Session #2

Take Home Assignment #1

- Feedback

- Google Form results

The GSBS Bootstrappers

More Complex Commands

grep	Search file for pattern
sort	Sort file based on columns

Pipes

a | b	Pipe result of a into b

Exercise Set #3

The GSBS
Bootstrappers

Break

Exercise Set #3 Solutions

Text Editors

- Allow users to edit documents in the terminal

- Important if you want to run scripts on a server or GHPCC cluster

- Many different editors: Emacs, Nano

- We will focus on vi (vim)

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vi

To start vi:

```
vi filename.txt
```

There are two modes in vi:
     1. Normal mode (ESC)
     2. Insert mode

vi- Save and Quit

- `:q`

- `:q!`

- `:w`

- `:wq`

vi- Navigation

- Arrow Keys

- (number)`G` – jump to line #number

- : (number) – jump to line #number

- `1G` – jump to last line

vi- Editing Text

- `i` – insert to the left of the cursor

- `I` – insert at the beginning of the line

- `a` – insert to the right of the cursor

- `A` – insert at the end of the line

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vi- Deleting Text

- `dd` – delete current line

- `dG` – delete entire document up until current line

- `D` – delete current line up to the cursor

- `u` – undo last action

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vi- Find and Replace

- `/foo` – find "foo" in document. Hit `n` to find next instance

- `: %s/foo/bar/g` – replace all instances of "foo" with "bar" in the document

- `: %s/foo/bar/gc` – replace instances of "foo" with "bar" in the document with confirmation

The GSBS Bootstrappers

Exercise Set #4

The GSBS
Bootstrappers

Exercise Set #4 Solutions

Take Home Assignment #2

You have a collection of genetic variants associated with Crohn's disease, epilepsy, hair color, leprosy, Parkinson's disease, type 1 diabetes, and type 2 diabetes that you downloaded from the NHGRI GWAS database. You want to perform additional analyses on your dataset.