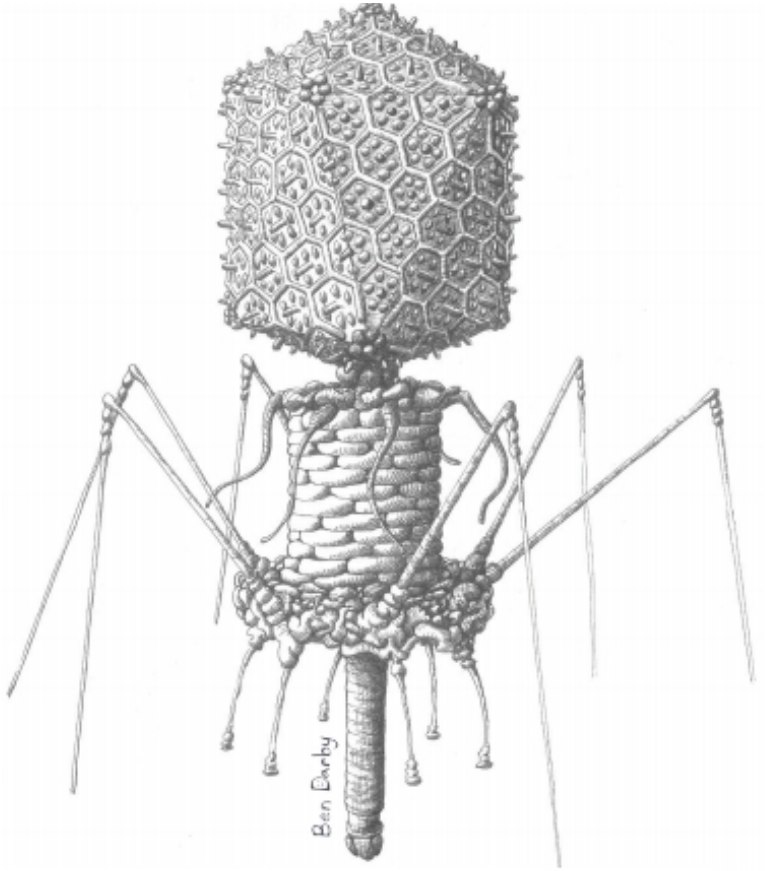
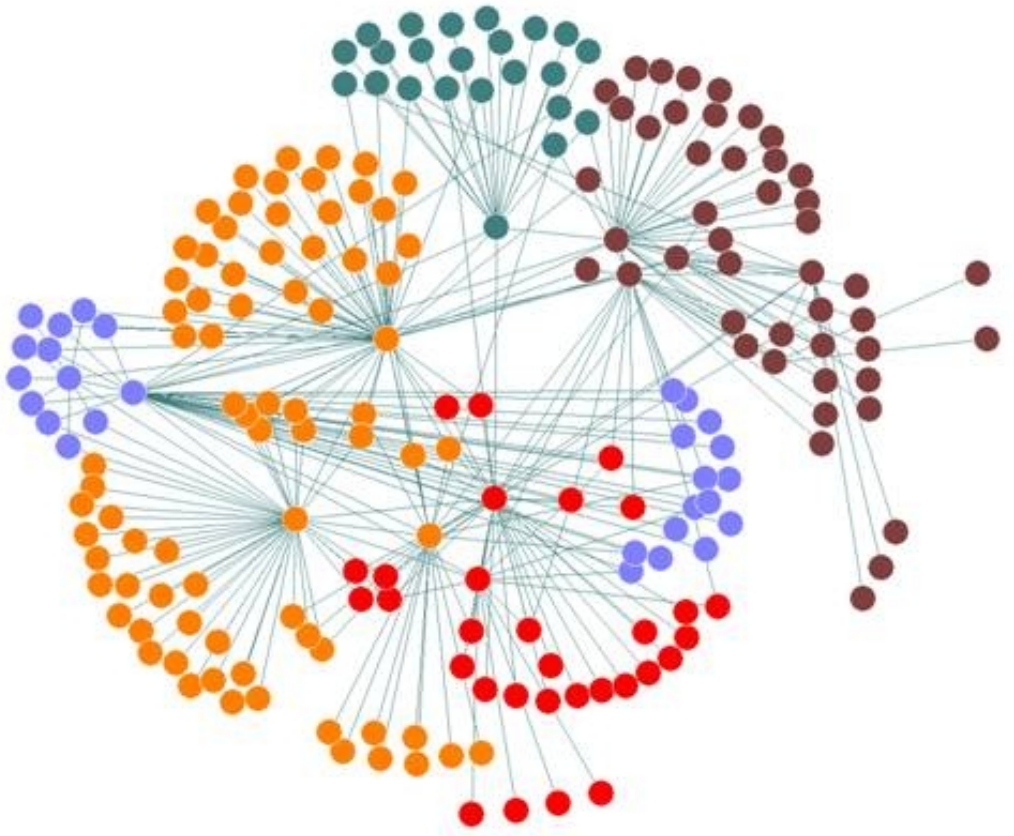




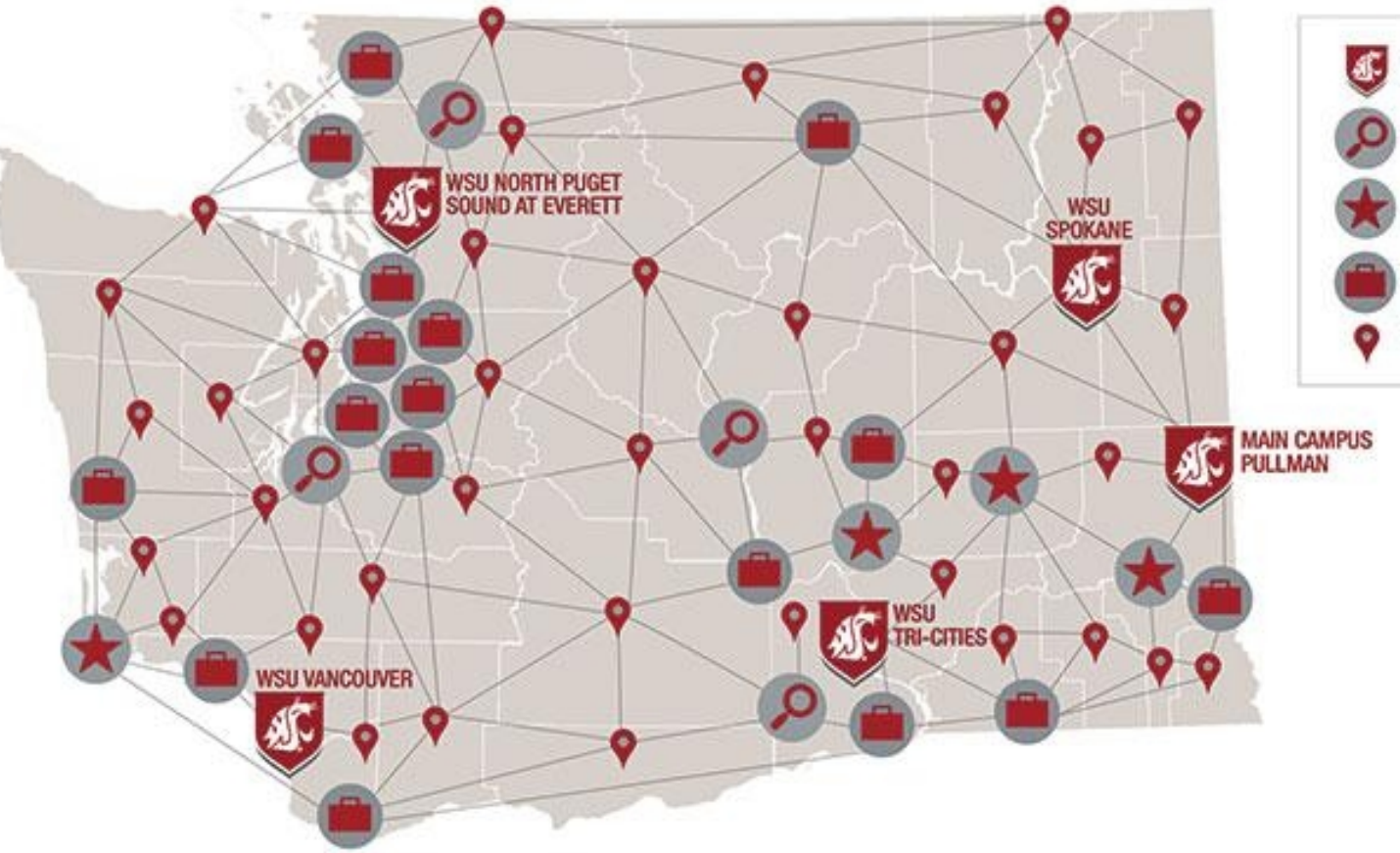
Dr. Richard Allen White III
Washington State University
FABI Workshop - Oct 21, 2018

Learning Objectives

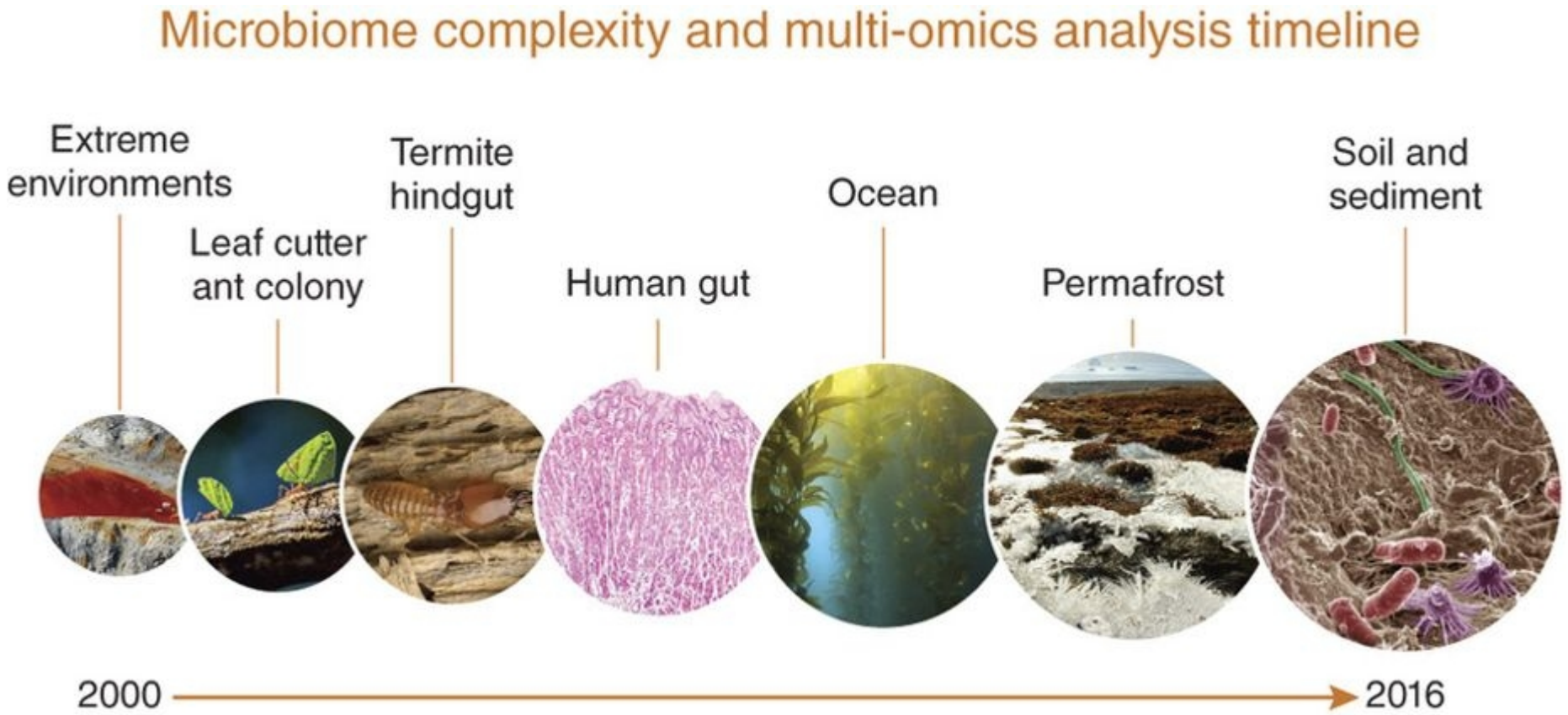
1. Brief introduction of me and my research
2. Learn about ‘Omics,’ technology terms
3. Introduction to multiomics
4. History of genome sequencing
5. Introduction to sequencing technologies
6. Unix/Linux command line
7. Grep -> text wrangling
8. Github
9. R intro
10. R ggplot2 intro

Introduction - Dr. RAWIII

Introduction - Dr. RAWIII

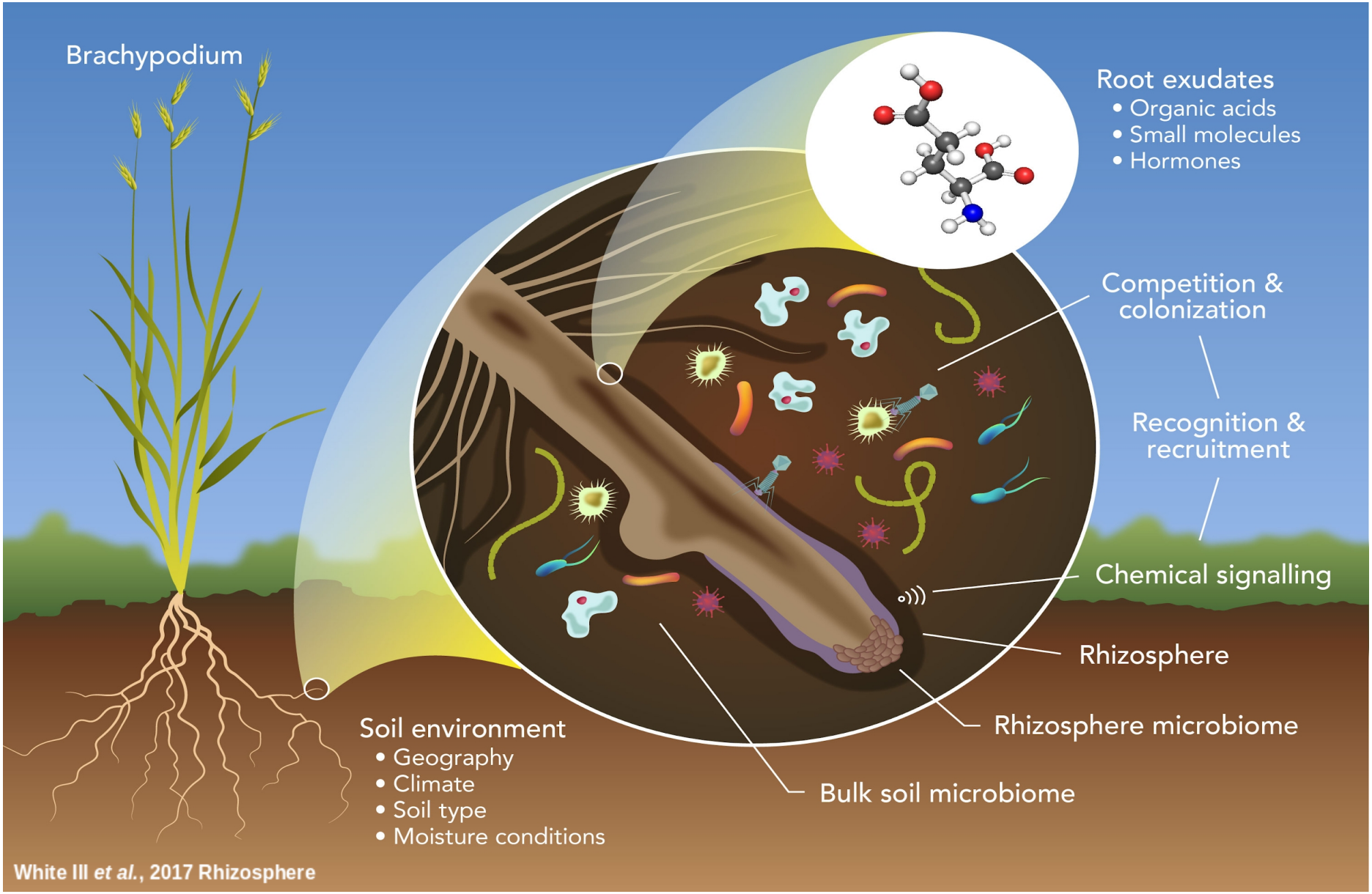


Research - Dr. RAWIII



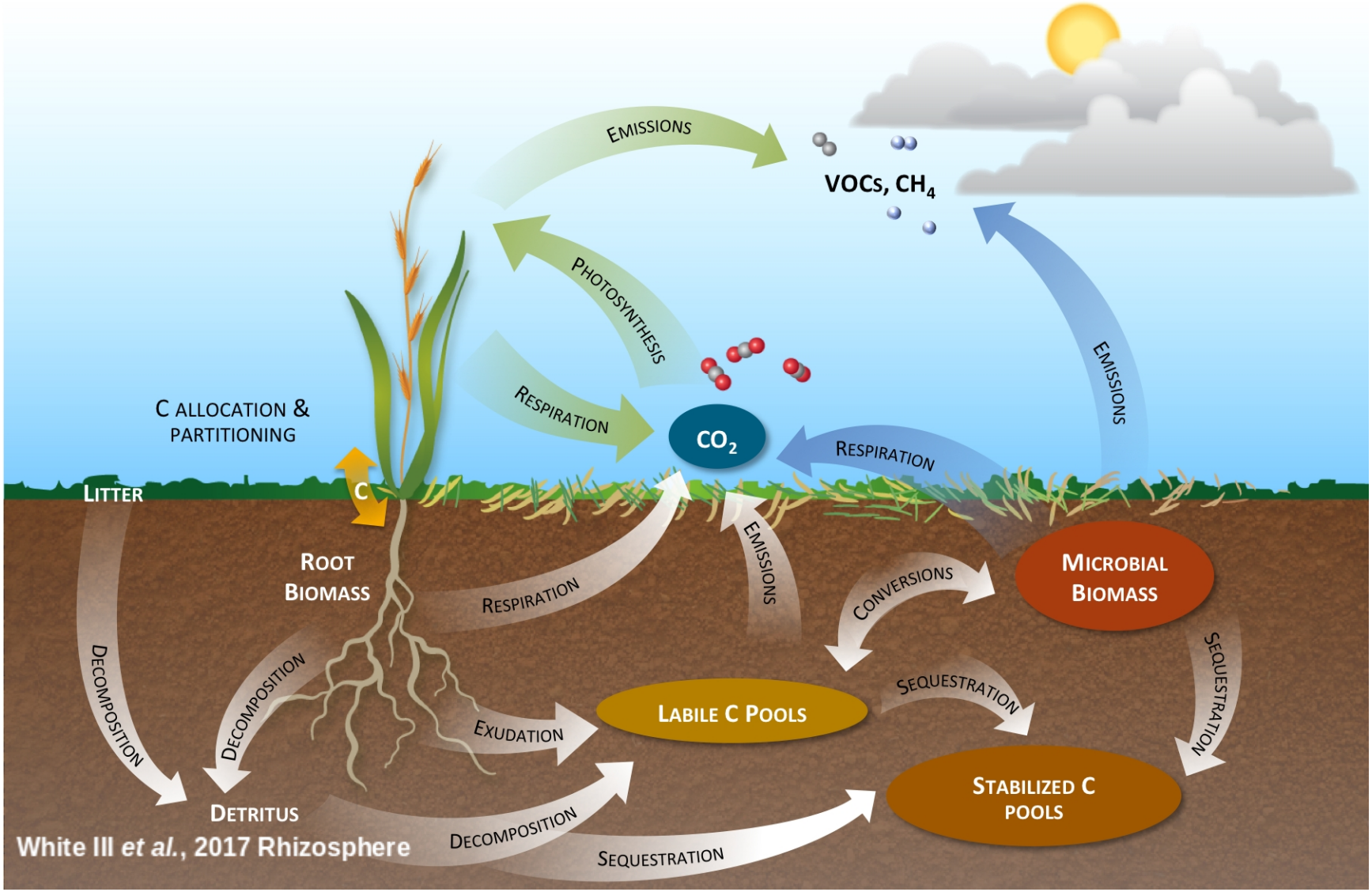
White III et al., 2016. Nature Protocols
Link to article:https://www.nature.com/articles/nprot.2016.148

Research - Dr. RAWIII



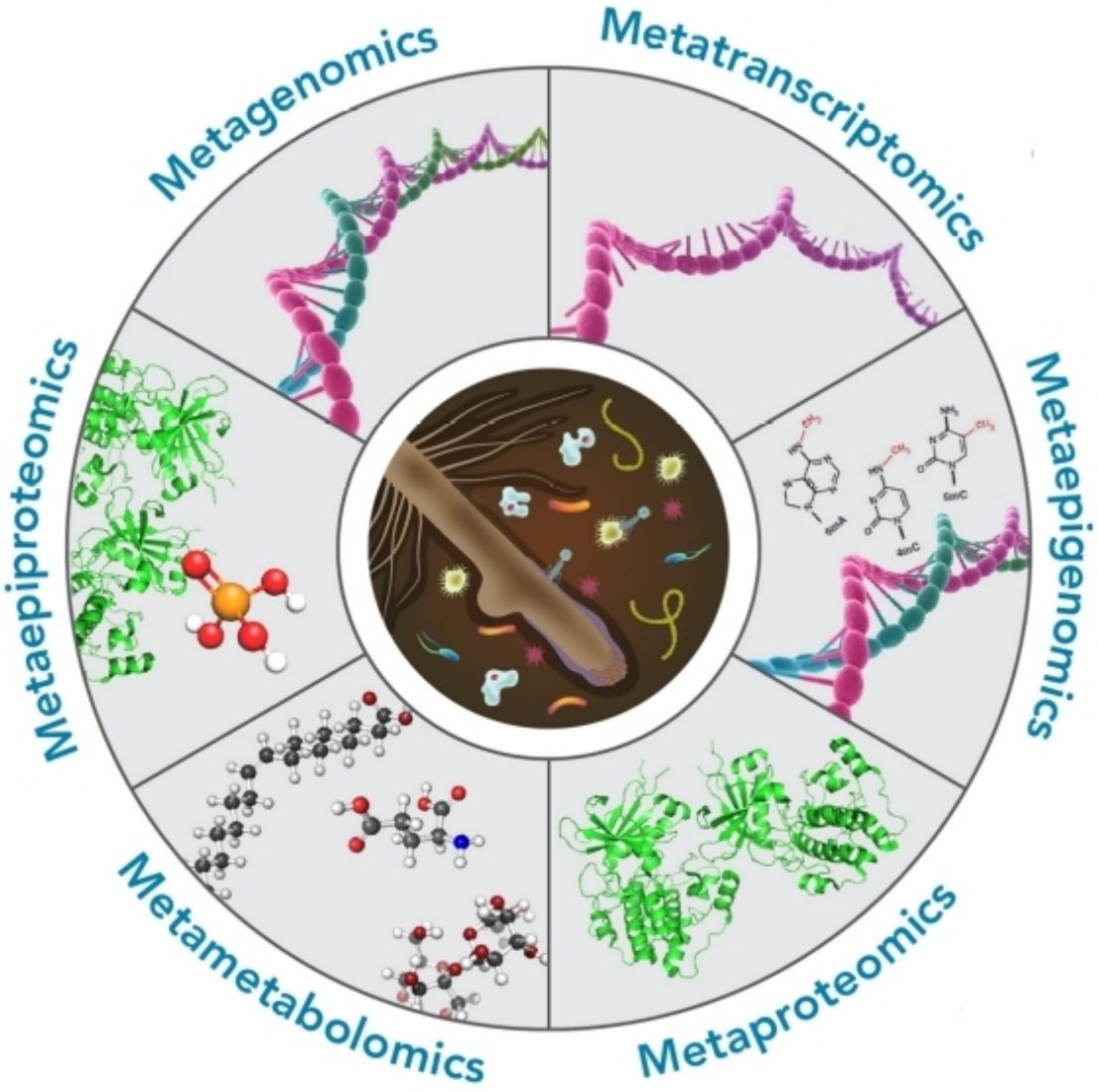
Link to article:https://www.sciencedirect.com/science/article/pii/S2452219817300666

Research - Dr. RAWIII



Link to article:https://www.sciencedirect.com/science/article/pii/S24522198173004596

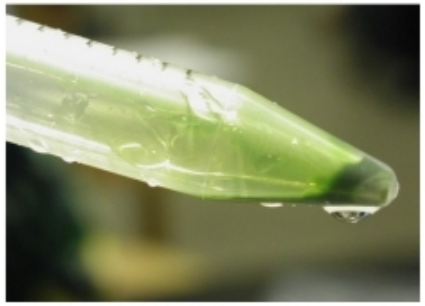
Omics terms



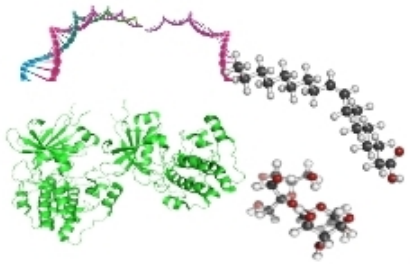
White III et al., 2017 Rhizosphere
Link to article: https://www.sciencedirect.com/science/article/pii/S2452219817300666#f0015

A workflow of a multiomic study

Environmental sample



Single step - multiomic extraction



Library prep (NGS) Fractionation (MS)

Sequencing

Mass Spectrometry

Data

Analysis

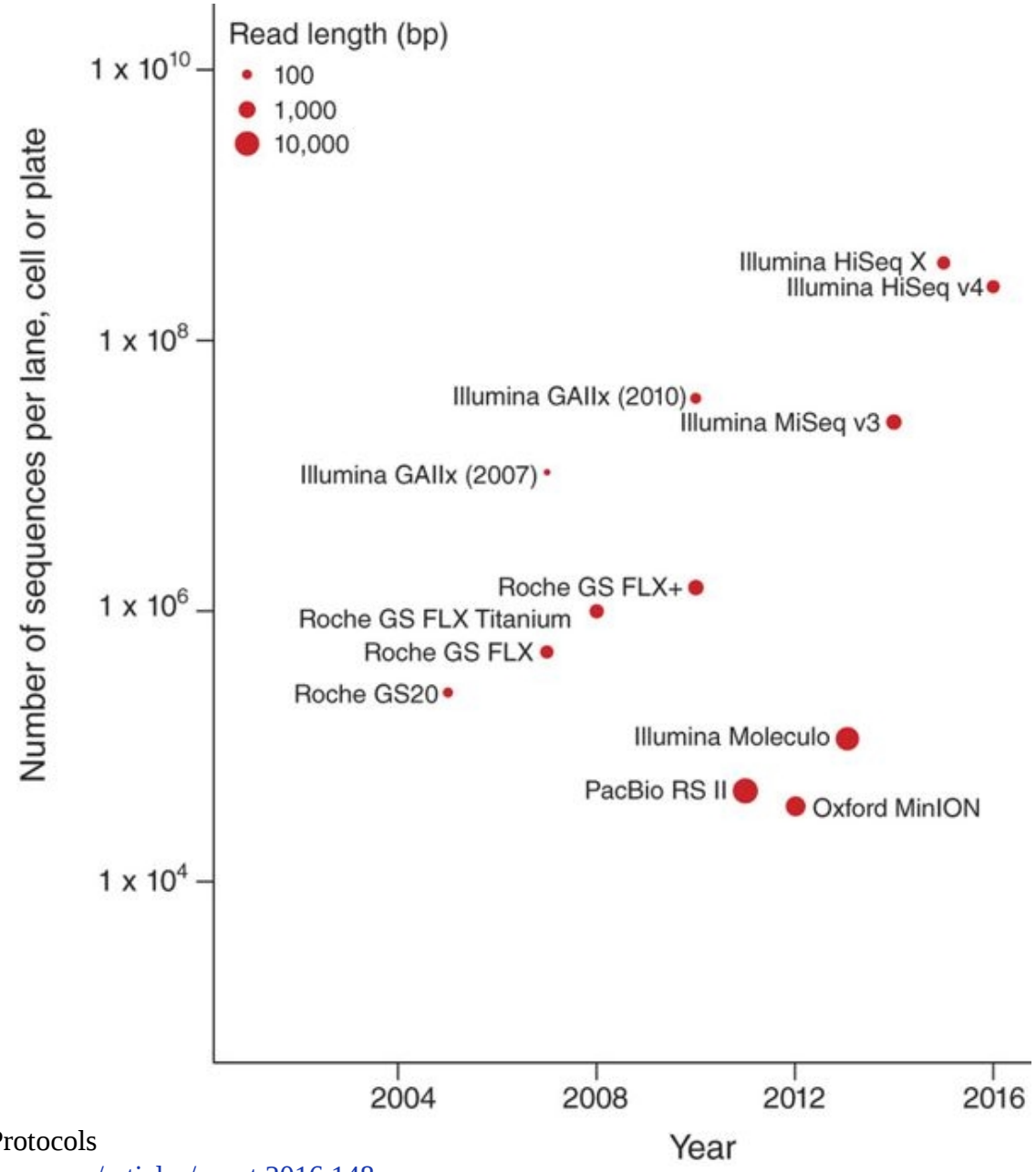
Direct Read or Assembly (NGS)

Spectral features analysis

White III et al., 2016. Nature Protocols

Link to article:https://www.nature.com/articles/nprot.2016.148

Sequencing technologies



White III et al., 2016. Nature Protocols

Link to article:https://www.nature.com/articles/nprot.2016.148

History of genome sequenced

1972 - First gene to be sequenced was MS2 coat protein (510 bp)
1976 - First RNA genome sequenced was Bacteriophage MS2 (3.56 kb)
1977 - First DNA genome sequenced was Bacteriophage phiX174 (5.38 kb)
1979 - First plasmid to be sequenced was pBR322 (4.3 kb)
1984 - First mammalian DNA virus sequenced was Epstein-Barr virus (172 kb)
1992 - First chromosome sequenced was Yeast chromosome III (315 kb)
1995 - First cellular genome sequenced was *Hemophilus influenzae* (1.8 Mb)
1995 - First archaeal genome sequenced was *Methanococcus jannaschii* (1.7 Mb)
1996 - First eukaryotic genome sequenced was *Saccharomyces cerevisiae* (12 MB)
1998 - First multicellular organism sequenced was *Ceanorhabditis elegans* (97 Mb)
2000 - First plant genome sequenced was *Arabidopsis thaliana* (125 Mb)
2001 - First mammalian draft genome *Homo sapiens* (3.3 Gb)

Super bonus -> Who sequenced the first cellular genome?

Data format

*.fna, .fasta, .fa ?

*.faa ?

*.gff ?

*.gbk ?

*.fq or fastq ?

*.gtf ?

Read vs. sequence?

Contig?

kmer?

What is Unix?

A multi-task and multi-user Operating System

Developed in 1969 at AT&T's Bell Labs by:

Ken Thompson (Unix)

Dennis Ritchie (C)

Douglas McIlroy (Pipes)

Some other variants: System V, Solaris, SCO Unix, SunOS, 4.4BSD, FreeBSD, NetBSD, OpenBSD, BSDI

What is Linux?

A clone of Unix
Developed in 1991 by Linus Torvalds, a Finnish graduate student
- Inspired by and replacement of Minix
  - Linus' Minix became Linux
  - Consist of :
- Linux Kernel
- GNU (GNU is Not Unix) Software

Software Package management
Others

What is Linux?

Originally developed for 32-bit x86-based PC Ported to other architectures, eg.

-> Alpha, VAX, PowerPC, IBM S/390, MIPS, IA-64 PS2, TiVo, cellphones, watches, Nokia N810, NDS, routers, NAS, GPS, ...

What is Linux?

> 300 Linux Distributions

Ubuntu (**Best for newbies, my fav, South African!**)

Slackware

Redhat RHEL (commercially support)

Fedora (free)

CentOS (free RHEL, based in England)

Debian (one of the few called GNU/Linux)

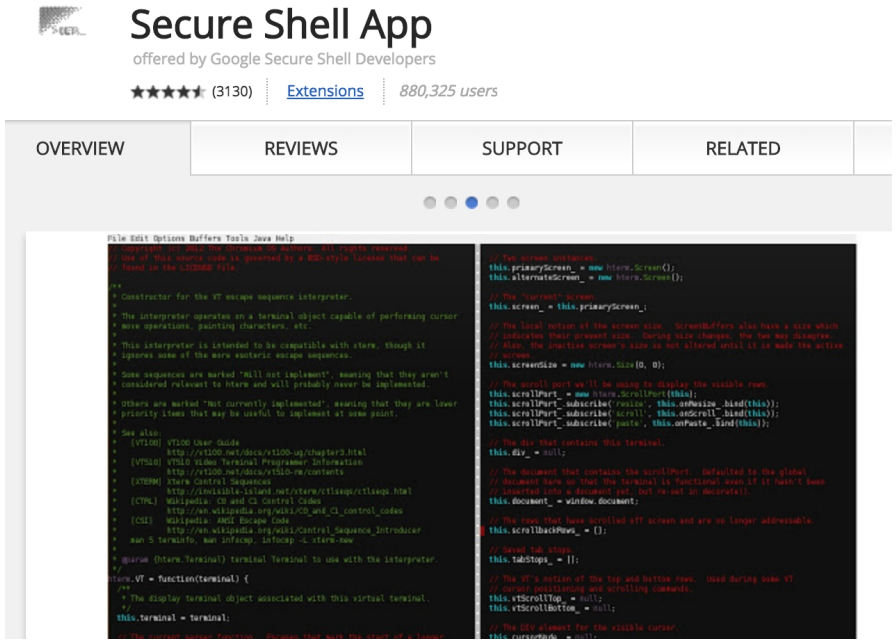
Knoppix (first LiveCD distro.) ...

Terminal for Unix/Bash

Mac: Terminal

Windows: PUTTY

Chrome: Secure Shell (extension; runs command line in your browser! How cool is that?)



Unix/Bash tutorial

>>Master page

https://github.com/raw937/FABI_workshop

https://github.com/raw937/FABI_workshop/blob/master/bin/Bash_tutorial.md

Command line review

cd	**?**	**tar**	**?**		
pwd	**?**	**scp**		**?**	
mkdir	**?**	**rm**	**?**		
head	**?**	**rm -r**	**?**		
tail	**?**	**echo**		**?**	
more	**?**	**|**	**?**		
less	**?**	**>**		**?**	
mv	**?**	**<**	**?**		
touch	**?**	**>>**	**?**		
cp	**?**	**cat**	**?**		

Unix/Bash - check point

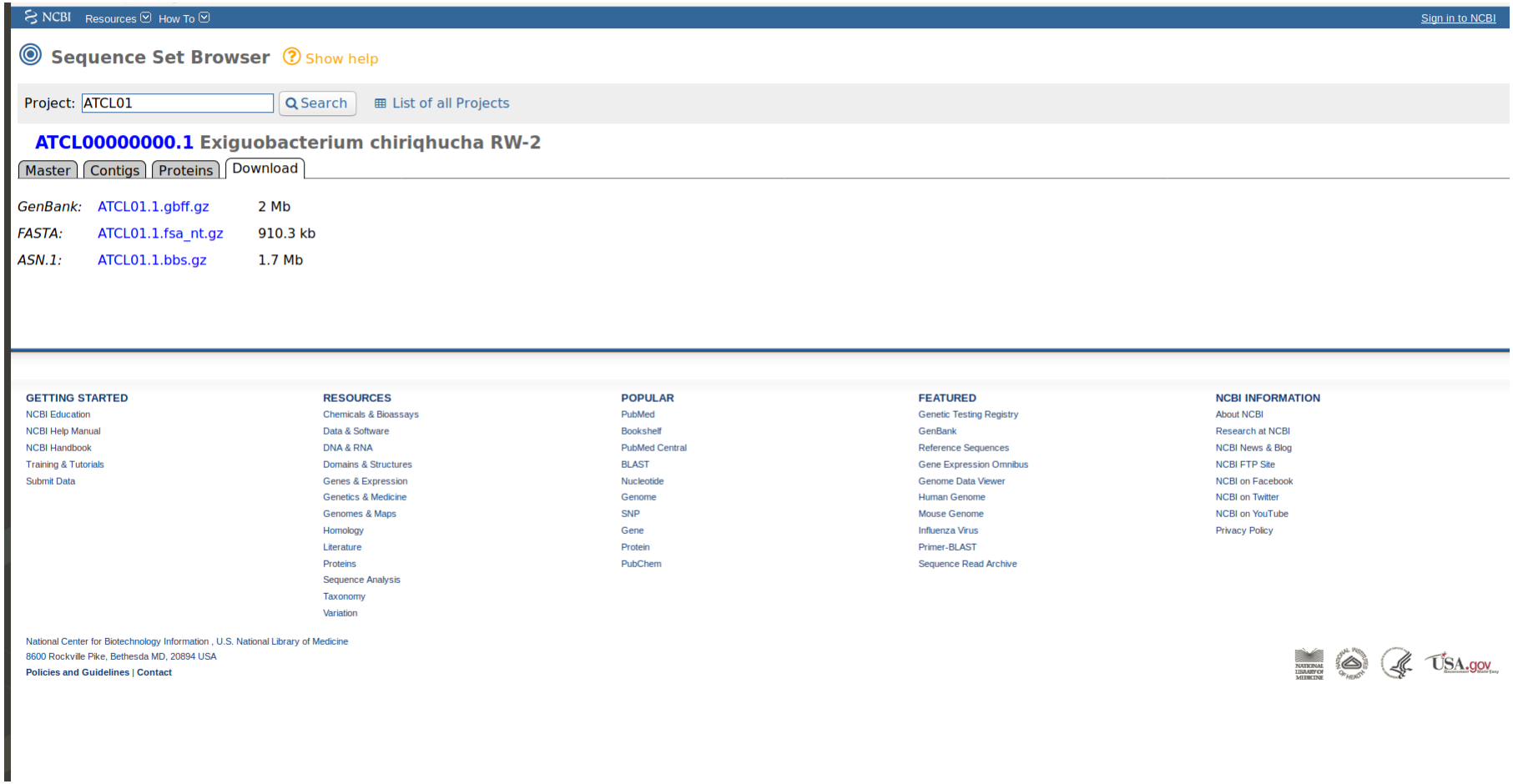
- Make a folder with your name
- Make two files in as .txt (labeled 1 and 2)
- Write your name in file 1
- Write your name in file 2 with _a at the end
- Combine those two files to a new file
- Copy the whole folder of your name with a new name

Grep “the hand of the gods”

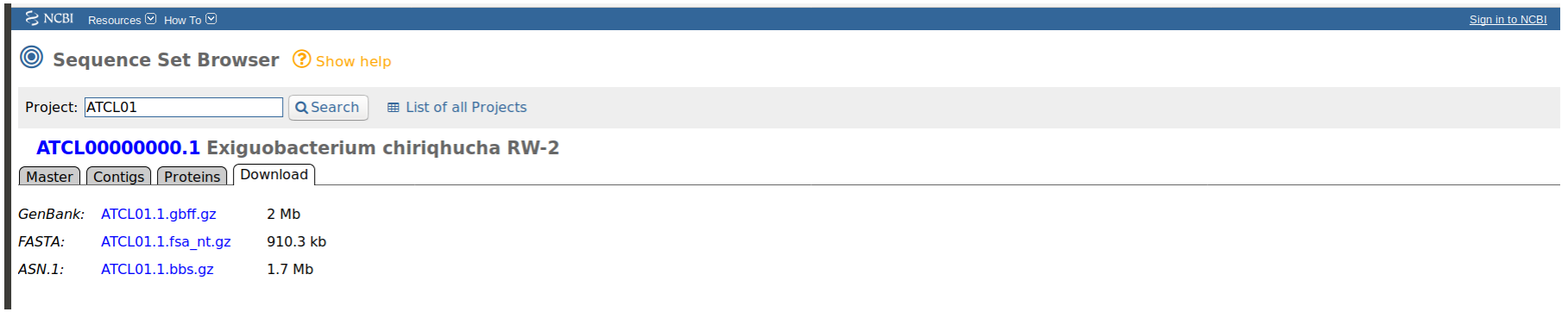
https://github.com/raw937/FABI_workshop/blob/master/bin/grep_tutorial.md

Grep “the hand of the gods”

https://www.ncbi.nlm.nih.gov/Traces/wgs/?val=ATCL01#contigs



Grep “the hand of the gods”



1. Download fasta file
2. Unzip the file
3. Rename file to “.fasta”
4. Give me the number of lines
5. Tell me the size of the file in bytes
6. Count the number of sequences using a command
7. Export all the headers into a new “.txt” file

Git tutorial

Make an account

https://github.com/

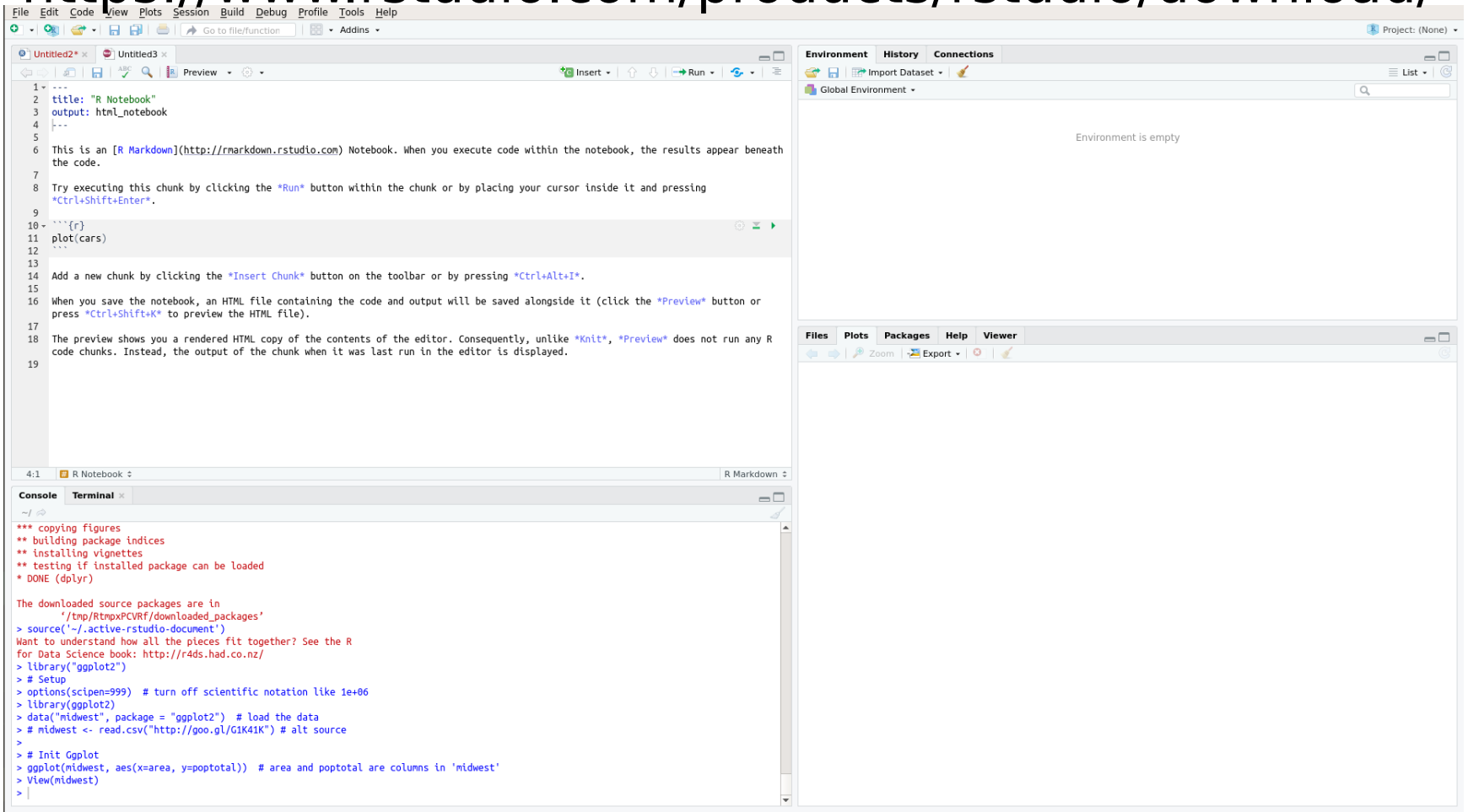
Follow tutorial on

https://github.com/raw937/FABI_workshop/edit/master/bin/git%20tutorial.md

R, Rstudio and Rnotebooks

Install Rstudio

https://www.rstudio.com/products/rstudio/download/



R, Rstudio and Rnotebooks

1. Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Ctrl+Shift+Enter*.

2. Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

3. When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

4. The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.

R, Rstudio and Rnotebooks

https://github.com/raw937/FABI_workshop/blob/master/bin/ggplot_tutorial.Rmd

VIEW ON SCREEN (HTML)

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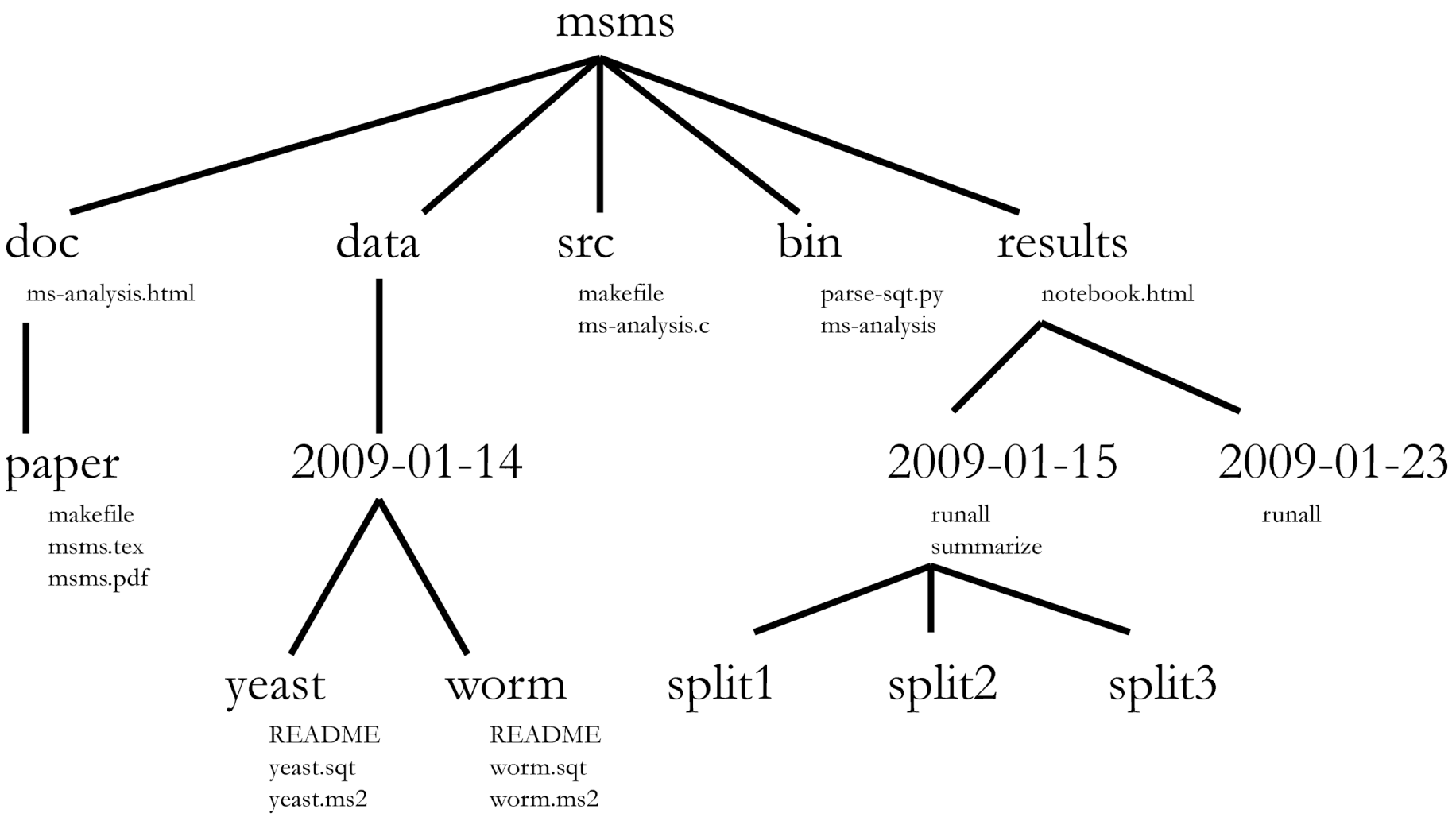
Reproducible research



Noble, 2009

Link to article:https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1000424

Reproducible research

http://joey711.github.io/phyloseq-demo/Restroom-Biogeography.html