then you can install it like any other program.

Install Packages

To install the main packages that will be required for meetups, open RStudio and copy and paste the code below into the **Console**.

```
install.packages('tidyverse')
```

If that doesn't work, copy and paste this code.

```
packages <- ('dplyr', 'forcats', 'ggplot2', 'purrr', 'readr', 'stringr', 'tibble', 'tidyr')
install.packages(packages)
```

Content

Week 1 (Sep 7)

Outline

- What's a meetup? / What's changing with meetups?
- Getting Started (same as above)
- Introduction to Rmarkdown

```
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Rmarkdown Demo