

# Experimental Design

# 4 Main Stages

**1**

Biological  
Question

**2**

Design &  
Conduct  
Experiment

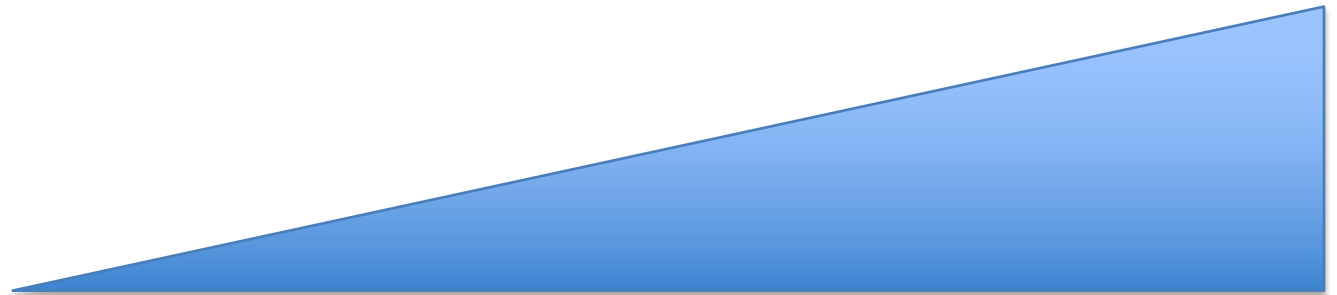
**3**

Prepare NGS  
Library &  
Sequence

**4**

Sequencing  
Analysis

Class time



2

Design &  
Conduct  
Experiment

## **2. DESIGN & CONDUCT EXPERIMENT**

# Types of sequencing

- Clonal sequencing
  - Expect a single genome to be present. Highly resilient to sequencing errors.
- Population sequencing
  - Multiple subpopulations and genomes expected to be present. Highly susceptible to sequencing errors especially when making quantitative analysis.
- Amplicon/targeted sequencing
  - Know all/most reads correspond to specific genomic locations. Can be dominated by sequencing errors.

Nice...

We have so many options!

- Deep whole genome
- Low pass whole genome
- Deep whole exome
- Genomewide array
- Exome array

How would you like to be sequenced?

Genomics  
Core  
Facility

3

Prepare NGS  
Library &  
Sequence

## **3. PREPARE NGS LIBRARY & SEQUENCE**

# Standard Library Prep

1. Fragment DNA
  1. Enzymatic, sonication, acoustic, nebulization
2. Blunt DNA
3. “A”-Tail DNA
4. Ligate adapters
5. PCR

# Standard library prep sufficient

- Clonal samples
  - Each base 0 or 100%
  - 50% possible in diploids
- Low to moderate coverage depth populations (<100)
  - Standard Illumina error rate 1%
  - Much more on this later
- Good reference
  - Typical want DNA fragment sizes 350 – 700 bp
  - miSeq: 700 – 1500 bp



# Standard library prep lacking

- High coverage populations (>100)
  - Error rate of 1% sets limit of detection at 1% regardless of depth
    - Error rate reduction
- Non-model organism
  - Difficult to generate good reference assemblies using 300 - 700bp
    - Mate-pair libraries several kb inserts
    - Combine with other long read sequencing solutions
- Repeat-mediated rearrangements
  - Repeats often 1.5kb+ long, difficult to get reads on both sides
    - Mate-pair libraries again

3. Prepare NGS Library & Sequence

# **ERROR RATE REDUCTION**

# Basic Principle

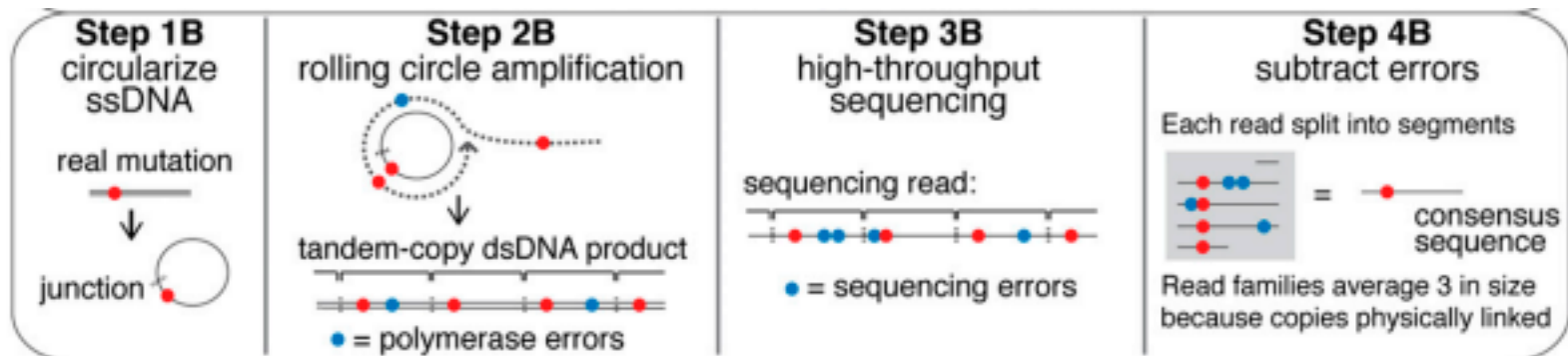
- Because majority of errors are randomly distributed along reads, several alternative library preparation methods exist to read the same original fragment of DNA multiple times to reduce error rates.
- 3 main ways.
  1. Molecular indexing
  2. Circle sequencing
  3. Short insert size approximately read length

# Alternative Library Preparation

- Duplex sequencing ([Schmidt et al 2012 PNAS](#))
  - Molecular index to identify original DNA fragments

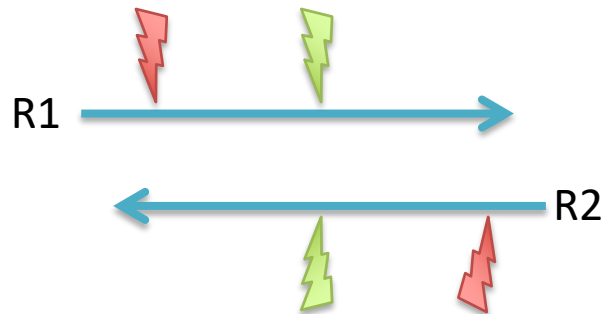


- Circle sequencing ([Lou et al 2013 PNAS](#))
  - Rolling circle amplification to reread same fragment



# Alternative Library Preparation

- Double read
  - Fragment DNA size to  $\sim$ read length.
  - Can be done with any paired end read.



3. Prepare NGS Library & Sequence

**“LONGER” READS**

# Illumina Options

- Technology:
  - Illumina: 2 x 300 miSeq runs
- Mate pair library:
  - Generates 2 outwardly facing reads separated by up to 25kb.
  - Allows connection of otherwise distant locations on a single read.



# 4

Sequencing  
Analysis

Read Sequence Quality control

## 4. SEQUENCING ANALYSIS





Garbage In, Garbage Out



Data Preprocessing

- Massaging standard Illumina data is always less effective than better experimental planning and design using alternative library preparation methods.

# Read Sequence Quality Control Questions

- Contaminated with other samples?
- Adapter dimers present?
  - Reads with no insert present.
- Adapters present on ends of reads?
  - Insert size smaller than read length.
- 3' end of reads quality decline?

# Onto the Tutorials.

- Some more basic bash/linux interrogation about reads, and working with TACC.
- FastQC can answer all questions about raw read quality and is pretty much the only game in town.
- Cutadapt is a tool for improving data when you identify a problem.