



MICROBIAL COMMUNITY PROFILING

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Bioinformatics
Core

Genome Center

UC Davis

DISCLAIMER

- This talk/workshop is full of opinion, there are as many different way to perform analysis as there are Bioinformaticians.
- My opinion is based on over a decade of experience and spending a considerable amount of time to understand the data and how it relates to the biological question.
- Each experiment is unique, this workshop is a starting place and should be adapted to the specific characteristics of your experiment.

OUTLINE

- 1. Introduction to High Throughput Sequencing and RNA-seq**
 - High throughput sequencing
 - RNA-seq Experimental Design
 - RNA Sequencing and Sample Preparation
- 2. Workshop Dataset**
- 3. Introduction to the Command Line**
- 4. Overview of RNA-seq Data Analysis**
 - Pipeline Workflow/Stages
 - Software
 - Metadata input
 - Files and Directory Structure

OUTLINE

5. Files and File Types

6. Read Preprocessing

- Description of the expHTS preprocess pipeline
- Parameters and what they mean
- Preprocessing the Workshop Data
- QA/QC

7. Read Mapping

- Description of the expHTS mapping pipeline
- Parameters and what they mean
- Mapping the Workshop Data
- QA/QC

8. Estimate known genes and transcripts expression – Counting

- Description of the expHTS counting pipeline
- Parameters and what they mean
- Counting the Workshop Data
- QA/QC

OUTLINE

9. Differential Expression Analysis using edgeR

- Overview of Differential Expression Analysis
- Models and model formulation
- QA/QC
- Perform Differential Expression the Workshop Data

10. Summarization and Visualization of Output

BIOINFORMATICS IS A DATA SCIENCE

Section

THE DATA DELUGE



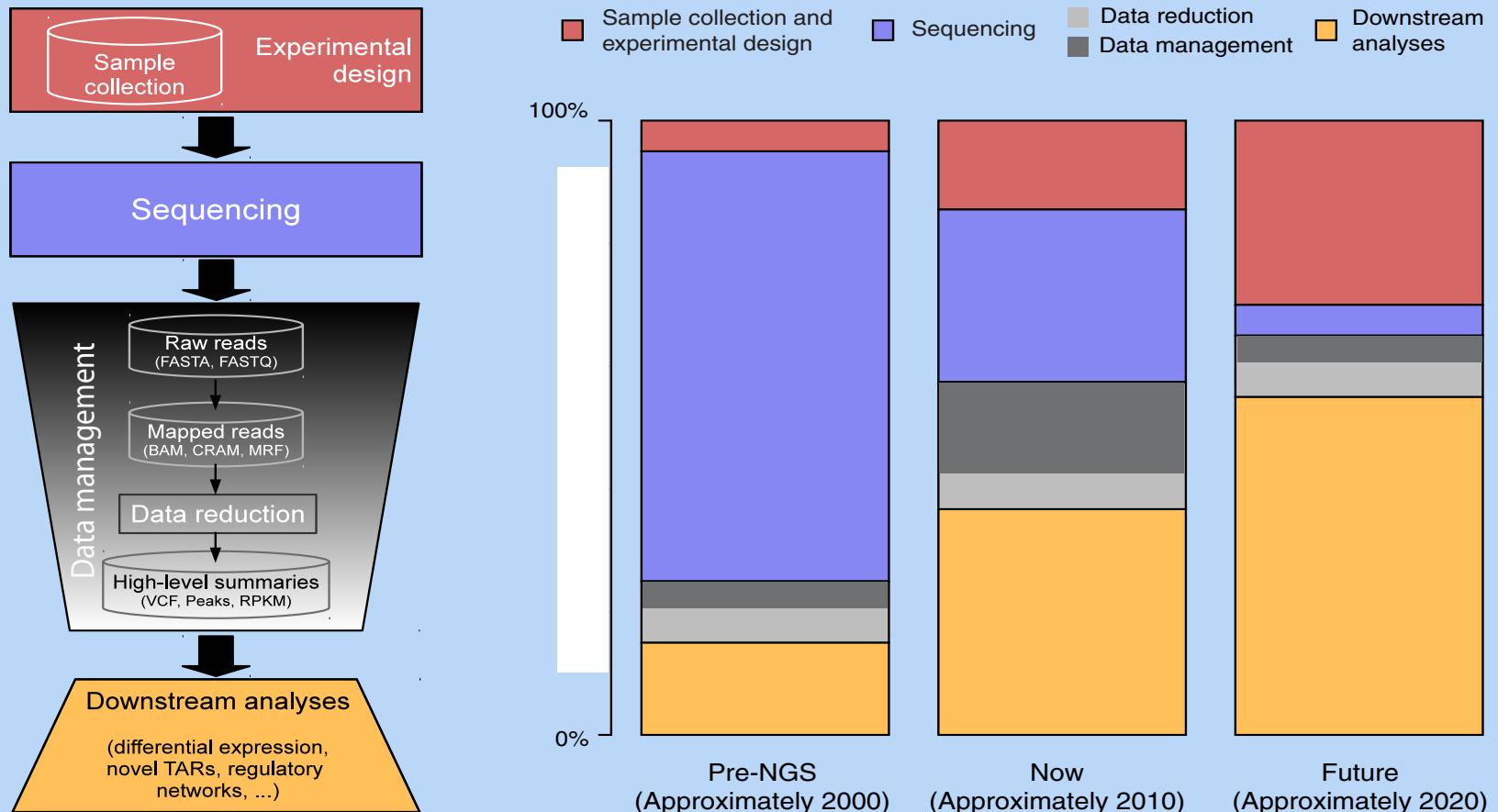
■ Plucking the biology from the Noise

REALITY



- Its much more difficult than we may first think

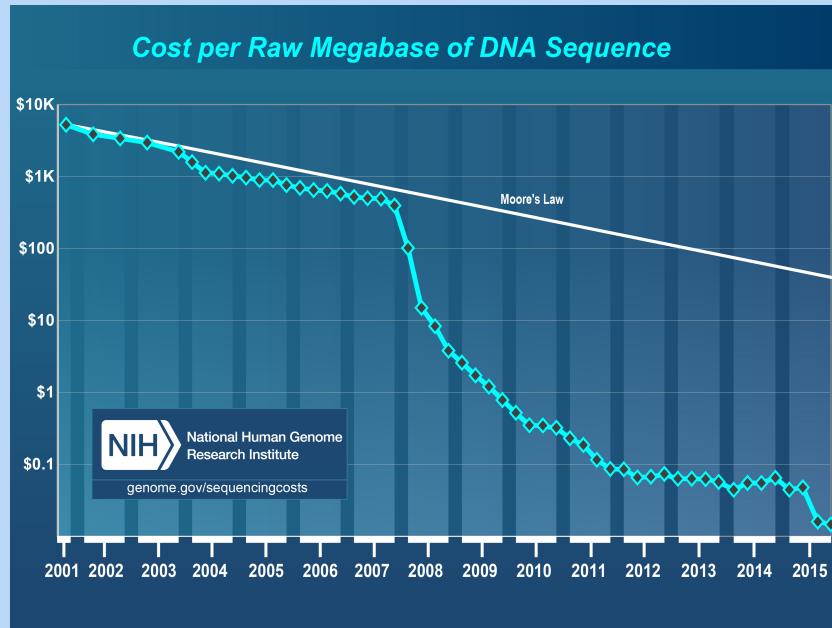
THE REAL COST OF SEQUENCING



The real cost of sequencing: higher than you think!

Sboner et al. Genome Biology 2011 12:125 doi:10.1186/gb-2011-12-8-125 (2011)

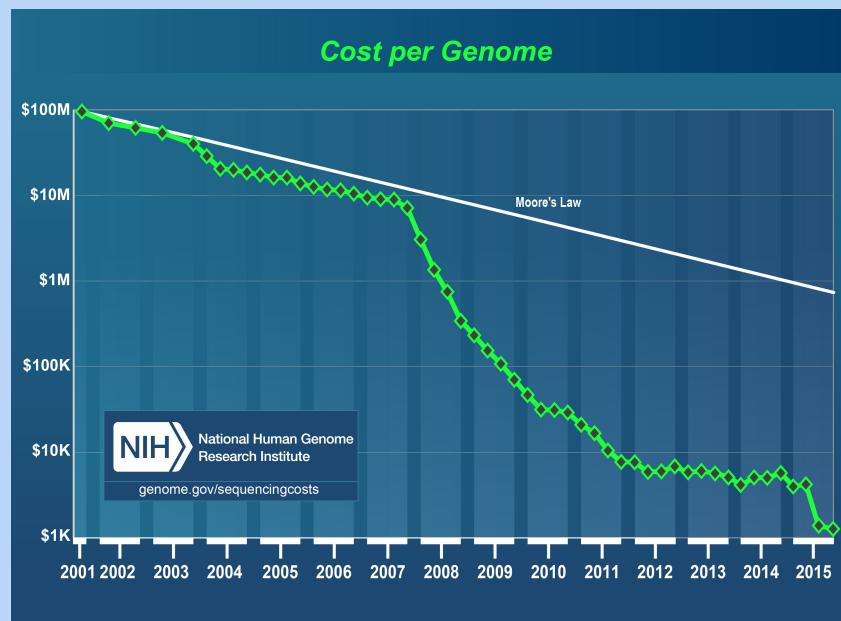
SEQUENCING COSTS



- October – 2015
 - \$0.014 per Megabase
 - \$1,245 per Human Sized Genome (30x coverage)

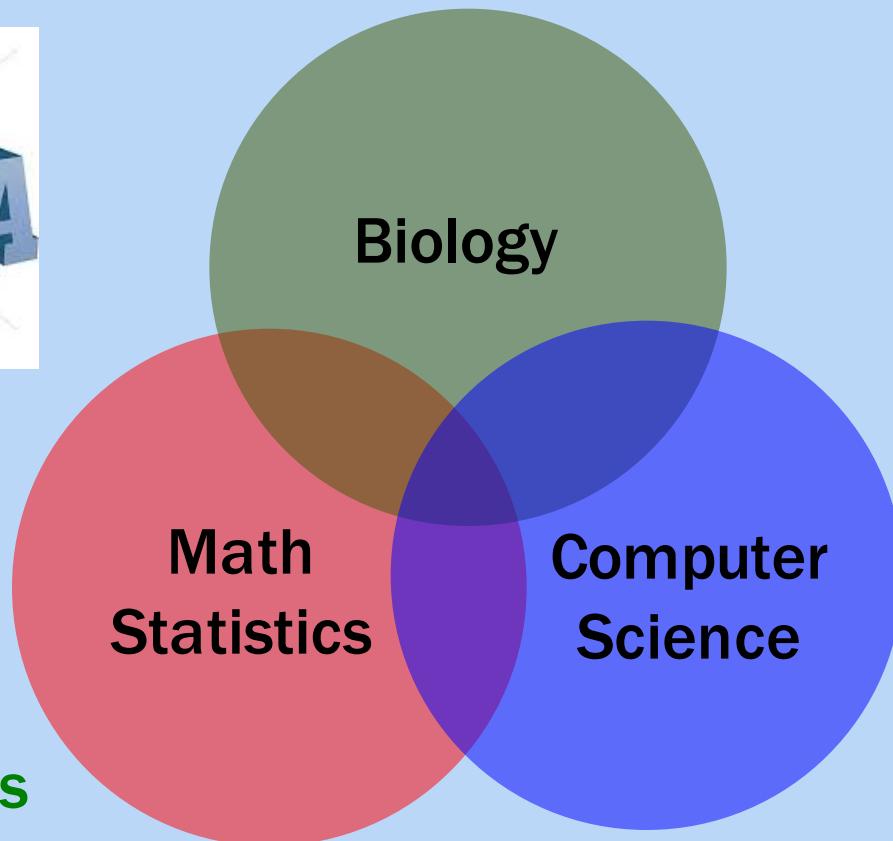
Data Only!!
Does not include any analysis or bioinformatics

GROWTH IN SEQUENCING



BIOINFORMATICS IS DATA SCIENCE

Computational Biology



Biostatistics

Bioinformatics

'The data scientist role has been described as “part analyst, part artist.”'
Anjul Bhambhani, vice president of big data products at IBM

DATA SCIENCE

Data science is the process of formulating a quantitative question that can be answered with data, collecting and cleaning the data, analyzing the data, and communicating the answer to the question to a relevant audience.

EXPERIMENT PHILOSOPHY

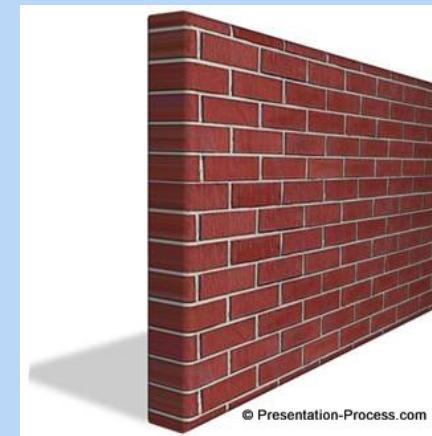
Design
Experiment

Perform
Experiment

Sample and
Extract
RNA/DNA

Prepare
Libraries

Sequence



Analyze

Interpret

7 STAGES TO DATA SCIENCE

1. Define the question of interest
2. Get the data
3. Clean the data
4. Explore the data
5. Fit statistical models
6. Communicate the results
7. Make your analysis reproducible

STAGE 1: DEFINE THE QUESTION

1. Define the question of interest

Begin with the end in mind!

what is the question

how are we to know we are successful

what are our expectations

dictates

the data that should be collected

the features being analyzed

which algorithms should be used

STAGES 2-4: COLLECTING AND CLEANING

2. Get the data
3. Clean the data
4. Explore the data

Know your data!

know what the source was
technical processing in producing
data (bias, artifacts, etc.)
“Data Profiling”



Data are never perfect but love your data anyway!

the collection of massive data sets often leads to unusual , surprising, unexpected and even outrageous.

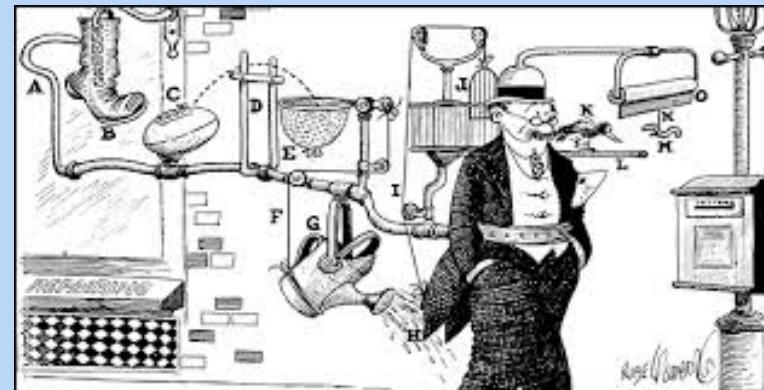
STAGE 5: ANALYZING THE DATA

5. Fit statistical models

Over fitting is a sin against data science!

Model's should not be over-complicated

- If the data scientist has done their job correctly the statistical models don't need to be incredibly complicated to identify important relationships
- In fact, if a complicated statistical model seems necessary, it often means that you don't have the right data to answer the question you really want to answer.



STAGES 6-7: COMMUNICATING YOUR RESULTS

6. Communicate the results
7. Make your analysis reproducible

Remember that this is ‘science’!

We are experimenting with data selections, processing, algorithms, ensembles of algorithms, measurements, models. At some point these ***must all be tested for validity and applicability*** to the problem you are trying to solve.



BIOINFORMATICS DONE WELL

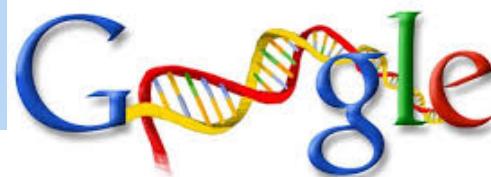
**Data science done well looks easy –
and that's a big problem for data
scientists**

simplystatistics.org

March 3, 2015 by Jeff Leek

SUBSTRATE

Cloud
Computing



Cluster
Computing



BAS™



LINUX Laptop & Desktop



ENVIRONMENT

“Command Line” and “Programming Languages”



Open
Source



VS
Bioinformatics Software Suite



PREREQUISITES

- Access to a multi-core (24 cpu or greater), ‘high’ memory 64Gb or greater Linux server [Metagenomics].
- Familiarity with the ‘command line’.
- Basic knowledge of how to install software
- Basic knowledge of R and statistical programming
- Basic knowledge of Statistics and model building

BIOINFORMATICS

- Know and Understand the experiment
 - “The Question of Interest”
- Develop a deep familiarity and understanding of the techniques/tools/methods
- Build a set of assumptions/expectations
 - Mix of technical and biological
 - Spend your time testing your assumptions/expectations
 - Don’t spend your time finding the “best” software
- Don’t under-estimate the time Bioinformatics may take
- Be prepared to accept ‘failed’ experiments

THE BOTTOM LINE

The Bottom Line:

- Spend the time (and money) planning and producing **good quality, accurate and sufficient data** for your experiment.
- Get to know to your data, develop and test expectations
- Result, you'll **spend much less time** (and less money) extracting biological significance and results during analysis.

INTRODUCTION TO SEQUENCING

Section

HISTORY

- It would take a few more decades after the discovery of the double helix in 1953 before we could readily analyze fragments of DNA.
- RNA sequencing actually preceded DNA sequencing when Walter Fiers from the University of Ghent published the first complete gene and genome of Bacteriophage MS2 in 1972 and 1976 respectively.
- Location specific primer extension: Raw Wu (1970), using DNA polymerase catalysis and specific nucleotide labeling.
- Chain-terminating inhibitors: Frederick Sanger (1977), aided in speeding up the process

HISTORY

- Leroy E. Hood's laboratory at the California Institute of Technology announced the first semi-automated DNA sequencing machine in 1986.
- Applied Biosystems' produced the first fully automated sequencing machine, the ABI 370, in 1987, followed by the ABI Prism 373, (1990), ABI Prism 377 (1995), ABI Prism 310 (also 1995) represented the first capillary sequencer, ABI Prism 3700 (1999, the workhorse of the human genome project), ABI 3730xl DNA analyzer (2002) @ **2M bases per day.**

HISTORY

- **Primer Walking**
 - Design a primer that matches the sequence neighboring the unknown sequence
 - Sequence the short DNA strand using the Sanger method
 - The new sequenced portion is used to design a new primer and repeat
- *de novo sequencing* or “shotgun sequencing”
 - High-molecular weight DNA is sheared into random fragments
 - ‘Shorter’ fragments are cloned into a vectors
 - clones are sequenced from both ends, creating two “reads”
 - original sequence is reconstitutes by “assembling” the reads

ROCHE 454

- The first massively parallel method (aka “next generation sequencing”) to become commercially available was developed by 454 Life Sciences in 2005 (acquired by Roche in 2007) and is based on the pyrosequencing technique. Similar to the Sanger method, sequencing is carried out using primed synthesis by DNA polymerase. However in the 454 pyrosequencing method, the DNA fragments are presented with each of the four dNTPs sequentially and without a dye-terminator, as is done with Sanger sequencing, allowing for multiple incorporation in the same flow. The amount of the incorporation is monitored by luminometric detection of the pyrophosphate released (hence the name ”pyrosequencing”).
- **700 Mb/day**

ILLUMINA (SOLEXA)

- The second “next generation” sequencing technology to be released (in 2006) was Illumina Solexa sequencing. A key difference between Roche 454 and Illumina sequencing was the use of chain-terminating nucleotides. The fluorescent label on the terminating base can be removed to leave an unblocked 3' terminus, making the chain termination a reversible process. The method thus sequences one base at a time, rather than 0 or more bases as does Roche 454.
- > 400Gb/day

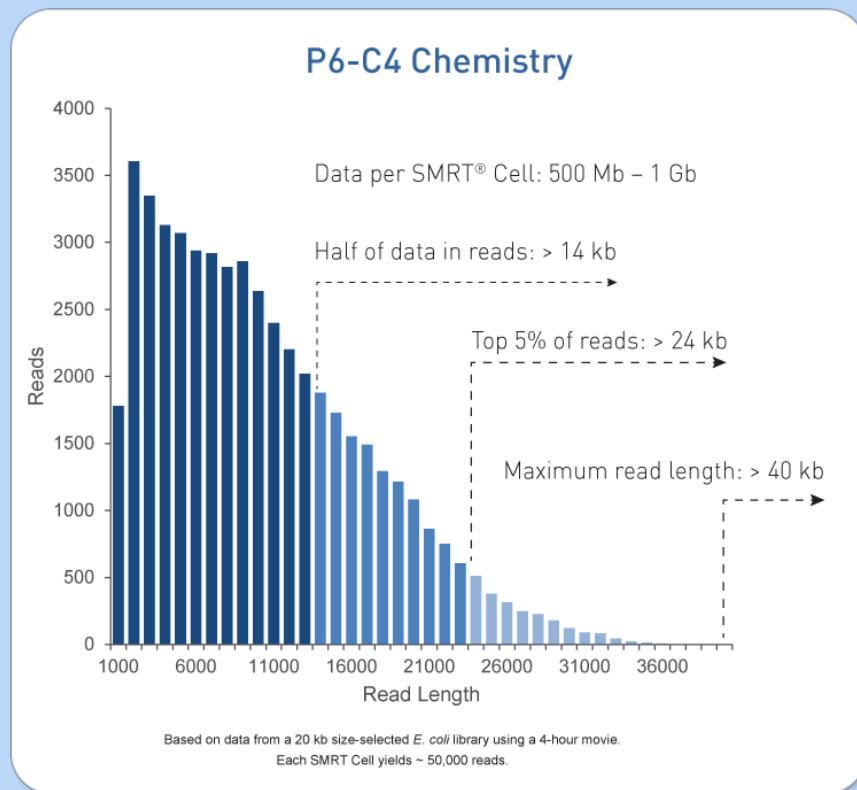
LIFE TECHNOLOGIES

- Ion Torrent PGM, first available in 2011, generates up to 400bp reads (reported) and up to 2Gb (5.5m reads) per run. Cheap fast runs. Ion Proton system can generate up to 10Gb per run. Generates flowgrams and SFF files similar to Roche 454 data as well as the standard fastq files. Ion Torrent is also considered a second generation sequencer.
- ~ 64Gb/day

PACIFIC BIOSYSTEMS

- Pacific Biosystems is so far the most successful third generation DNA sequencing system. Key differences are that its a single molecule, real time (SMRT) technology and capable of producing sequences of multi-kilobases.
- ~ 2Gb/day (20Gb/day)

Third generation sequencers are single molecule sequencers.



OXFORD NANOPORE

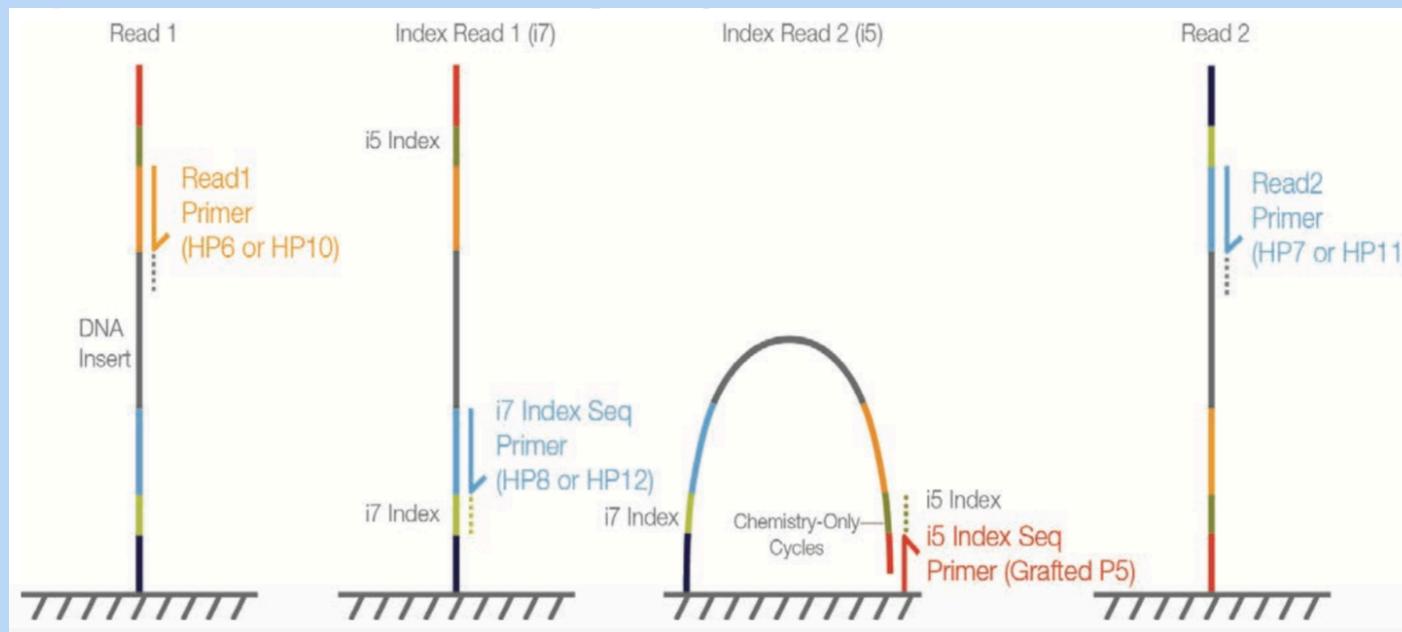
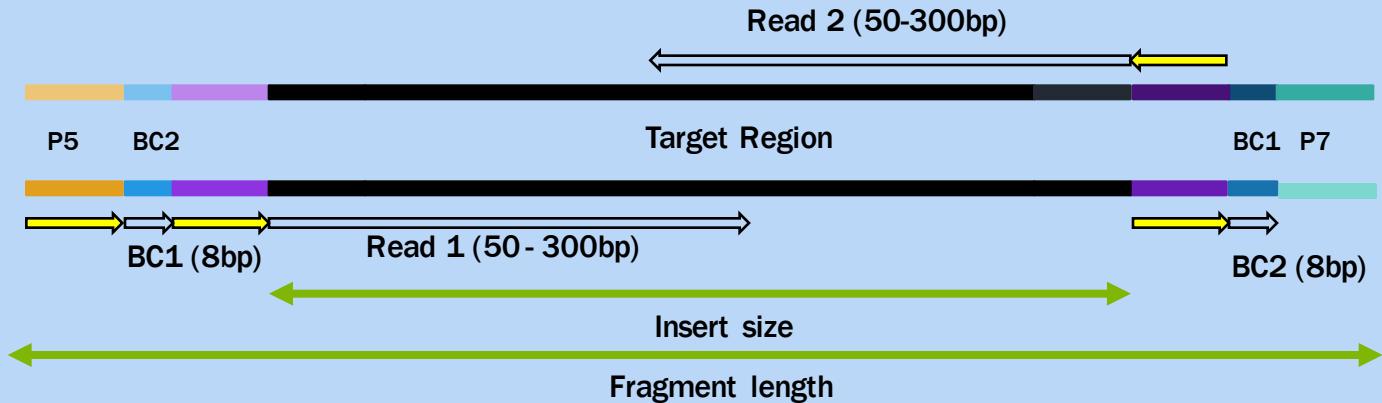
- Another 3rd generation sequencer, founded in 2005 and recently (May 2015) produced a commercial product, the MinION. The sequencer uses nanopore technology developed in the 90's to sequence single molecules.
- > 1Gb per flowcell

FYI: 4th generation sequencing is being described as “In-situ sequencing”, for applications such as “spatial transcriptomics”

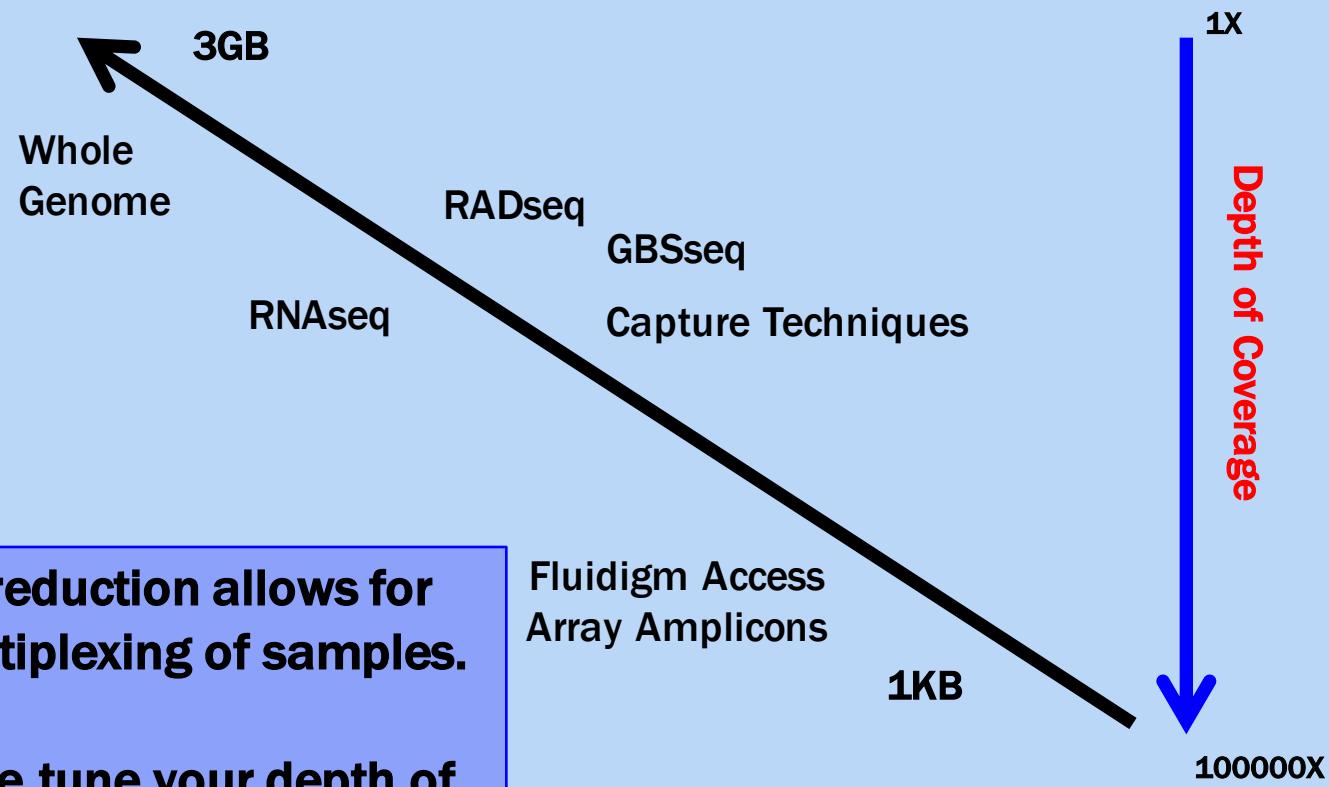


ILLUMINA SEQUENCING

Illumina SBS



GENOMIC REDUCTION



Genomic reduction allows for greater multiplexing of samples.

You can fine tune your depth of coverage needs and sample size with the reduction technique

ILLUMINA HISEQ SEQUENCING

- <http://www.illumina.com/systems/hiseq-3000-4000/specifications.html> 2500
MiSeq

	HISEQ 3000 SYSTEM	HISEQ 4000 SYSTEM
No. of Flow Cells per Run	1	1 or 2
Data Yield:		
2 × 150 bp	650-750 Gb	1300-1500 Gb
2 × 75 bp	325-375 Gb	650-750 Gb
1 × 50 bp	105-125 Gb	210-250 Gb
Clusters Passing Filter (Single Reads) (8 lanes per flow cell)	2.1-2.5 billion	4.3-5 billion
Quality Scores:		
2 × 50 bp	≥ 85% bases above Q30	≥ 85% bases above Q30
2 × 75 bp	≥ 80% bases above Q30	≥ 80% bases above Q30
2 × 150 bp	≥ 75% bases above Q30	≥ 75% bases above Q30
Daily Throughput	> 200 Gb	> 400 Gb
Run Time	< 1-3.5 days	< 1-3.5 days
Human Genomes per Run*	up to 6	up to 12
Exomes per Run**	up to 48	up to 96
Transcriptomes per Run***	up to 50	up to 100



ILLUMINA MISEQ SEQUENCING

MISEQ REAGENT KIT V2			MISEQ REAGENT KIT V3		
READ LENGTH	TOTAL TIME*	OUTPUT	READ LENGTH	TOTAL TIME*	OUTPUT
1 × 36 bp	~4 hrs	540-610 Mb	2 × 75 bp	~21 hrs	3.3-3.8 Gb
2 × 25 bp	~5.5 hrs	750-850 Mb	2 × 300 bp	~56 hrs	13.2-15 Gb
2 × 150 bp	~24 hrs	4.5-5.1 Gb			
2 × 250 bp	~39 hrs	7.5-8.5 Gb			

Reads Passing Filter†
MISEQ REAGENT KIT V2

Single Reads	12-15 M
Paired-End Reads	24-30 M

Quality Scores††	
MISEQ REAGENT KIT V2	MISEQ REAGENT KIT V3
> 90% bases higher than Q30 at 1 × 36 bp	> 85% bases higher than Q30 at 2 × 75 bp
> 90% bases higher than Q30 at 2 × 25 bp	> 70% bases higher than Q30 at 2 × 300 bp
> 80% bases higher than Q30 at 2 × 150 bp	
> 75% bases higher than Q30 at 2 × 250 bp	



Perform

Visit the Illumina website

- How many sequencing machines does Illumina Have?
- What are the differences between the HiSeq 2500 series and HiSeq 3000/4000 series machines?
- What are differences in read length options between the MiSeq and HiSeq?
- What are the differences between the HiSeq's High Output Run Mode and the Rapid Run Mode
- How many reads (and bp) do you get on one lane of a HiSeq 2500 in High Output Run Mode for 1x50 and 2x100, compare those to what you get on the HiSeq 3000
- How many reads (and bp) do you get from one run of a MiSeq 2x300.

HOMEWORK

Getting to know
Illumina

EXPERIMENTAL DESIGN: COMMUNITY PROFILING

Section

EXPERIMENTAL DESIGN

- In high throughput biological work (Microarrays, Sequencing, HT Genotyping, etc.), what may seem like small technical artifacts introduced during sample extraction/preparation can lead to large changes, or technical bias, in the data.
 - Not to say this doesn't occur with smaller scale analysis such as Sanger sequencing or qRT-PCR, but they do become more apparent and may cause significant issues during analysis.

GENERAL RULES FOR PREPARING SAMPLES

- Prepare more samples than you are going to need, i.e. expect some will be of poor quality, or outright fail
- Preparation stages should occur across all samples at the same time (or as close as possible) and by the same person
- Spend time practicing a new technique to produce the highest quality product you can, reliably
- Quality should be established using Fragment analysis traces (pseudo-gel images, FOR RNA RIN > 7.0)
- DNA/RNA should not be degraded
 - 260/280 ratios for RNA should be approximately 2.0 and 260/230 should be between 2.0 and 2.2. Values over 1.8 are acceptable
- Quantity should be determined with a Fluorometer, such as a Qubit.

BE CONSISTENT ACROSS ALL SAMPLES!!!

SEQUENCING DEPTH

- The first and most basic question is how many base pairs of sequence data will I get

Factors to consider are:

- 1. Number of reads being sequenced
- 2. Read length (if paired consider them as individuals)
- 3. Number of samples being sequenced
- 4. Expected percentage of usable data

$$bpPerSample = \frac{readLength * readCount}{sampleCount} * 0.8$$

- The number of reads and read length data are best obtained from the manufacturer's website (search for specifications) and always use the lower end of the estimate.

SEQUENCING COVERAGE

- Once you have the number of base pairs per sample you can then determine expected coverage

Factors to consider are:

- 1. Length of the genome (in bp)
- 2. Any extra-genomic sequence, or contamination

$$\text{expectedCoverage} = \frac{\text{bpPerSample}}{\text{totalGenomicContent}}$$

- Coverage is determined differently for "Counting" based experiments (RNAseq, amplicons) where an expected number of reads per sample is typically more suitable.

MG SEQUENCING DESIGNS

- Taxonomic Identification
 - Amplicon based (e.g. 16s variable regions)
 - Shotgun Metagenomics
- Functional Characterization
 - Shotgun Metagenomics
 - Shotgun Metatranscriptomics (active)
- Genome Assembly, Function and Variation
 - Shotgun Metagenomics
 - Shotgun Metatranscriptomics

PROPOSAL STAGE

Considerations (when a literature search turns up nothing)

- Proportion that is host (non-microbial genomic content)
- Proportion that is microbial (genomic content of interest)
 - Number of species
 - Genome size of each species
 - Relative abundance of each species

The back of the envelope calculation

$$\# \text{Reads} = \frac{\text{Coverage} * \text{Average_Genome_Size}}{0.8 * \text{Read_Len} * \text{Dilution_factor} * 1 - \text{Host_prop}}$$

RAREFACTION CURVES

Plot rarefactions curves of Amplicons, or reconstituted 16S sequence to determine if saturation is achieved

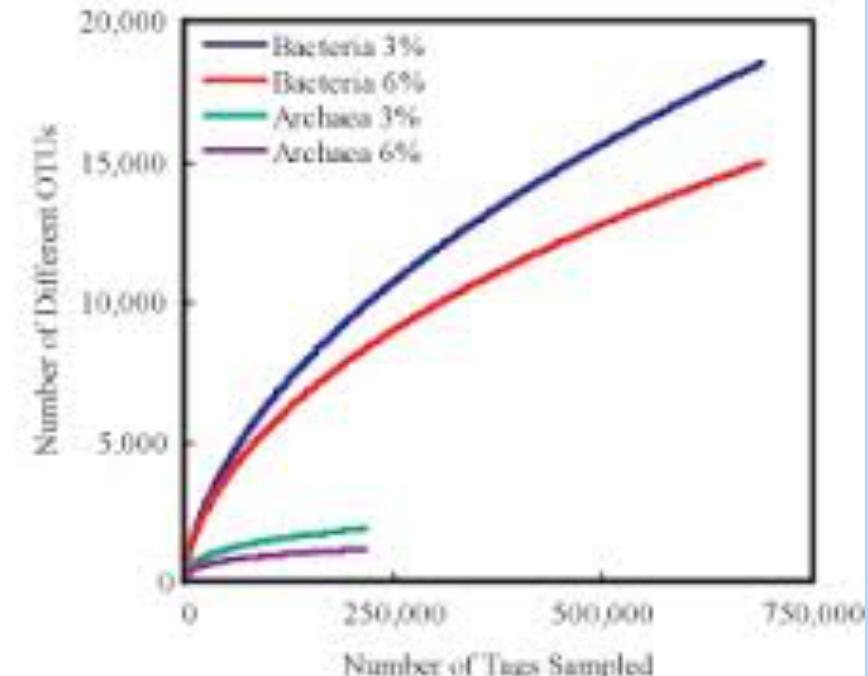
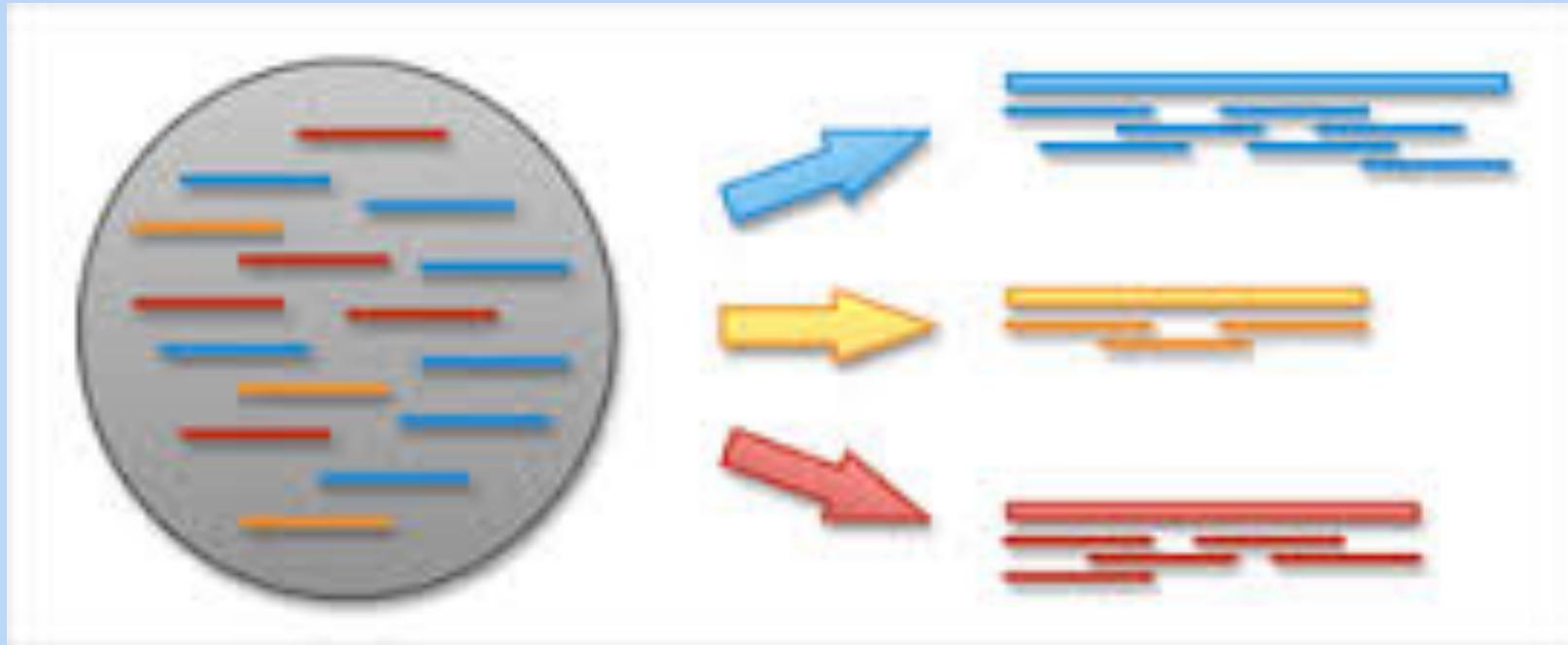


Figure 2

Miller CS, Baker BJ, Thomas BC, Singer SW, Banfield JF (2011) EMIRGE: reconstruction of full-length ribosomal genes from microbial community short read sequencing data. *Genome biology* 12: R44 doi:10.1186/gb-2011-12-5-r44.

METAGENOMICS ASSEMBLY



To determine if you've sequenced 'enough' to re-assemble 'most' of the community member's genetic content, look to what is left over - proportionally

TAKE HOMES

- Experience and/or literature searches (other peoples experiences) will provide the best justification for estimates on needed depth.
- Don't forget about 'contamination' can often be a large source of reads.
- 'Longer' reads are better than short reads, especially for assembly.
- Libraries can be sequenced again, so do a pilot, estimate 'contamination', compute rarefaction/16s coverage then sequence more accordingly.

■ Given

- Read length = 200
 - Desired coverage = 30
 - Average genome size = 5Mb
 - Host = 95%
 - Dilution factor = 1%
- ## ■ How many reads do you need per samples?

HOMEWORK
Depth of coverage

COST ESTIMATION

- DNA/RNA extraction QA/QC (Bioanalyzer/Gels)
- Metatranscriptomes: Enrichment of RNA of interest and RNA library preparation
 - Library QA/QC (Bioanalyzer and Qubit)
 - Pooling (\$10/library)
- Metagenomes: DNA library preparation
 - Library QA/QC (Bioanalyzer and Qubit)
 - Pooling (\$10/library)
- Community Profiling: PCR reactions
 - Library QA/QC (Bioanalyzer and Qubit/microplate reader)
 - Pooling
- Sequencing (Number of Lanes / runs)
- Bioinformatics (General rule is to estimate the same amount as data generation, i.e. double your budget)

<http://dnatech.genomecenter.ucdavis.edu/prices/>

Perform

- Search the web for 16s reads per sample recommendations.
- Cost estimate a metagenomics (DNA) project analysis on 8 samples, 2x100 on a HiSeq 3000 using the number of reads target determined in the last homework

HOMEWORK
COVERAGE

WORKSHOP DATASET

Section

SLASHPILE

- Slash Pile – Accumulated debris from cutting brush or trimming trees
 - Measured, bacteria and fungal communities using 5 amplicons
 - 16sV1V3
 - 16sV4V5
 - ITS1
 - ITS2
 - LSU
- 3 – slashpiles
- 2 depths
- Distance from slashpile

Perform

- Briefly scan the metadata files on the github page
- Upload the fastq reads files to AWS, then extract them
 - https://drive.google.com/open?id=0B_3ITFvg_WhxMVQwUEtZaV9rQzA

HOMEWORK
Workshop Data

THE COMMAND LINE

SECTION

THE COMMAND LINE

- The command line is powerful and the preferred way to run bioinformatics tools

BASICS:

Prompt msettles@MacBook-Pro:~\$
 ~ is your home director
 ... \$ **command [parameters] [files]** ENTER
parameters begin with a - short parameter or
 -- long parameter

Help ... \$ **man command**
 ... \$ **command -h**
 ... \$ **command -help**

Tab complete!!

THE COMMAND LINE

Command input/output:

file/folder on the command line, either as a positional argument or a parameter, or defaults

stdin aka 'standard in', input pipe

stdout aka 'standard out', output pipe

stderr aka 'standard error', pipe for error messages

Special characters:

- | vertical bar is the pipe, it pipes the stdout of one command to the stdin of another cmd
- < > 2> feeds stdin, stdout, stderr to the command
- >> append
- & at the end of a command will run the command in the background
- .
- .. Up one folder
- / folder delimiter
- *
- wild character, match anything

When naming files/folders avoid special characters and spaces (use . and _)!!

THE COMMAND LINE

Basics Commands:

pwd	print the working directory (current dir)
ls [file/dir]	list the current contents of the directory
ls -lah [file/dir]	long list, human readable, show hidden of the directory
cd to	change directory
cp f1 f2	copy file f1 to file f2
mv from to	mv directory (also way to rename)
mkdir dir	make directory
rm file	remove file
rmdir dir	remove an empty directory
rm -r dir	recursively remove a non-empty directory
nano file	edit a document
cat f1 [f2]	print to stdout file f1 then if provided file f2 (concatenate)
less file	view file, one page at a time
head file	view the first 10 lines of a file
tail file	view the last 10 lines of a file

CHEAT SHEETS

Perform

- Look at your home directory, what files are already there, what files are hidden
- Create a new folder
- Move into that folder and create a file (write anything)
- Show that file, using less and cat
- Go back to your home directory
- Create a second folder
- Copy the file from the first directory to the new directory
- Move to your home directory
- Remove both folders
- Learn to use the command 'wc' with 'man wc'
- Play with the new commands

HOMEWORK

Playing with
the command
line

GIT

- Git is an open source program for tracking changes in text files. It was written by the author of the Linux operating system, Linus Torvalds. Use git for:
 - Tracking software changes
 - Tracking notes changes
 - Tracking document changes
- Github is a web-based Git repository hosting service, free to use for open repositories
 - This workshop is available via git and github
 - https://github.com/msettles/Workshop_Community-Profiting

GIT

- **git clone [repo]** – to clone a copy of a repository from the remote server (github) onto your workstation. With your clone you can edit the documents as you please
- **git status** – displays the differences between your repositories and the current working head (changes you've made).
- **git pull** – when you fetch in changes to the repository and merging them in. for example if I edited the workshop repository, you can then pull in those changes to your workstation
- **git checkout** – to checkout different branches

Perform

- **Install system software**
 - `sudo apt-get install bowtie2`
 - `sudo apt-get install openjdk-7-jdk`
 - `sudo apt-get install ant`
- **Using git clone, install from repositories on github**
 - **FLASH2**
 - Using Make, link onto the Path
 - **RDPtools**
 - Using Make
 - **dbcAmplicons**
 - `python setup.py install`

HOMEWORK

Install expHTS
using git and
python

DBCAMPLICONS

Section

MICROBIAL COMMUNITY ANALYSIS

Goal: A culture independent method for profiling the diversity of a community.

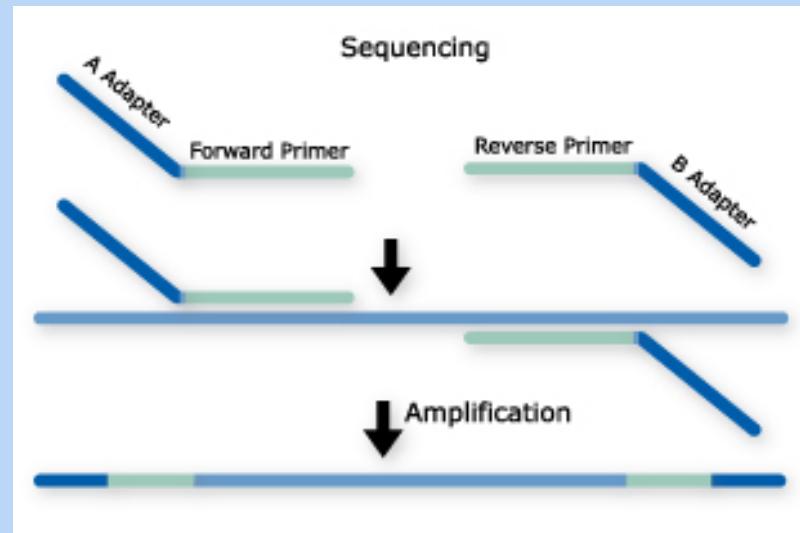
High-throughput sequencing technologies (such as Illumina) can generate millions of amplicons, across thousands of samples in a single run, and are today our best approach to deeply assess the environmental or clinical diversity of complex microbial assemblages of archaea, bacteria, and eukaryotes.

Using sequence variation within a common gene (e.g. 16s) to assign and count community members rather than counting individual cells. Assume each sequence variant is one community member.

AMPLICONS: COMMON APPROACH

- Single PCR
- Long primer sequences (~75bp) that contain barcodes and sequencing adapters
- Single or dual barcodes
(dual barcode often within read 2)

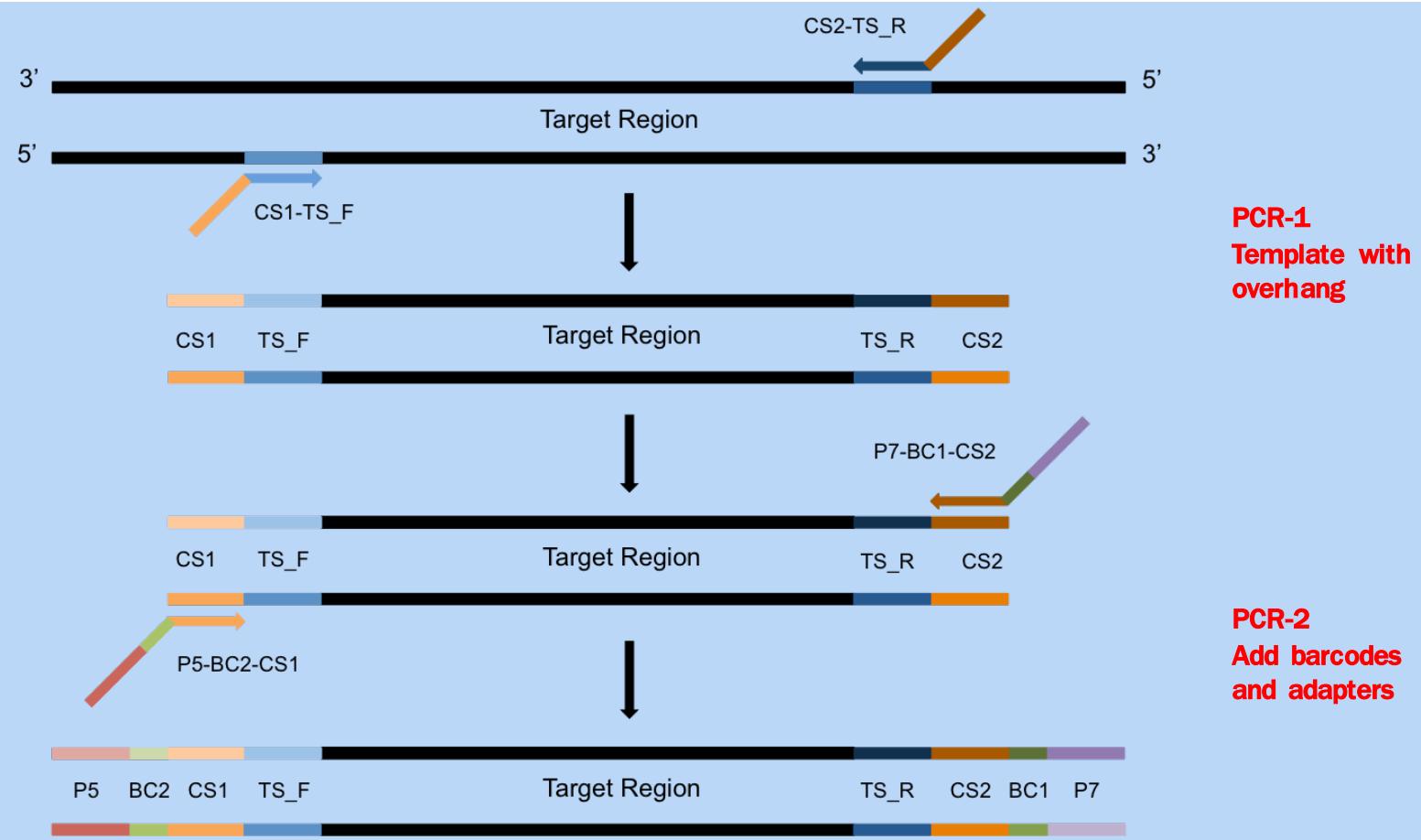
Common approach



DBCAMPLICONS

- Originally conceived in late 2012 to lower per sample costs on relatively short targeted (PCR) regions
 - 16S, ITS, LSU, 18S, etc. Community profiling
 - Extraction of mitochondria, virae, chloroplast regions, plasmids by PCR
 - Genotyping of samples for phylogenomics, genome to phenotype interactions
- Uses the Illumina platform, capable of pooling thousands, or even tens of thousands of barcoded samples/targets per sequencing run.
- Core Facility friendly, facilitates interactions between and across individual labs, standardizing workflows.

AMPLICONS: ALTERNATIVE APPROACH



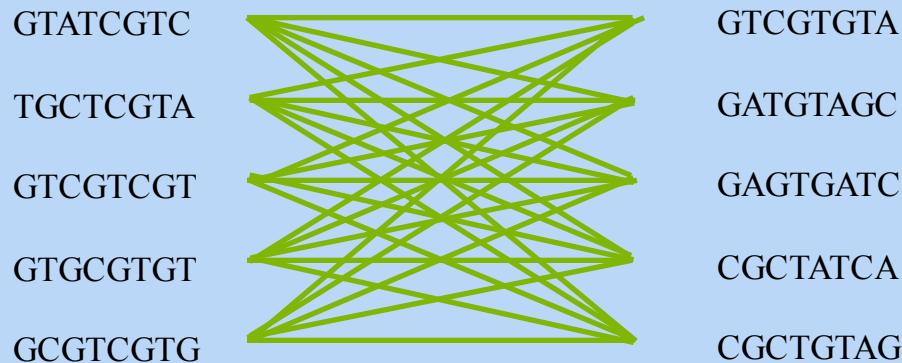
Barcodes and adapters are added in the second round of PCR

MULTIPLEX SAMPLES

Dual barcoding allows for massively multiplexing of samples using only a relatively few primers

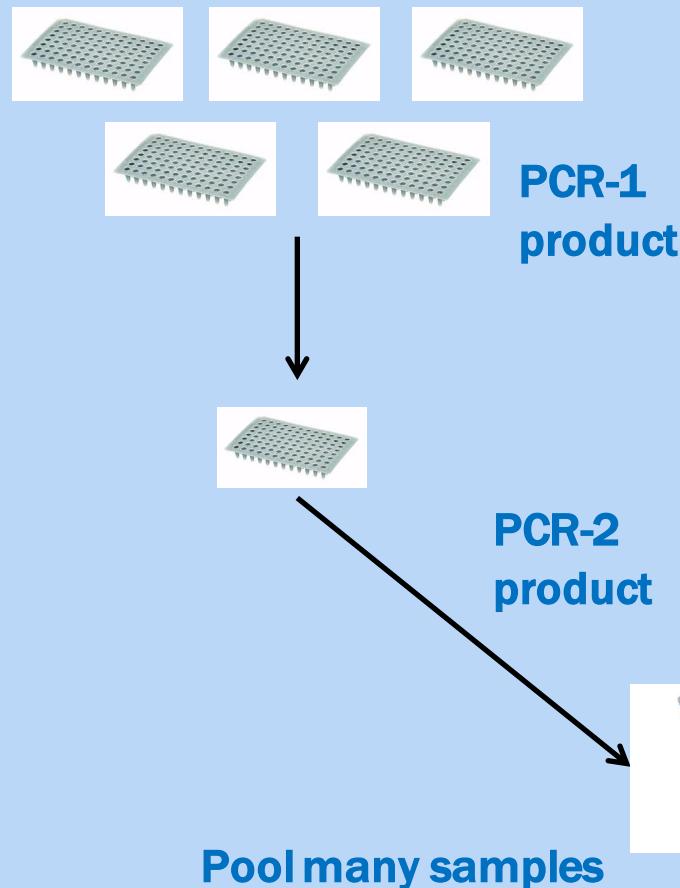
Pairing of BC1 and BC2 uniquely identifies sample

8bp [Error-Correcting] Barcodes

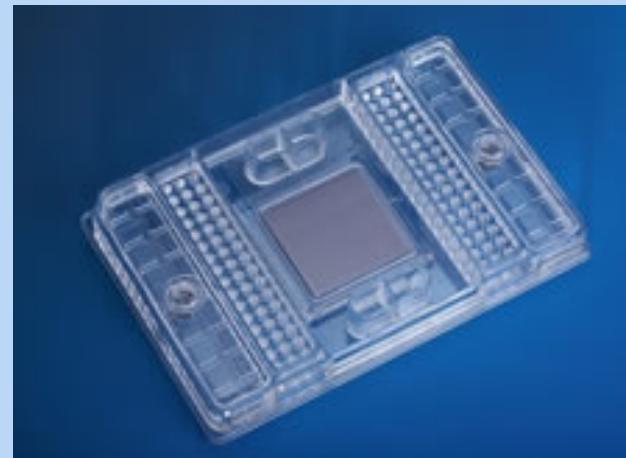


5 Pairs of Barcodes allows for multiplexing of 25 samples.
32 Pairs can multiplex 1024 samples in the same sequencing reaction

MULTIPLEX AMPLICON TARGETS

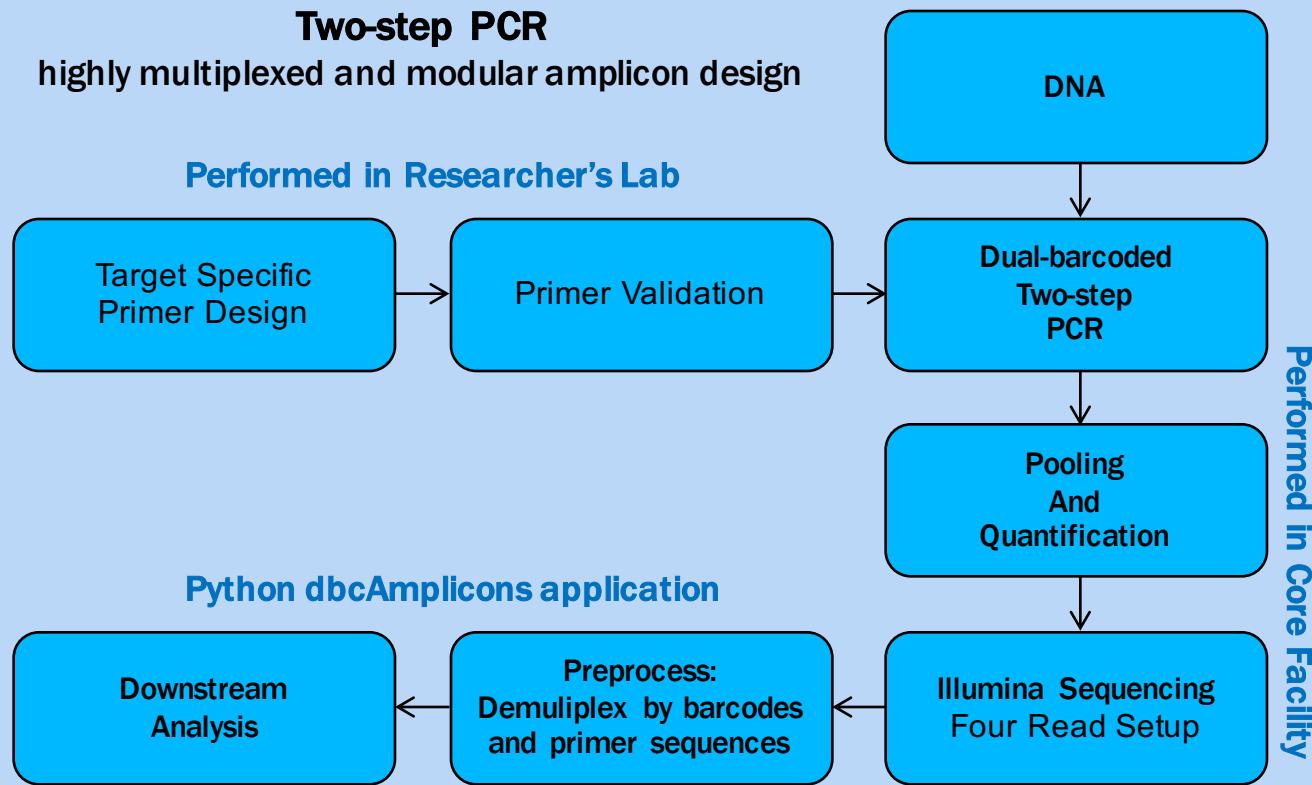


Fluidigm Access Array System



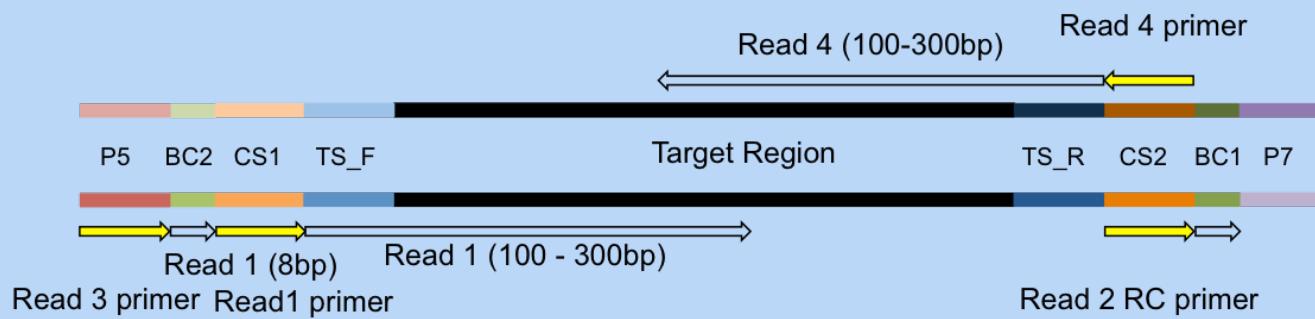
48 samples X 48 amplicons
2304 Two-step PCR reactions

DBCAMPLICONS



SEQUENCING

Illumina four read sequencing run



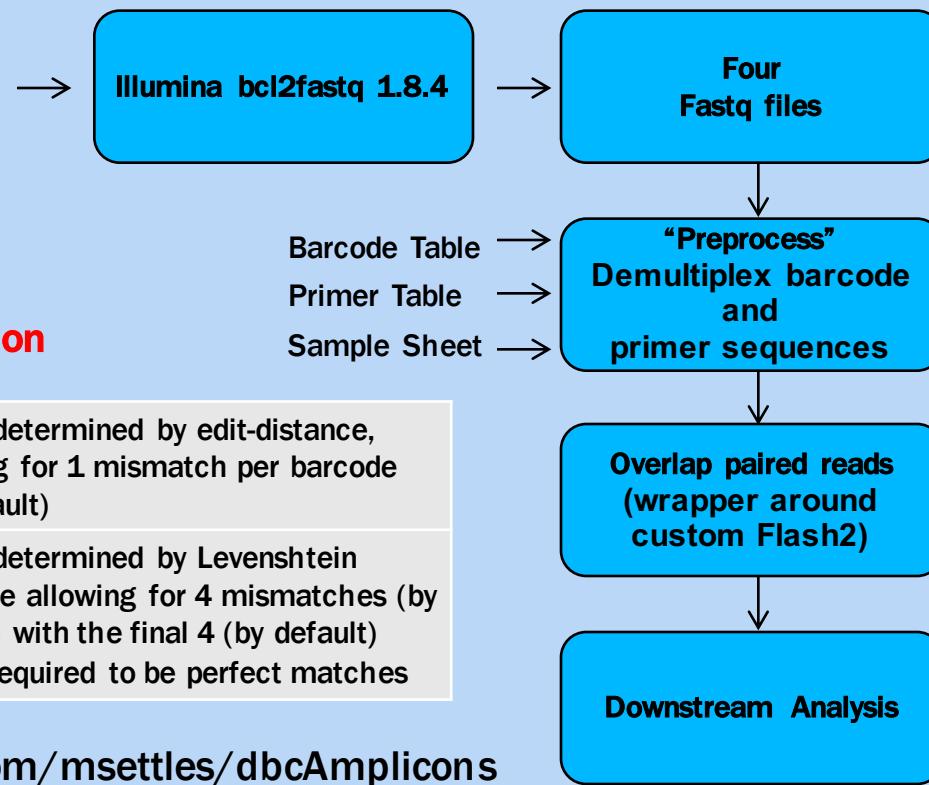
Read	Sequencing Primer
Read1 primer	CS1 - 5' ACACTGACGACATGGTTCTACA
Read2 primer	CS2 - 5' TACGGTAGCAGAGACTTGGTCT
BC1 primer	CS2rc - 5' AGACCAAGTCTTGCTACCGTA
BC2 primer	Uses the P5 amplification primer

BIOINFORMATICS



dbcAmplicons Python Application

Barcode	Match determined by edit-distance, allowing for 1 mismatch per barcode (by default)
Primers	Match determined by Levenshtein Distance allowing for 4 mismatches (by default) with the final 4 (by default) bases required to be perfect matches



<https://github.com/msettles/dbcAmplicons>

DOWNSTREAM ANALYSIS

Population Community Profiling (i.e. microbial, bacterial, fungal, etc.)

[dbcAmplicons Python Application](#)

Screen	Using Bowtie2, screen targets against a reference fasta file, separating reads by those that produce matches and those that do not match sequences in the reference database.
Classify	Wrapper around the MSU Ribosomal Database Project (RDP) Classifier for Bacterial and Archaeal 16S rRNA sequences, Fungal 28S rRNA, fungal ITS regions
Abundance	Reduce RDP classifier results to abundance tables (or biom file format), rows are taxa and columns are samples ready for additional community analysis.

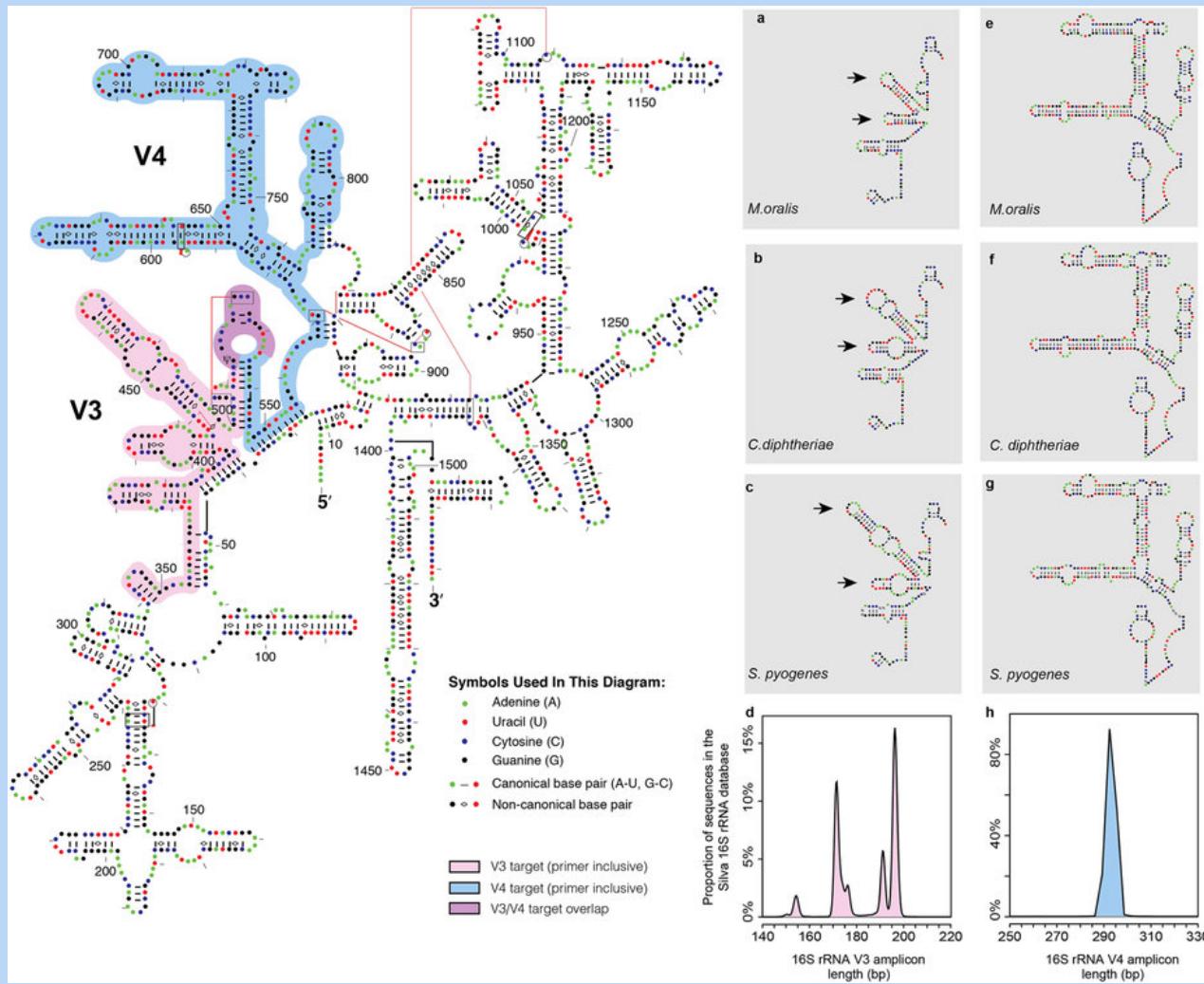
[Targeted Re-sequencing](#)

	Consensus - Reduce reads to consensus sequence for each sample and amplicon
R-functions to be added into dbcAmplicons	Most Common – Reduce reads to the most commonly occurring read in the sample and amplicon (that is present in at least 5% and 5 reads, by default)
	Haplotypes – Impute the different haplotypes in the sample and amplicon

SUPPLEMENTAL SCRIPTS

- `convert2Readto4Read.py`
 - For when samples are processed by someone else
- `splitReadsBySample.py`
 - To facilitate upload to the SRC

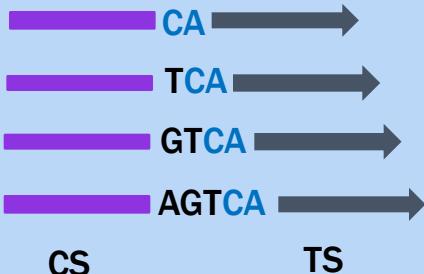
PRIMER DESIGN



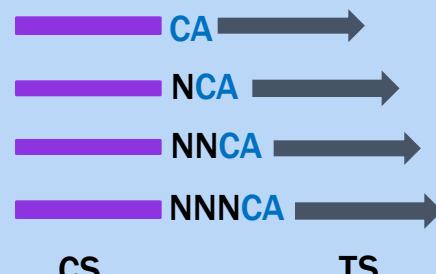
TEMPLATE SPECIFIC PRIMER DESIGN

- Each primer pair contains the following parts
 - CS1 or CS2 to attach second adapter/barcode primer
 - Phase-shifting bases [see below]
 - Linker sequence
 - Template specific primer sequence

Phase shifting primer



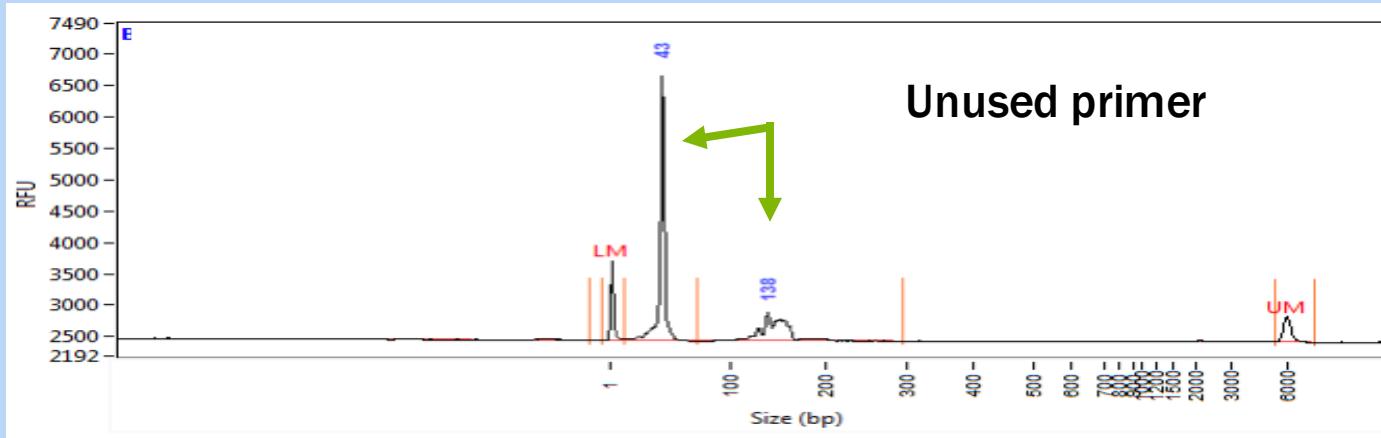
Phase shifting primers with PCR duplicate detection



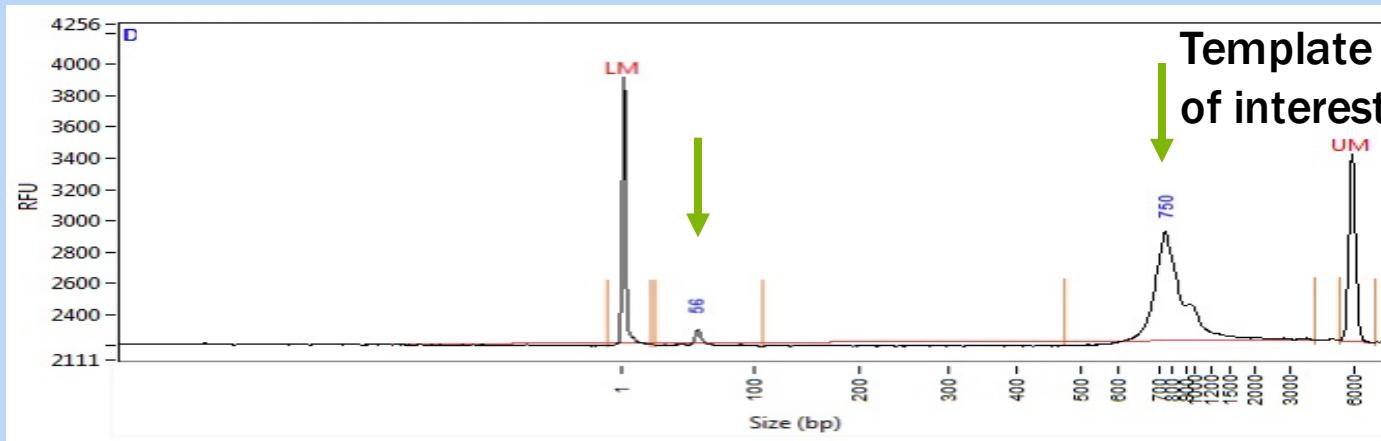
Ns, resolve to be PCR
duplicate keys and should
only ever appear once

QC: WHAT IS A “GOOD” LIBRARY?

Unused primers and adapters



BAD!



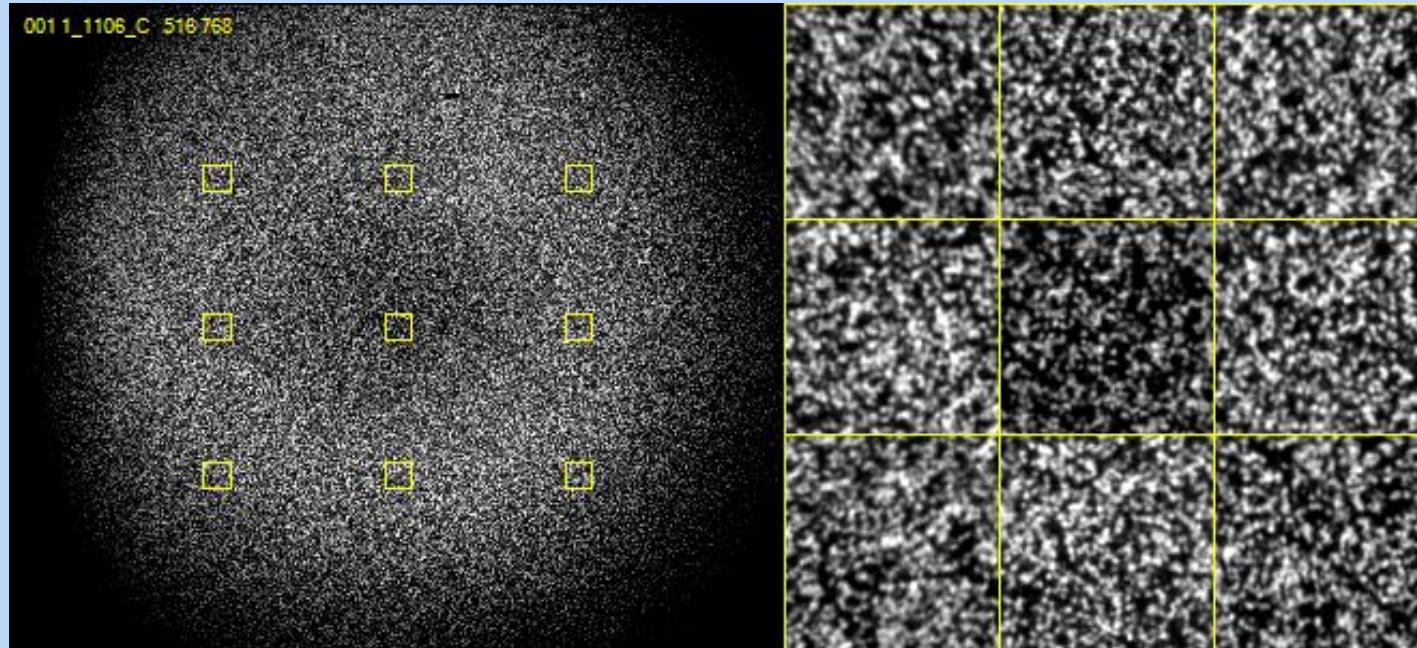
Good!

POOLING SAMPLES/AMPLICONS

- Even amplicon representation is important and difficult to achieve. Amplicon counts can vary from sample to sample by 100x
- Each amplicon should be evaluated by quality (ideally by trace) and quantity (fluourometry). Both qualities will effect final counts.
- Best practices
 - First group amplicons by quality/quantity profiles
 - Pool each group separately
 - If a small number of groups consider qPCR on each group for final pooling concentrations
 - If a large number re-quantify and pool to final pool.

NUCLEOTIDE DIVERSITY

Critically important for imaging clusters



AMPLICON RUNS ARE LOW COMPLEXITY

- Sequencing with lower cluster density
- Adding in highly diverse libraries (shotgun libraries ~15%)
- Phase-shifting template specific primers:

What is nucleotide diversity?

The term "nucleotide diversity" describes the proportion of each nucleotide (A, T, C, and G) at each position in a sequencing library. A "balanced" or "diverse" library has *equal proportions* of A, C, G, and T nucleotides at each base position in a sequencing library. Figure 9 illustrates cluster images and SAV data by cycle plots from diverse/balanced, low-diversity, and unbalanced libraries.

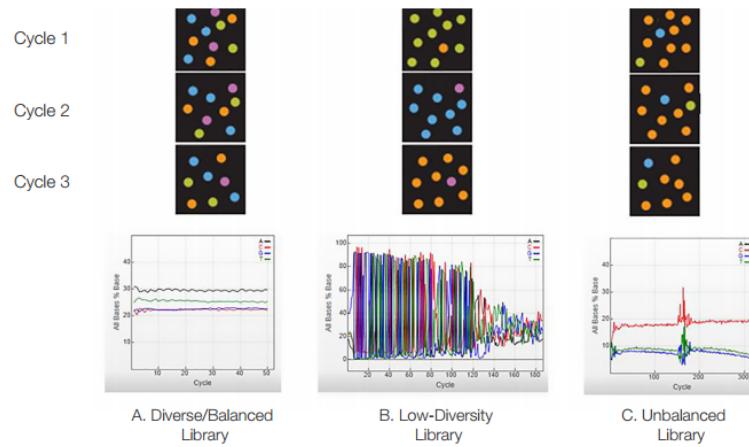


Figure 9: Nucleotide Diversity and Data by Cycle: % Base Plots. A) Diverse/balanced libraries contain equal proportions of A, T, C, and G nucleotides. The Data by Cycle: % Base plot shows even, horizontal curves centered around 25%. B) Low-diversity libraries, such as amplicon, enriched/targeted, or ChIP libraries, have an uneven proportion of nucleotides across the flow cell from one cycle to the next. The Data by Cycle: % Bases plot shows large intensity spikes at each cycle. C) Unbalanced libraries, such as bisulfite converted or Tetrahymena libraries, have one base at a much lower percentage than the others. This example shows a library with a low percentage of the "A" nucleotide.

BENEFITS/DRAWBACKS

Benefits

- Maximum Flexibility, fewer target specific primers needed.
- Dual barcoding, allowing for massively multiplexing of samples to occur.
- Pool multiple targets per run
- Software for demultiplexing

Drawbacks

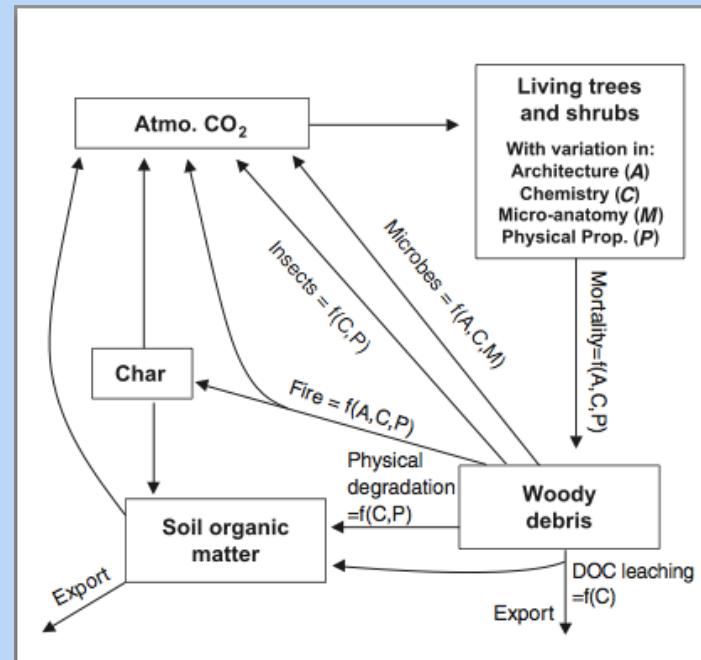
- Two – step PCR reaction
- Sequence the target specific primer

COMMUNITY PROFILING (ZANNE LAB GWU)

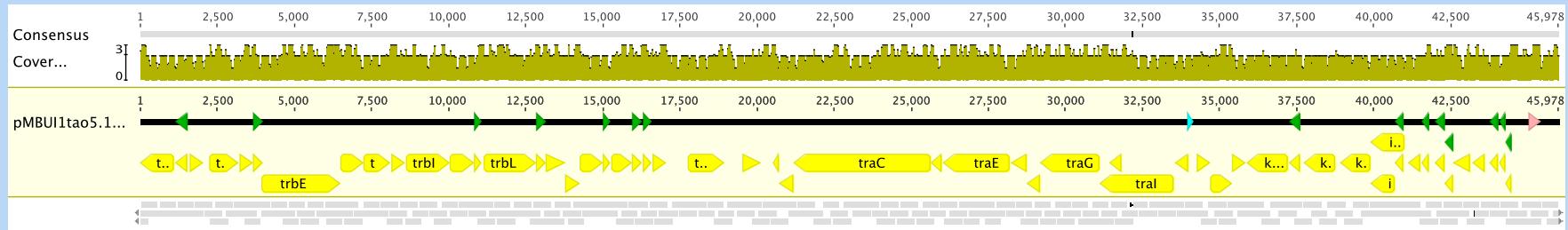
Examine differences in wood decomposition rates across 21 species in two environmental settings (ridge tops and valley bottoms) and how these rates relate to plant functional traits and their fungal and microorganism communities.

Characterize the bacterial, fungal and 'other' microorganisms (2x16S, 2xITS, and LSU)

576 samples X 5 amplicons
2,880 unique amplicon products
~6,000 reads per amplicon



SMALL GENOME SEQUENCING (TOP LAB UI)



Resequencing of the pMBUI1 plasmid from three evolution experiments in *E. coli*, *C. necator* and a combination of the two (i.e. host switching) in order to identify plasmid encoded mutations that may be involved in plasmid host range expansion and evolution

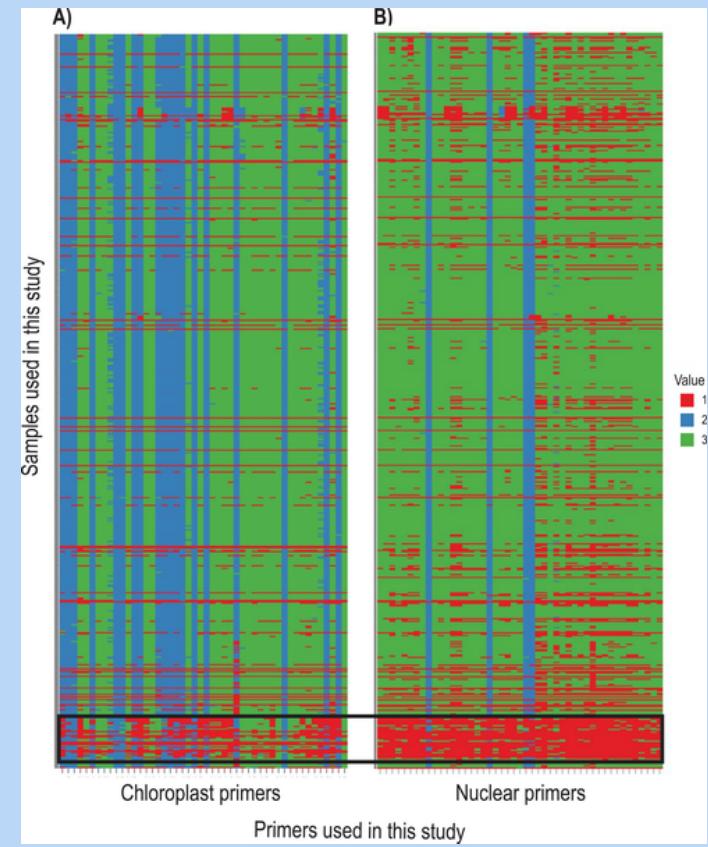
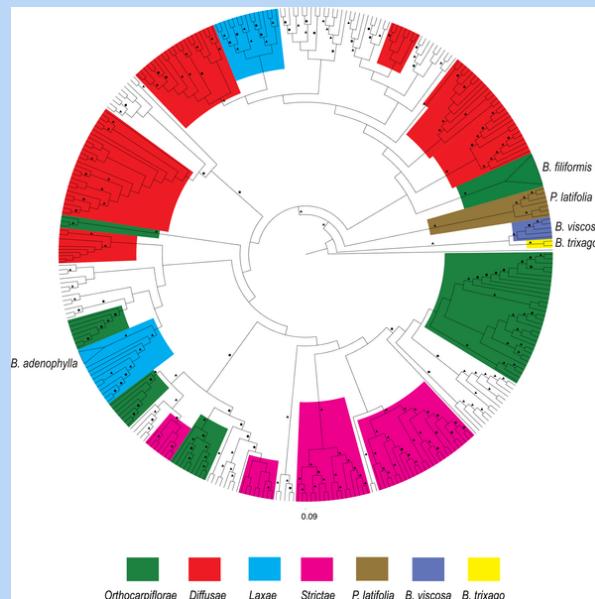
1 – Fluidigm Chip
47 samples X 192 amplicons
9,024 unique amplicon products
~900 reads per amplicon

Fluidigm Chip	\$710
Pooling/Primers	\$220
1/2 MiSeq run (2x300)	\$1,100
Total	\$2,030
	\$43/genome

PHYLOGENOMICS (TANK LAB UI)

24 – Fluidigm Chips
576 samples X 96 amplicons
55,296 unique amplicon products
~300 reads per amplicon ~\$35/sample

Sequence
phylogenetically
informative regions
(Chloroplast and
Nuclear)
across many, many
samples



FUTURE DIRECTIONS

- Include error-correcting barcodes in demultiplexing
- Identification of PCR duplicates
- Replace RDP classification with another scheme
 - Have ideas (for years) but no time
- Extend to community analysis (maybe a Shiny app).
dbcAmplicons is a data reduction pipeline, not a complete analysis pipeline
- Incorporate the R genotyping pipeline into dbcAmplicons
 - Extend to inferring copy number (or ploidy levels)

DBCAMPLICONS ANALYSIS

- Approach is an DNA-result pipeline
- Requires
 - Illumina bcl2fastq
 - Python
 - Few python libs, like biom
 - Flash2 (<https://github.com/dstreett/FLASH2>)
 - Bowtie2 – for off-target screening
 - RDP (<https://github.com/rdpstaf/RDPTools>) - for classification
- dbcAmplicons
 - <https://github.com/msettlesdbcAmplicons>

```
mattsettles@Matts-MBP:~$ dbcAmplicons -h
usage: dbcAmplicons [-h] [--version]
                     {validate,preprocess,join,screen,classify,abundance} ...
```

dbcAmplicons, a python package for preprocessing of massively multiplexed,
dual barcoded Illumina Amplicons

positional arguments:

{validate,preprocess,join,screen,classify,abundance}	commands
validate	validate the sample, barcode and primer sheets
preprocess	Preprocess four read raw amplicon data, identifying barcode and primer sequence
join	join reads using flash2
screen	screen reads using bowtie2 and a reference sequence file
classify	classify reads using RDP generating a fixrank formatted file
abundance	Generate an abundance table from a fixrank formatted file

optional arguments:

-h, --help	show this help message and exit
--version	show program's version number and exit

For questions or comments, please contact Matt Settles <settles@ucdavis.edu>

```
mattsettles@Matts-MBP:~$
```

Stages of the Pipeline

BARCODES SHEET

#BarcodeID	Read2RC	Read3
Alpha1	TAAGGCGA	TAGATCGC
Alpha2	TAAGGCGA	CTCTCTAT
Alpha3	TAAGGCGA	TATCCTCT
Alpha4	TAAGGCGA	AGAGTAGA
Alpha5	TAAGGCGA	GTAAGGAG
Alpha6	TAAGGCGA	ACTGCATA
Alpha7	TAAGGCGA	AAGGAGTA
Alpha8	TAAGGCGA	CTAACGCCT
Alpha9	TAAGGCGA	TGAACCTT
Alpha10	TAAGGCGA	TGCTAAGT
Alpha11	TAAGGCGA	TGTTCTCT
Alpha12	TAAGGCGA	TAAGACAC
Alpha13	TAAGGCGA	CTAATCGA
Alpha14	TAAGGCGA	CTAGAAACA
Alpha15	TAAGGCGA	TAAGTTCC
Alpha16	TAAGGCGA	TAGACCTA
Alpha17	TAAGGCGA	TATAGCCT
Alpha18	TAAGGCGA	ATAGAGGC
Alpha19	TAAGGCGA	CCTATCCT
Alpha20	TAAGGCGA	GGCTCTGA
Alpha21	TAAGGCGA	AGGCGAAG
Alpha22	TAAGGCGA	TAATCTTA
Alpha23	TAAGGCGA	CAGGACGT

- Tab-separated text file, 3 columns
 - Barcode name
 - sequence of read 2
 - sequence of read 3
- Orientation is important, read 2 comes off in reverse complement

PRIMER SHEET

#Read	Pair_ID	Primer_ID	Sequence
P5	16S	27F_YM1	GTAGAGTTGATCCTGGCTCAG
P5	16S	27F_YM2	CGTAGAGTTGATCATGGCTCAG
P5	16S	27F_YM3	ACGTAGAGTTGATTCTGGCTCAG
P5	16S	27F_YM4	TACGTAGAGTTGATTATGGCTCAG
P5	16S	27F_Bif	GTACGTAGGGTTCGATTCTGGCTCAG
P5	16S	27F_Bor	CGTACGTAGAGTTGATCCTGGCTTAG
P5	16S	27F_Chl	ACGTACGTAGAATTGATCTGGTTCA
P7	16S	534R_1	CCATTACCGCGGCTGCTGG
P7	16S	534R_2	GCCATTACCGCGGCTGCTGG
P7	16S	534R_3	TGCCATTACCGCGGCTGCTGG
P7	16S	534R_4	ATGCCATTACCGCGGCTGCTGG
P7	16S	534R_5	CATGCCATTACCGCGGCTGCTGG
P7	16S	534R_6	TCATGCCATTACCGCGGCTGCTGG
P7	16S	534R_7	ATCATGCCATTACCGCGGCTGCTGG

- Tab-separated text file, 4 columns
 - Read from machine
 - primer pair ID
 - individual primer ID
 - sequence of primer (without CS tag!)
- accepts IUPAC ambiguity codes

SAMPLE METADATA SHEET

- Tab-separated text file
- 4 columns required, additional metadata in additional columns will be added to biom file
- Formatting is important! (no #\$\$%^|\{\}; characters)
- can search multiple primers (comma separated or * [any]) or no primer (-)

- can make
subdirectories for
individual projects

SampleID	BarcodeID	PrimerPairID	ProjectID
1	Delta146	16S	subfolder/match_16S
2	Delta147	16S	subfolder/match_16S
3	Delta148	16S	subfolder/match_16S
4	Delta149	16S	subfolder/match_16S
5	Delta150	16S	subfolder/match_16S
6	Delta151	16S	subfolder/match_16S
7	Delta152	16S	subfolder/match_16S
8	Delta153	16S	subfolder/match_16S
9	Delta154	16S	subfolder/match_16S
10	Delta155	16S	subfolder/match_16S
11	Delta156	16S	subfolder/match_16S
12	Delta157	16S	subfolder/match_16S
13	Delta158	16S	subfolder/match_16S
14	Delta159	16S	subfolder/match_16S
15	Delta160	16S	subfolder/match_16S

```
mattsettles@Matts-MBP:~$ dbcAmplicons validate -h
usage: dbcAmplicons validate [-h] -B FILENAME -P FILENAME -S FILENAME [-v]
                               [--debug]

optional arguments:
  -h, --help            show this help message and exit
  -B FILENAME, --barcodes_file FILENAME
                        file with barcodes
  -P FILENAME, --primer_file FILENAME
                        file with primers
  -S FILENAME, --sample_metadata FILENAME
                        file with sample metadata
  -v, --silent          silences verbose output [default: False]
  --debug              show traceback on error
mattsettles@Matts-MBP:~$
```

dbcAmplicons
validate
command

- Generate the
 - Barcode, primer and sample input files
- Use dbcAmplicons validate to validate the files

HOMEWORK
Validate

SEQUENCING READ FILES

fasta files

>sequence1

ACCCATGATTGCGA

qual files

>sequence1

40 40 39 39 40 39 40 40 40 40 40 20 20 36 39 39

fastq files

@sequence1

ACCCATGATTGCGA

+

IHHIHII55EHH

QUALITY SCORES

$$Q = -10 \log_{10} P$$

Phred Quality Score	Probability of incorrect base call	Base call accuracy
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1000	99.9%
40	1 in 10000	99.99%

QSCORE CONVERSION

$Q_{\text{sanger}} = -10 \log_{10} P$ - based on probability (aka phred)

$Q_{\text{solexa}} = -10 \log_{10} \frac{P}{1-P}$ - based on odds

S - Sanger	Phred+33,	raw reads typically (0, 40)
X - Solexa	Solexa+64,	raw reads typically (-5, 40)
I - Illumina 1.3+	Phred+64,	raw reads typically (0, 40)
J - Illumina 1.5+	Phred+64,	raw reads typically (3, 40)
L - Illumina 1.8+	Phred+33,	raw reads typically (0, 41)

ILLUMINA READ NAMING CONVENTIONS

CASAVA 1.8 Read IDs

- @EAS139:136:FC706VJ:2:2104:15343:197393 1:Y:18:ATCACG
 - EAS139 the unique instrument name
 - 136 the run id
 - FC706VJ the flowcell id
 - 2 flowcell lane
 - 2104 tile number within the flowcell lane
 - 15343 'x'-coordinate of the cluster within the tile
 - 197393 'y'-coordinate of the cluster within the tile
 - 1 the member of a pair, 1 or 2 (paired-end or mate-pair reads only)
 - Y Y if the read fails filter (read is bad), N otherwise
 - 18 0 when none of the control bits are on, otherwise it is an even number
 - ATCACG index sequence

dbcAmplicons preprocess command

```
mattsettles@Matts-MBP:~$ dbcAmplicons preprocess -h
usage: dbcAmplicons preprocess [-h] -B FILENAME [-d BARCODEDIFF] [-P FILENAME]
                               [-D PRIMERDIFF] [-e PRIMEREND] [-f DEDUP_FLOAT]
                               [-S FILENAME] [-q MINQ] [-l MINL]
                               [-b BATCHSIZE] [-O PREFIX] [-U] [-u] [-v] -1
                               read1 [read1 ...] [-2 read2 [read2 ...]]
                               [-3 read3 [read3 ...]] [-4 read4 [read4 ...]]
                               [--test] [--keepPrimers] [--debug]

optional arguments:
-h, --help            show this help message and exit
-B FILENAME, --barcodes_file FILENAME
                     file with barcodes
-d BARCODEDIFF, --barcodediff BARCODEDIFF
                     max hamming dist from barcode [default: 1]
-P FILENAME, --primer_file FILENAME
                     file with primers
-D PRIMERDIFF, --primerdiff PRIMERDIFF
                     max hamming dist from primer [default: 4]
-e PRIMEREND, --primerend PRIMEREND
                     required number of matching bases at end of primer
                     [default: 4]
-f DEDUP_FLOAT, --dedup_float DEDUP_FLOAT
                     number of bases preceding primer used to deduplicate
                     reads [default: 0]
-S FILENAME, --sample_metadata FILENAME
                     file with sample metadata
-q MINQ, --minQ MINQ trim 3' end of sequences to minQ [default: None]
-l MINL, --minL MINL if minQ is not None, only keep reads that are at least
                     minL length [default: 0]
-b BATCHSIZE, --batchsize BATCHSIZE
                     batch size to process reads in [default: 100000]
-O PREFIX, --output_prefix PREFIX
                     output file basename [default: fastq_prefix]
-U, --output_unidentified
                     output unidentified reads [default: False]
-u, --uncompressed leave output files uncompressed [default: False]
-v, --silent    silences verbose output [default: False]
-1 read1 [read1 ...] read1 of an amplicon fastq four file set
-2 read2 [read2 ...] read2 of an amplicon fastq four file set
-3 read3 [read3 ...] read3 of an amplicon fastq four file set
-4 read4 [read4 ...] read4 of an amplicon fastq four file set
--test          exit after the first batch in order to test the inputs
--keepPrimers  Don't cut off the primer sequence, leave it as a part
                     of the read [default: 0]
--debug         show traceback on error
```

```
mattsettles@Matts-MBP:~$ █
```

BARCODE/PRIMER COMPARISON

Barcode Comparison

ACTGACTG
GTCAGCTA
TCAGTCAG
CGTACGTA

ACTTACTG

Compares each barcode to all possible barcodes and returns the best match < desired **edit distance**

Primer Comparison

GGCTTGGTCATTTAGAGGAA**GTAA** Primer 1
TACGGCTTGGTCATTTAGAGGAA**GTAA** Primer 2
CGGCTTGGTCATTTAGAGGAA**GTAA** Primer 3
ACGGCTTGGTCATTTAGAGGAA**GTAA** Primer 4
TACGGCTTGGTCATTTAGAGGAA**GTAA****AAGTCGTAA** Read

Compares the beginning (primer region) of each read to all possible primers and returns the best match < specified maximum **Levenshtein distance**
+ final 4 exact match

PREPROCESS COMMAND

The Minimal preprocess command

Takes:

- 4 fastq files (Read 1, Index 1, Index 2, Read 2)
- Table of barcodes (indices) used in the run
- Table of sequences and names of template-specific primers
- Table of sample names and the assigned barcodes and primers for each

```
dbcAmplicons preprocess \  
-B barcodeLookupTable.txt \  
-P primerLookupTable.txt \  
-S sampleLookupTable.txt \  
-1 data_R1_001.fastq.gz
```

STANDARD OUTPUT

```
alida@alida:~/Documents/Idaho/IBEST/dbcAmplicons workshops/tests$ dbcAmplicons preprocess -b 10000 -B barcodeLookupTable.txt  
-P primerLookupTable.txt -S sampleLookupTable.txt -1 Test100K_16S_R1_001.fastq.gz  
barcode table length: 864  
primer table length P5 Primer Sequences:7, P7 Primer Sequences:7  
sample table length: 130, and 3 projects.  
processed 10000 total reads, 6859.0 Reads/second, 4901 identified reads(49.0%), 5099 unidentified reads  
processed 20000 total reads, 6686.0 Reads/second, 9948 identified reads(49.7%), 10052 unidentified reads  
processed 30000 total reads, 6656.0 Reads/second, 14981 identified reads(49.9%), 15019 unidentified reads  
processed 40000 total reads, 6666.0 Reads/second, 20041 identified reads(50.1%), 19959 unidentified reads  
processed 50000 total reads, 6641.0 Reads/second, 25166 identified reads(50.3%), 24834 unidentified reads  
processed 60000 total reads, 6640.0 Reads/second, 30166 identified reads(50.3%), 29834 unidentified reads  
processed 70000 total reads, 6593.0 Reads/second, 35203 identified reads(50.3%), 34797 unidentified reads  
processed 80000 total reads, 6584.0 Reads/second, 40309 identified reads(50.4%), 39691 unidentified reads  
processed 90000 total reads, 6580.0 Reads/second, 45322 identified reads(50.4%), 44678 unidentified reads  
processed 100000 total reads, 6554.0 Reads/second, 50353 identified reads(50.4%), 49647 unidentified reads  
100000 reads processed in 0.25 minutes, 50353 (50.4%) identified  
  
29914 reads (29.9% of total run) found for project      match_twoprimer  
2195 reads (2.2% of total run) found for project      subfolder/match_16S  
18244 reads (18.2% of total run) found for project    match_wildcard  
Cleaning up.
```

OUTPUTS: IDENTIFIED_BARCODES.TXT

Barcode	X16S	None
Delta146	44	0
Delta147	44	0
Delta148	44	0
Delta149	63	0
Delta150	50	0
Delta151	29	0
Delta152	49	0
Delta153	60	0
Delta154	32	0
Delta155	95	0
Delta156	63	0
Delta157	110	0
Delta158	67	0
Delta159	74	0
Delta160	14	0
Delta161	1	0
Delta162	130	0
Delta163	171	0
Delta164	100	0
Delta165	115	0
Delta166	118	0

- Tab-separated text file listing all barcodes that had at least 1 read
- Rows list number of reads per barcode
- Columns list the primers provided

OUTPUTS: DIRECTORIES AND FILES

```
alida 23K Feb 11 11:11 barcodeLookupTable.txt
alida 2.0K Feb 11 13:04 Identified_Barcodes.txt
alida 3.9M Feb 11 13:04 match_twoprimer_R1.fastq.gz
alida 4.1M Feb 11 13:04 match_twoprimer_R2.fastq.gz
alida 2.5M Feb 11 13:04 match_wildcard_R1.fastq.gz
alida 2.6M Feb 11 13:04 match_wildcard_R2.fastq.gz
alida 579 Feb 11 11:34 primerLookupTable.txt
alida 5.2K Feb 11 13:03 sampleLookupTable.txt
alida 4.0K Feb 11 13:03 subfolder/
alida 3.3K Feb 11 12:02 table.txt
alida 15M Feb 11 11:11 Test100K_16S_R1_001.fastq.gz
alida 794K Feb 11 11:11 Test100K_16S_R2_001.fastq.gz
alida 893K Feb 11 11:11 Test100K_16S_R3_001.fastq.gz
alida 16M Feb 11 11:11 Test100K_16S_R4_001.fastq.gz
```

- ProjectID column from the sample sheet determines the resulting output structure
- A “folder/name” structure creates a directory with the named files within it

```
alida@alida:~/Documents/Idaho/IBEST/dbcAmplicons workshops/tests$ ll subfolder/
total 620K
drwxrwxr-x 2 alida alida 4.0K Feb 11 13:17 .
drwxrwxr-x 3 alida alida 4.0K Feb 11 13:28 ..
-rw-rw-r-- 1 alida alida 295K Feb 11 13:17 match_16S_R1.fastq.gz
-rw-rw-r-- 1 alida alida 314K Feb 11 13:17 match_16S_R2.fastq.gz
```

OUTPUTS: FASTQ FILES

Header format of all identified sequences:

@HWI-M01380:13:000000000-AAJFM:1:1101:15579:1503 1:N:0:Sample1:PrimerPair6 GCTCAGGA|0|CCTATCCT|0|Primer6Forward|0|23

The diagram illustrates the structure of a FASTQ header. It starts with the sequence identifier '@HWI-M01380:13:000000000-AAJFM:1:1101:15579:1503 1:N:0'. A bracket above the first 16 characters is labeled 'Sequence ID (Illumina header)'. Below the colon is a blue box containing 'Sample1:PrimerPair6', which is bracketed by 'Assigned sample ID' below it and 'Assigned primer pair ID' above it. To the right of the colon is a green box containing 'GCTCAGGA|0|CCTATCCT|0|Primer6Forward|0|23', which is bracketed by 'Barcodes with number of differences from the reference barcodes' above it and 'Primer ID with number of differences from the reference primer and length of primer that was trimmed' below it.

@HWI-M01380:50:000000000-A641U:1:1101:17127:1556 1:N:0:Sample97:16S GTCGTGAT|0|TAAGTTCC|0|27F_Bif|0|26
GATGAACGCTAGCTACAGGCTAACACATGCAAGTCGAGGGCATCAGGAAGAAAGCTTGCTTCTTGCTGGCACGGGTGAGTAACACGTATC

SUMMARY OF PREPROCESS

- Read 1 and Read 2 files for each unique Project_ID
- Each sequence identified by barcode, primer and/or sample name
- Table of identified barcodes from the run
- A number of parameters available, however defaults work most of the time

- Run
 - `dbcAmplicons preprocess`
- Try `--test` to play with a few parameters

HOMEWORK
preprocess

NEXT: OVERLAPPING READS

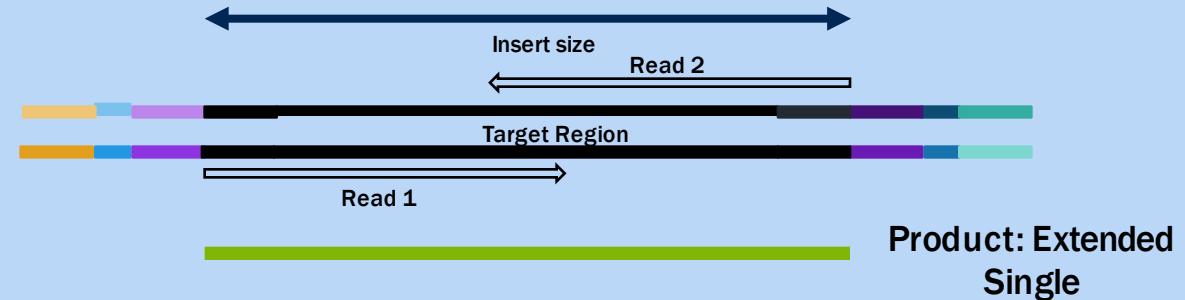
- dbcAmplicons join builds off of preprocess
- Uses FLASH2, a modified version of flash (Fast Length Adjustment of SHort reads, <http://ccb.jhu.edu/software/FLASH/>) to merge paired-end reads.
- Modification include:
 - Performs complete overlaps with adapter trimming
 - Allows for different sized reads (after cutting primer off)
 - Discards reads with > 50% Q of 2 (changed to Q10 in dbcAmplicons), which are indicative of adapter/primer dimers

FLASH2 – OVERLAPPING OF READS

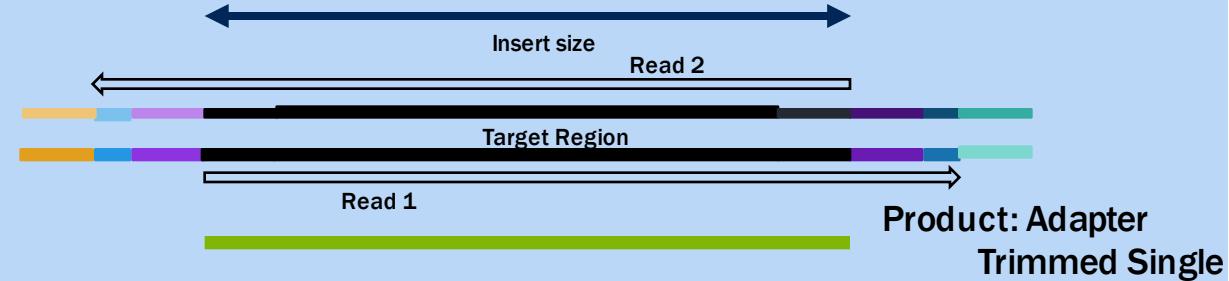
Insert size > length of the number of cycles



Insert size < length of the number of cycles (10bp min)



Insert size < length of the read length



dbcAmplicons join parameters

```
mattsettles@Matts-MBP:~$ dbcAmplicons join -h
usage: dbcAmplicons join [-h] [-O PREFIX] [-u] [-x NUM] [-t NTHREADS] [-v] -1
                           read1 [-2 read2]

optional arguments:
  -h, --help            show this help message and exit
  -O PREFIX, --output_path PREFIX
                        path for output files [default: joined]
  -u, --uncompressed    leave output files uncompressed [default: False]
  -x NUM, --max-mismatch-density NUM
                        Maximum allowed ratio between the number of mismatched
                        base pairs and the overlap length. Two reads will not
                        be combined with a given overlap if that overlap
                        results in a mismatched base density higher than this
                        value. Note: Any occurrence of an "N" in either read
                        is ignored and not counted towards the mismatches or
                        overlap length. [default:0.25]
  -t NTHREADS, --threads NTHREADS
                        Set the number of worker threads. [default: 1]
  -v, --verbose         verbose output [default: True]
  -1 read1              read1 of an amplicon fastq (or fastq.gz) two file set
  -2 read2              read2 of an amplicon fastq (or fastq.gz) two file set
mattsettles@Matts-MBP:~$
```

EXECUTING DBCAMPLICONS JOIN

```
dbcAmplicons join -O join/match -1 match_16S_R1.fastq.gz -2  
match_16S_R2.fastq.gz -v
```

```
alida@alida:~/Documents/Idaho/IBEST/dbcAmplicons workshops/tests/subfolder$ dbcAmplicons join  
-O join/match -1 match_16S_R1.fastq.gz -2 match_16S_R2.fastq.gz -v  
Using Flash_version:v2.2.00  
Min_overlap:10  
Min_overlap_outie:35  
Max_overlap:600  
Max_mismatch_density:0.250000  
Allow_"outie"_pairs:true  
Cap_mismatch_quals:false  
Combiner_threads:1  
Input_format:FASTQ, phred_offset=33  
Output_format:FASTQ, phred_offset=33, gzip  
Total_pairs:2195  
Combined_pairs:1893  
Innie_pairs:1847 (97.57% of combined)  
Outie_pairs:46 (2.43% of combined)  
Uncombined_pairs:302  
Percent_combined:86.24%
```

DBCAMPLICONS JOIN OUTPUTS

```
alida 451K Feb 11 13:55 match.extendedFrags.fastq.gz
alida 695 Feb 11 13:55 match.hist
alida 469 Feb 11 13:55 match.hist.innie
alida 2.6K Feb 11 13:55 match.histogram
alida 1.5K Feb 11 13:55 match.histogram.innie
alida 1.9K Feb 11 13:55 match.histogram.outie
alida 226 Feb 11 13:55 match.hist.outie
alida 54K Feb 11 13:55 match.notCombined_1.fastq.gz
alida 51K Feb 11 13:55 match.notCombined_2.fastq.gz
```

- 3 fastq files: 1 of overlapped pairs [extendedFrags], 2 remaining single [notCombined_1/2] reads that didn't overlap
- Histogram showing the length of reads that overlapped and the frequency
Ignore “innie” and “outie” designations for now

HISTOGRAM

```
468 *
469 ***
470 **
471 **
472
473 *****
474
475
476
477 *
478 *
479 *
480 *
481
482 *
483 *
484
485 *
486
487
488 *
489
490 ****
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505 **
506
507
508
509
510 *
511 ****
512 ****
513
514
515
516
517
518
519 ****
520
521
522
```

- “more match.histogram” will scroll through the file showing the lengths (symbolic)
- “match.hist” gives the number of sequences that fall into each numerical category
- Useful for determining the lengths of the amplicons that were sequenced

- Using dbcAmplicons
 - Join the preprocessed reads
- Modify the parameter
 - -x see how the results change

HOMEWORK
Join

DBCAMPLICONS CLASSIFY

- Uses the RDP (Ribosomal Database Project) classifier for bacterial and archaeal 16S, fungal LSU, ITS warcup/unite databases.
- Classifies sequences to the closest taxonomic reference provides a bootstrap score for reliability

dbcAmplicons classify command

```
attsettles@Matts-MBP:~$ dbcAmplicons classify -h
sage: dbcAmplicons classify [-h] [-b BATCHSIZE] [-q MINQ] [-l MINL]
                           [-p PROCS] --rdpPath PATH [-g <arg>] [-t TRAIN]
                           [-O outputPrefix] [-1 read1 [read1 ...]]
                           [-2 read2 [read2 ...]] [-U single [single ...]]
                           [-v] [--debug]

optional arguments:
-h, --help            show this help message and exit
-b BATCHSIZE, --batchsize BATCHSIZE
                      batch size to process reads in [default: 100000]
-q MINQ, --minQ MINQ trim 3' end of sequences to minQ (paired-end reads
                      only) [default: None]
-l MINL, --minL MINL if minQ is not None, only keep reads that are at least
                      minL length (paired-end reads only) [default: 0]
-p PROCS, --processors PROCS
                      number of processors to use, [default: 1]
--rdpPath PATH        path to the RDP classifier
-g <arg>, --gene <arg>
                      16srrna, fungallsu, fungalits_warcup, or
                      fungalits_unite [default: 16srrna]
-t TRAIN, --train TRAIN
                      RDP property file containing the mapping of the
                      training files for a custom RDP training set, if not
                      using the default.
-O outputPrefix, --output_path outputPrefix
                      path for output files [default: classify]
-1 read1 [read1 ...]  read1 of an amplicon fastq two file set
-2 read2 [read2 ...]  read2 of an amplicon fastq two file set
-U single [single ...]
                      single-end amplicon, typically from joined paired
                      reads
-v, --silent          silences verbose output [default: False]
--debug              show traceback on error
attsettles@Matts-MBP:~$ █
```

USING DBCAMPLICONS CLASSIFY

```
dbcAmplicons classify -b 7500  
-O classify/classified  
-U join/match.extendedFrags.fastq.gz  
--rdpPath ~/RDPTools/classifier.jar  
-p 1  
-1 join/match.notCombined_1.fastq.gz  
-2 join/match.notCombined_2.fastq.gz
```

USING DBCAMPLICONS CLASSIFY

```
Starting rdp for file classify/classified.1893.fasta
Finished processing classify/classified.1893.fasta in 0.16 minutes
Starting rdp for file classify/classified.2195.fasta
Finished processing classify/classified.2195.fasta in 0.08 minutes
Combining temporary files
2195 reads processed in 0.25 minutes
Cleaning up.
alida@alida:~/Documents/Idaho/IBEST/dbcAmplicons workshops/tests/subfolder$ ll classify/
total 448K
drwxrwxr-x 2 alida alida 4.0K Feb 11 15:21 ./
drwxrwxr-x 4 alida alida 4.0K Feb 11 14:46 ../
-rw-rw-r-- 1 alida alida 440K Feb 11 15:21 classified.fixrank
```

FIXRANK FILES

HWI-M01380:50:000000000-A641U:1:1101:18594:1568 Sample26:16S				Bacteria	domain
1.0	"Actinobacteria"	phylum	1.0	Actinobacteria	class
1.0	Actinomycetales	order	1.0	Actinomycetaceae	family
1.0	Varibaculumgenus	1.0			
HWI-M01380:50:000000000-A641U:1:1101:17948:1574 Sample28:16S				Bacteria	domain
1.0	"Actinobacteria"	phylum	0.96	Actinobacteria	class
0.96	Bifidobacteriales	order	0.9	Bifidobacteriaceae	family
0.9	Aeriscardovia	genus	0.23		
HWI-M01380:50:000000000-A641U:1:1101:14301:1587 Sample12:16S				Bacteria	domain
1.0	Firmicutes	phylum	0.98	Bacilli	class
order	0.86	Lactobacillaceae	family	0.81	0.97 Lactobacillales
genus	0.61				Lactobacillus
HWI-M01380:50:000000000-A641U:1:1101:18207:1603 Sample19:16S				Bacteria	domain
1.0	Firmicutes	phylum	1.0	Bacilli	class
Lactobacillales		order	1.0	Lactobacillaceae	family
Lactobacillus		genus	1.0		1.0
HWI-M01380:50:000000000-A641U:1:1101:17585:1630 Sample17:16S				Bacteria	domain
1.0	Firmicutes	phylum	1.0	Bacilli	class
Lactobacillales		order	1.0	Lactobacillaceae	family
Lactobacillus		genus	1.0		1.0
HWI-M01380:50:000000000-A641U:1:1101:22144:1652 Sample26:16S				Bacteria	domain
1.0	"Actinobacteria"	phylum	1.0	Actinobacteria	class
1.0	Actinomycetales	order	1.0	Actinomycetaceae	family
1.0	Actinomycesgenus	1.0			

```
mattsettles@Matts-MBP:~$ dbcAmplicons abundance -h
usage: dbcAmplicons abundance [-h] [-r <arg>] [-t VALUE] [-m VALUE] [-M VALUE]
                               [-S FILE] [-O FILE_PREFIX] -F FILE [FILE ...]
                               [-b] [-v] [--debug]

optional arguments:
  -h, --help            show this help message and exit
  -r <arg>, --rank <arg>
                        taxonomic rank to build table from, allowable values
                        are (domain, phylum, class, order, family, genus, and
                        species{if performed}, [default: genus])
  -t VALUE, --threshold VALUE
                        Threshold bootstrap value to use for assignment, first
                        taxon level greater than threshold
  -m VALUE, --minsize VALUE
                        Min size of amplicon to consider
  -M VALUE, --maxsize VALUE
                        Max size of amplicon to consider
  -S FILE, --sample_metadata FILE
                        file with sample metadata
  -O FILE_PREFIX, --output_path FILE_PREFIX
                        path for output files [default: table]
  -F FILE [FILE ...]   fixrank formated classification file generated by
                      classify
  -b, --biom           output biom formatted file [default: False]
  -v, --silent         verbose output [default: False]
  --debug             show traceback on error
mattsettles@Matts-MBP:~$
```

dbcAmplicons abundance

DBCAMPLICONS ABUNDANCE

`dbcAmplicons abundance -F
classify/classified.fixrank`

Outputs 3 files:

`table.abundance.txt`
`table.proportions.txt`
`table.taxa_counts.txt`

TABLE.ABUNDANCE.TXT

	A	B	C	D	E	F	G	H	I	J	K	L
1	Taxon_Name	Level	MeanBootstrapValue	Sample1	Sample10	Sample11	Sample12	Sample13	Sample14	Sample15	Sample16	Sample17
2	Acidovorax	genus	0.973	0	0	0	0	0	0	0	0	0
3	Actinobaculum	genus	1	0	0	0	0	0	0	0	0	0
4	Actinomyces	genus	0.988	0	0	0	0	0	0	0	0	0
5	Actinomycetaceae	family	0.83	0	0	0	0	0	0	0	0	0
6	Actinomycetales	order	0.923	0	0	0	0	0	0	0	0	0
7	Aeriscardovia	genus	0.68	0	0	0	0	0	0	0	0	0
8	Aerococcus	genus	1	0	0	0	0	0	1	0	0	0
9	Alloiscardovia	genus	1	0	3	0	0	0	0	0	0	0
10	Lactobacillus	genus	0.977	41	75	55	96	56	66	12	0	114
11	Anaerococcus	genus	0.946	0	1	0	0	0	1	0	0	0
12	Anaerospaera	genus	0.582	0	0	0	0	0	0	0	0	0
13	Archaea	domain	0.587	0	0	0	0	0	0	0	0	0
14	Atopobium	genus	1	0	0	0	0	0	0	0	0	0
15	Bacilli	class	0.606	0	1	1	2	1	0	0	0	5
16	Bacillus	genus	0.9	0	0	0	0	0	0	0	0	0

Can open file in spreadsheet; lists lowest taxonomically classified level for each sample by read count

TABLE.PROPORTIONS.TXT

	A	B	C	D	E	F	G
1	Taxon Name	Level	MeanBootstrapValue	Sample1	Sample10	Sample11	Sample12
2	Acidovorax	genus	0.973	0	0	0	0
3	Actinobaculum	genus	1	0	0	0	0
4	Actinomyces	genus	0.988	0	0	0	0
5	Actinomycetaceae	family	0.83	0	0	0	0
6	Actinomycetales	order	0.923	0	0	0	0
7	Aeriscardovia	genus	0.68	0	0	0	0
8	Aerococcus	genus	1	0	0	0	0
9	Alloiscardovia	genus	1	0	0.0315789474	0	0
10	Anaerococcus	genus	0.946	0	0.0105263158	0	0
11	Anaerospaera	genus	0.582	0	0	0	0
12	Archaea	domain	0.587	0	0	0	0
13	Atopobium	genus	1	0	0	0	0
14	Bacilli	class	0.606	0	0.0105263158	0.0158730159	0.0181818182
15	Bacillus	genus	0.9	0	0	0	0
16	Bacteria	domain	0.885	0.0227272727	0	0.0158730159	0.0090909091
17	Bacteroidales	order	0.57	0	0	0	0
18	Bacteroidetes	phylum	0.85	0	0	0	0
19	Bifidobacteriaceae	family	0.905	0	0	0	0
20	Bifidobacterium	genus	0.965	0	0	0	0
21	Blautia	genus	0.99	0.0227272727	0	0	0
22	Burkholderiales	order	0.76	0	0	0	0

Similar to abundance.txt, but instead lists proportions of each taxonomic level found per sample

TABLE.TAXA_COUNTS.TXT

	A	B
1	Taxon_Name	Count
2	Klebsiella genus	21
3	Aerococcus genus	1
4	Porphyromonadaceae family	2
5	Clostridiales order	2
6	Varibaculum genus	7
7	Turicella genus	1
8	Burkholderiales order	1
9	Paralactobacillus genus	4
10	Phyllobacteriaceae family	1
11	Lactobacillales order	68
12	Bacillus genus	2
13	Peptoniphilus genus	11
14	Clostridium XIX genus	2
15	Bacteria domain	95
16	Parascardovia genus	1
17	Thermoprotei class	1
18	Leclercia genus	3
19	Bacilli class	19
20	Actinobaculum genus	1
21	Propionibacterium genus	8
22	Bacteroidales order	1
23	Acidovorax genus	8
24	Mobiluncus genus	1
25	Dechloromonas genus	2
26	Clostridiales_Incertae_Sedis XII family	1
27	Lachnospiraceae family	1
28	Unknown Root	38
29	Lactobacillaceae family	28

**Summary of each classification
and the number of counts for that
level across all samples**

CONVERT2READTO4READ

Back-converts a set of 2 Illumina paired-end files that have already been preprocessed by *dbcAmplicons* into 4 reads, splitting the 2 barcodes into separate reads.

Useful for reprocessing datasets and analyzing barcode counts.

SPLITREADSBYSAMPLE (UPLOAD TO SRA)

Takes processed reads from *dbcAmplicons* and bins each read by its sample ID. If no sample IDs are assigned, reads will be split by individual barcode.

Each sample receives a Read 1 and Read 2.

Designed for easy upload to the SRA