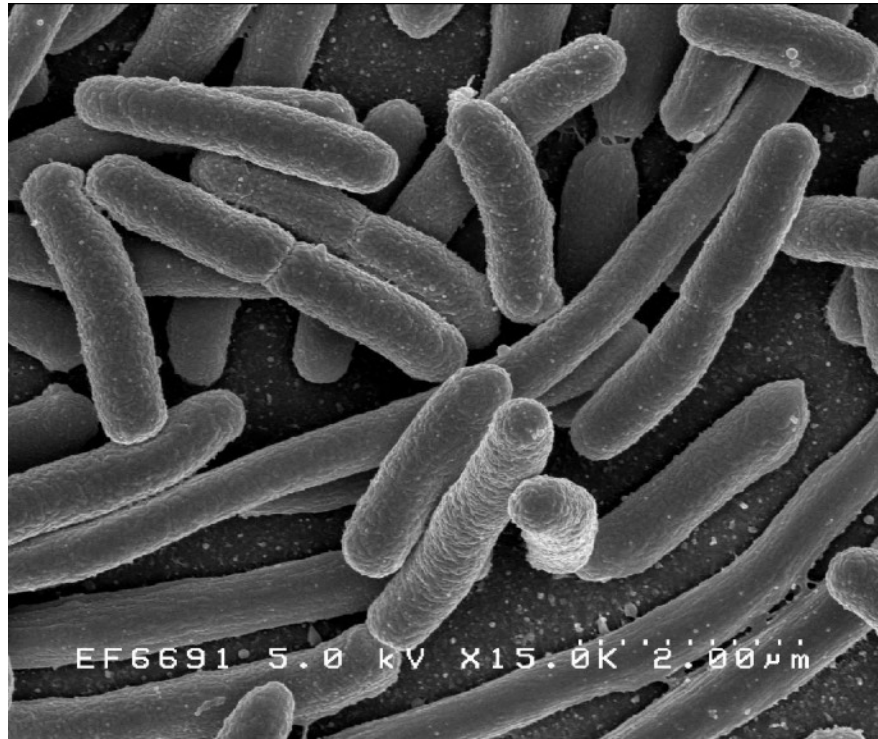


**Exact Sequences  
from  
Marker-gene sequencing**

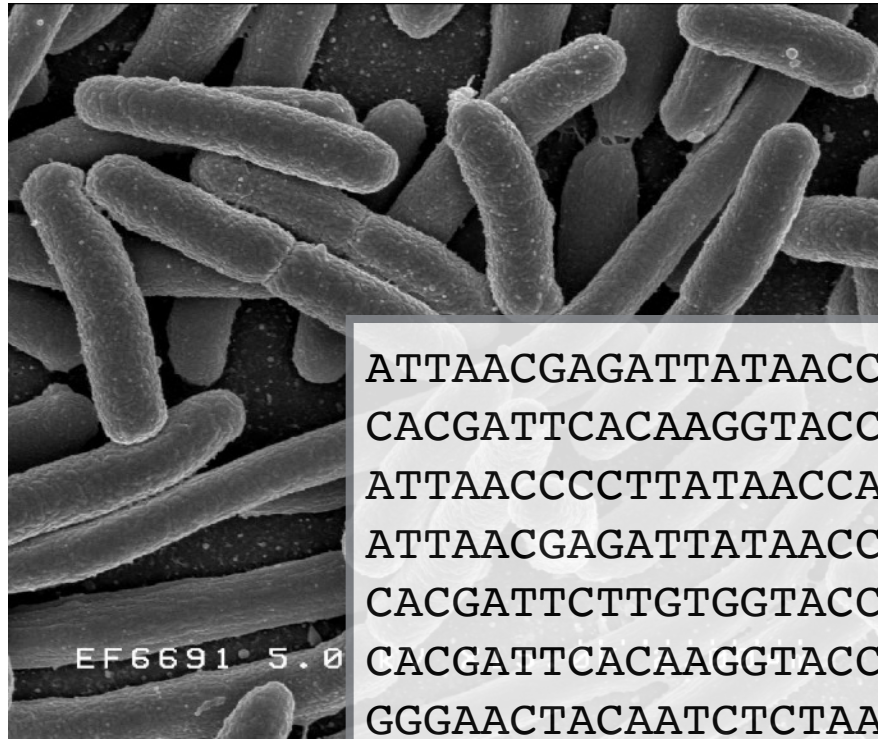
# A Microbial Census

*Marker-gene or Metagenomics Sequencing (MGS)*



# A Microbial Census

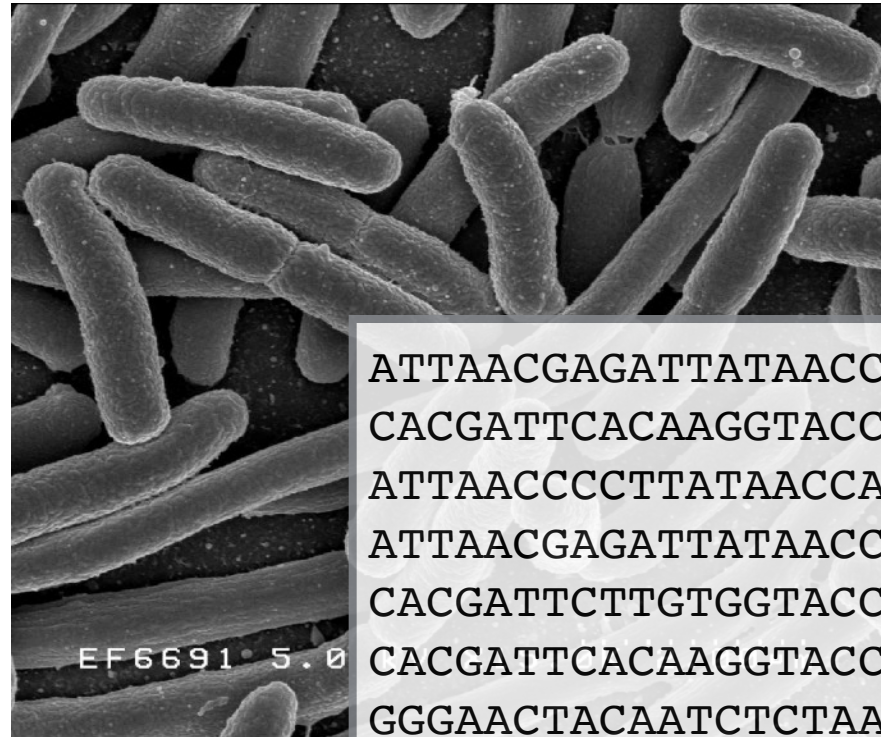
## *Marker-gene or Metagenomics Sequencing (MGS)*



```
ATTAACGAGATTATAACCAGAGTACGAATACCGAAC  
CACGATTCACAAGGTACCACAAGGTAACATAGCTCC  
ATTAACCCCTTATAACCAGAGTACGAATACCGAAC  
ATTAACGAGATTATAACCAGAGAGAGAATACCGAAC  
CACGATTCTTGTGGTACCACAAGGTAACATAGCTCC  
CACGATTCACAAGGTACCACAAGGTAACATAGCTCC  
GGGA ACTACAATCTCTAAGGTGAAGTCTCAGTCTAT  
ATTAACGAGATTATAACCAGAGTACGAATACCGAAC  
CACGATTCACAAGGTACCACAAGGTAACATAGCTCC  
ATTAACGAGATTATAACCAGAGTACGAATACCGAAC
```

# A Microbial Census

## Marker-gene or Metagenomics Sequencing (**MGS**)



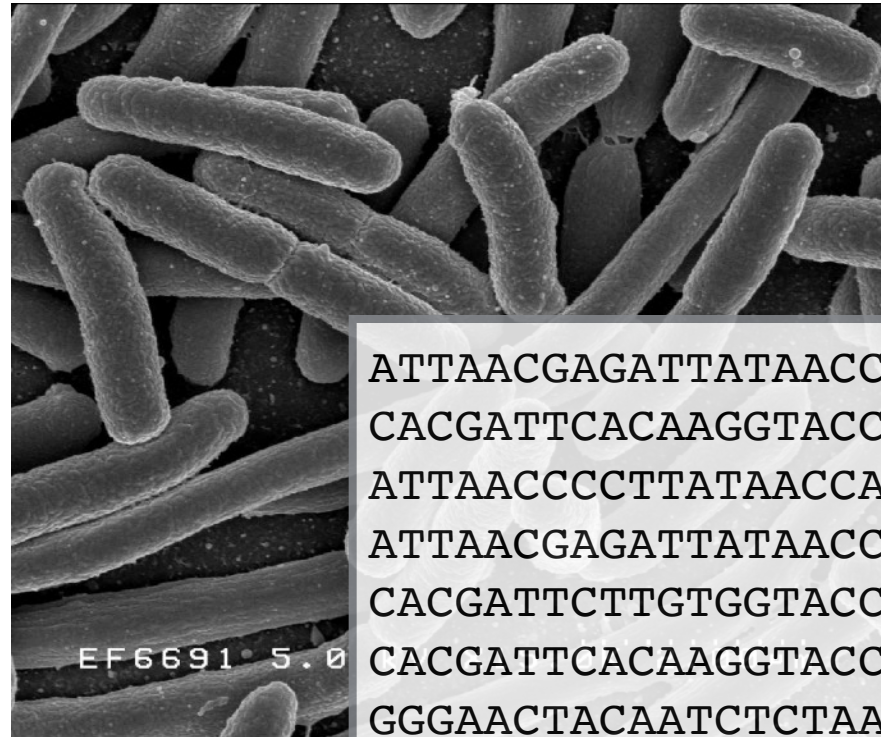
ATTAACGAGATTATAACCAGAGTACGAATACCGAAC  
CACGATTCACAAGGTACCACAAGGTAACATAGCTCC  
ATTAACCCCTTATAACCAGAGTACGAATACCGAAC  
ATTAACGAGATTATAACCAGAGAGAGAATACCGAAC  
CACGATTCTTGTGGTACCACAAGGTAACATAGCTCC  
CACGATTCACAAGGTACCACAAGGTAACATAGCTCC  
GGGA ACTACAATCTCTAAGGTGAAGTCTCAGTCTAT

ATTAACGAGATTATAACCAGA  
CACGATTCACAAGGTACCACA  
ATTAACGAGATTATAACCAGA

<i>Lactobacillus crispatus</i>	1300	5	0	882	596
<i>Ureaplasma urealytica</i>	15	0	220	0	0
<i>Gardnerella vaginalis</i>	22	0	1	0	412
<i>Prevotella intermedia</i>	0	0	8	12	0
...	...	...	...	...	...

# A Microbial Census

## Marker-gene or Metagenomics Sequencing (**MGS**)



ATTAACGAGATTATAACCAGAGTACGAATACCGAAC  
CACGATTCACAAGGTACCACAAGGTAACATAGCTCC  
ATTAACCCCTTATAACCAGAGTACGAATACCGAACA  
ATTAACGAGATTATAACCAGAGAGAGAATACCGAAC  
CACGATTCTTGTGGTACCACAAGGTAACATAGCTCC  
CACGATTCACAAGGTACCACAAGGTAACATAGCTCC  
GGGA ACTACAATCTCTAAGGTGAAGTCTCAGTCTAT  
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CACGATTCACAAGGTACCACAAGGTAACATAGCTCC  
ATTAACGAGATTATAACCAGAGTACGAATACCGAAC

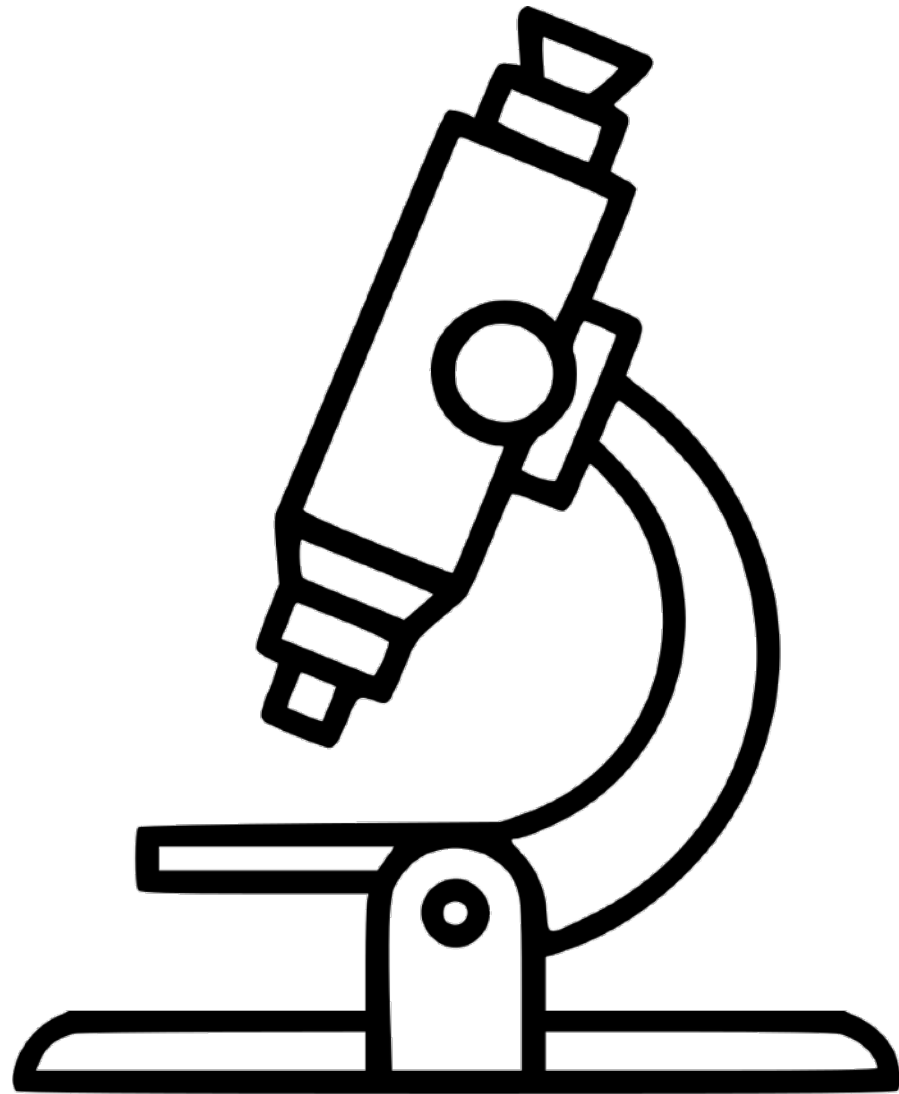
<i>Lactobacillus crispatus</i>	1300	5	0	882	596
<i>Ureaplasma urealytica</i>	15	0	220	0	0
<i>Gardnerella vaginalis</i>	22	0	1	0	412
<i>Prevotella intermedia</i>	0	0	8	12	0
...	...	...	...	...	...

Visualization

Exploration

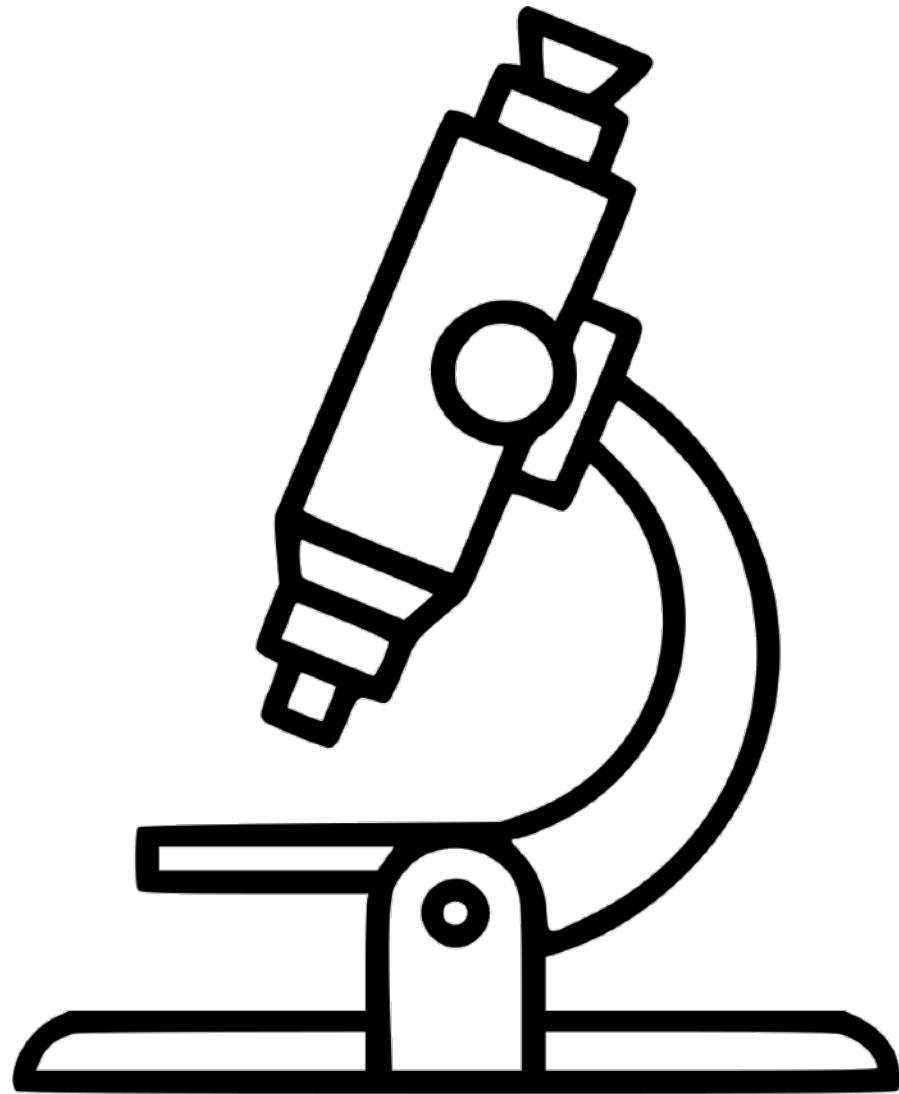
Inference

# The MGS Microscope



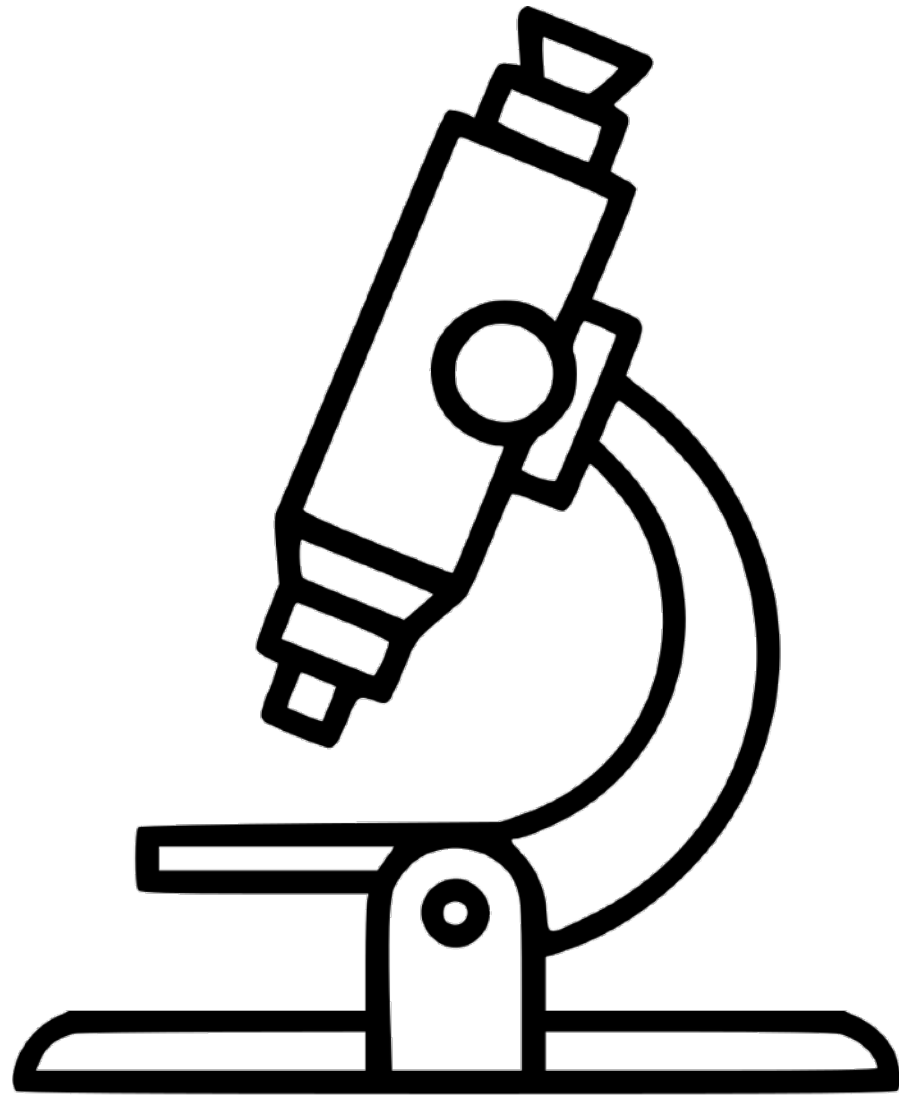


# The MGS Microscope



- **sample collection**
- **sample storage**
- **DNA extraction**
- **library preparation**
- **PCR**
- **sequencing instrument**
- **bioinformatics**

# The MGS Microscope



?

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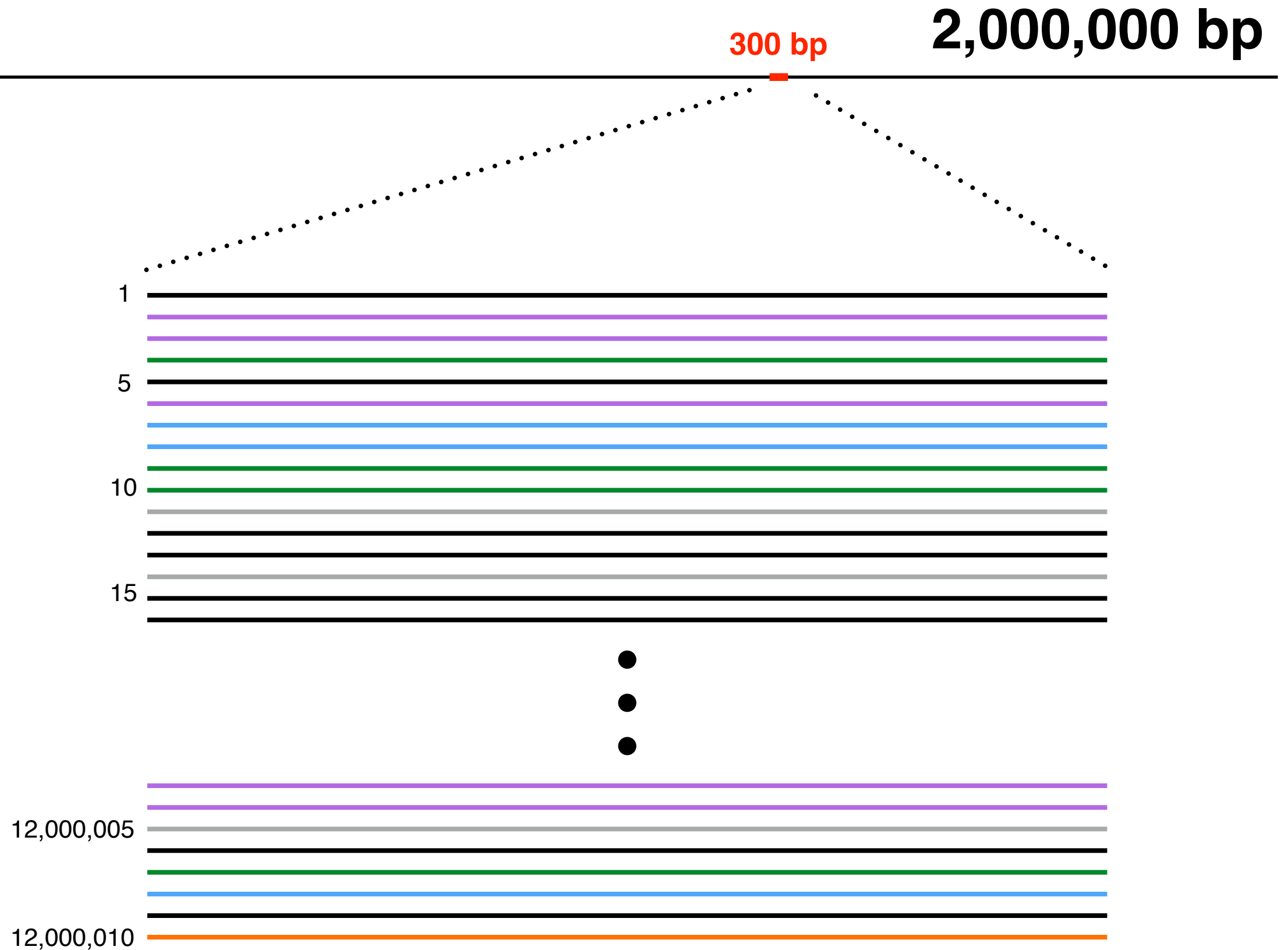
# Marker-gene Sequencing

300 bp

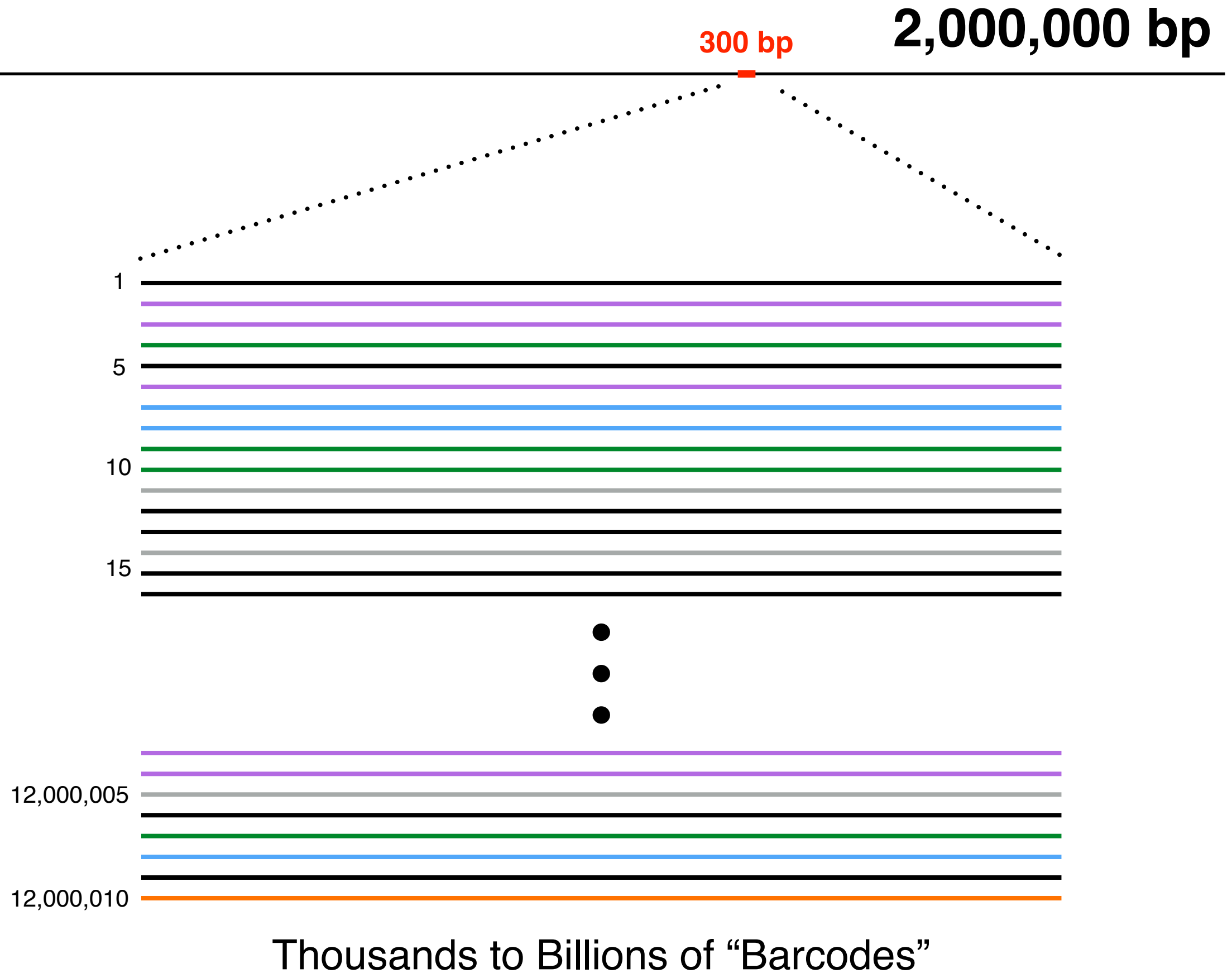
2,000,000 bp



# Marker-gene Sequencing

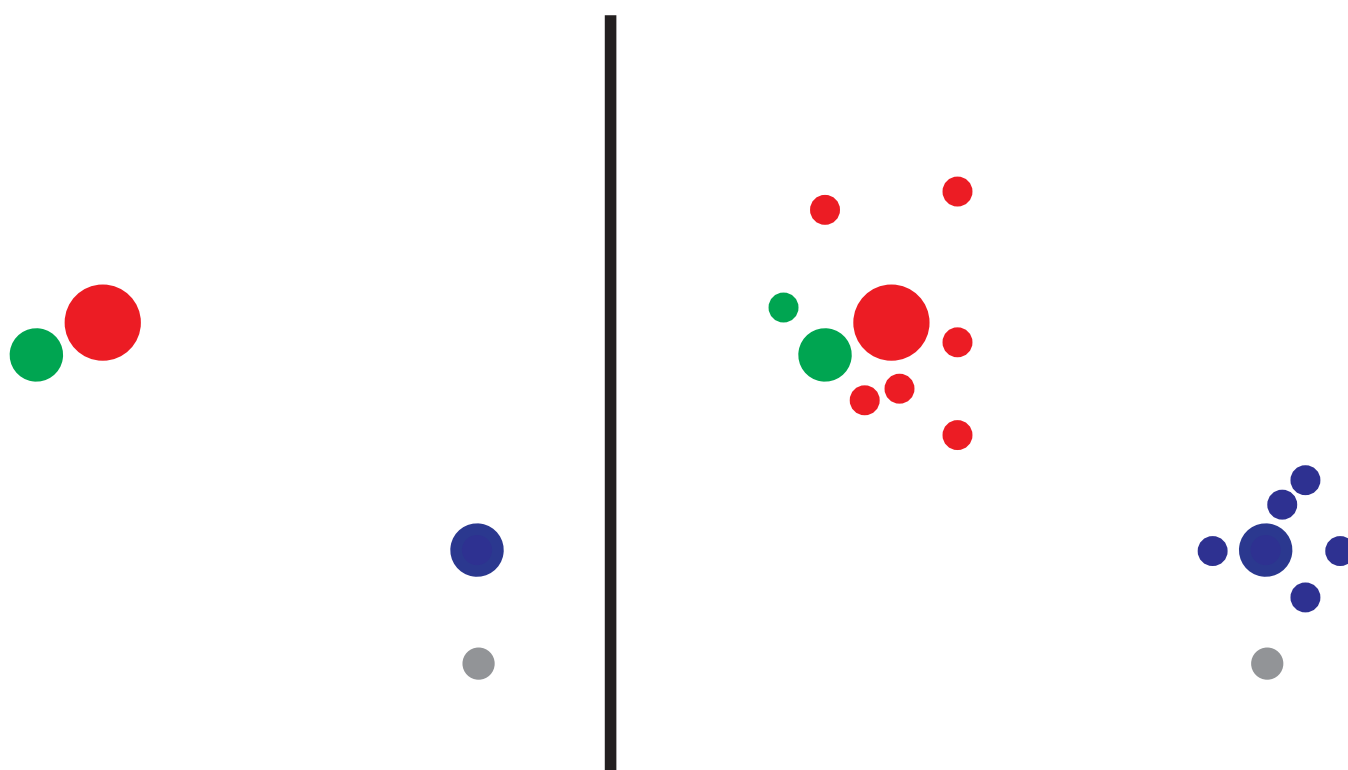


# Marker-gene Sequencing



**Sample  
Sequences**

**Amplicon  
Reads**



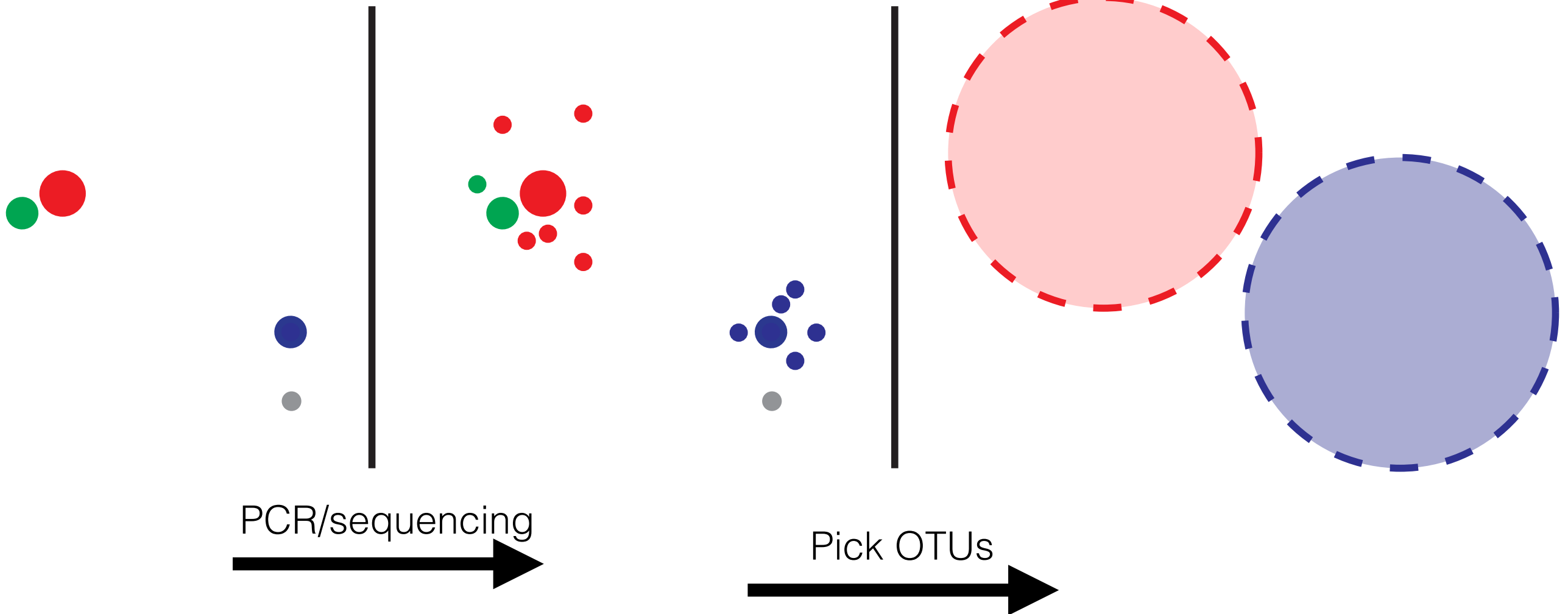
PCR/sequencing



## Sample Sequences

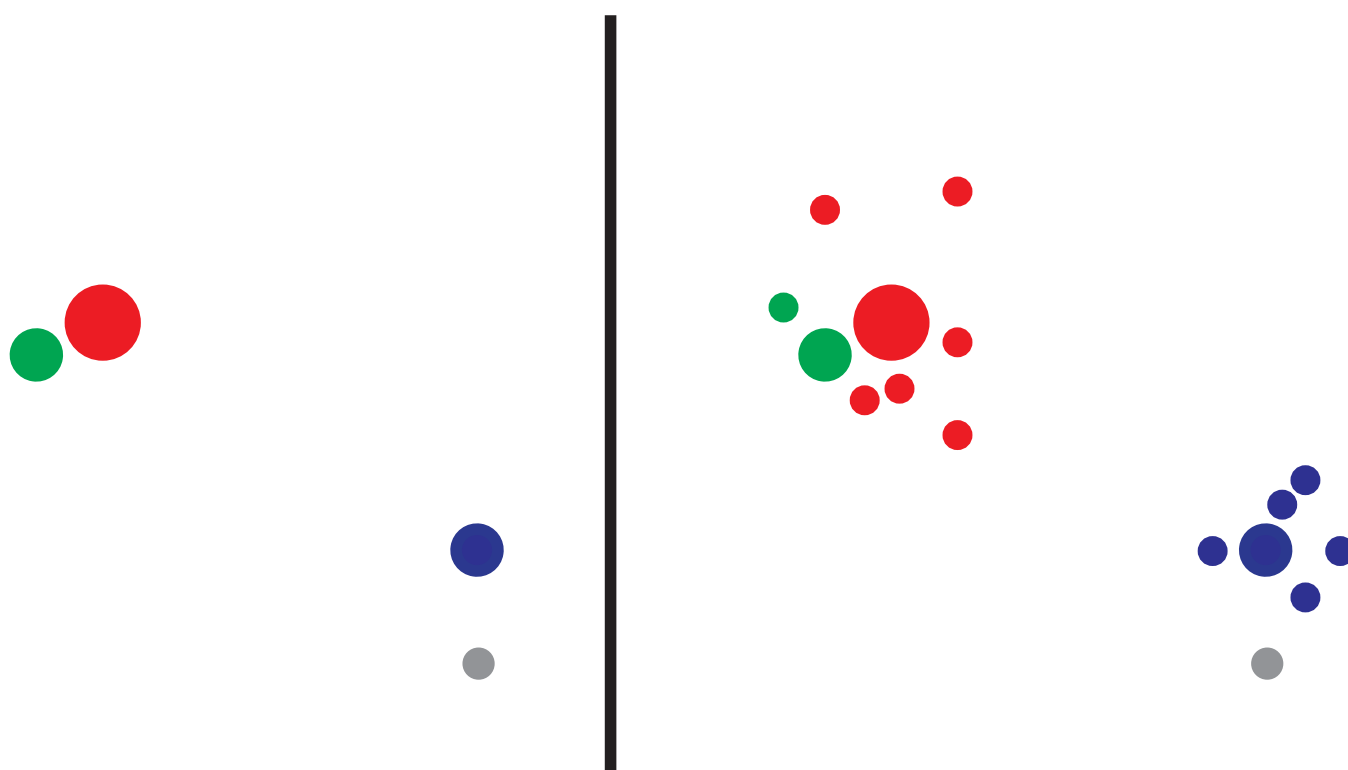
## Amplicon Reads

## Operational Taxonomic Units



**Sample  
Sequences**

**Amplicon  
Reads**

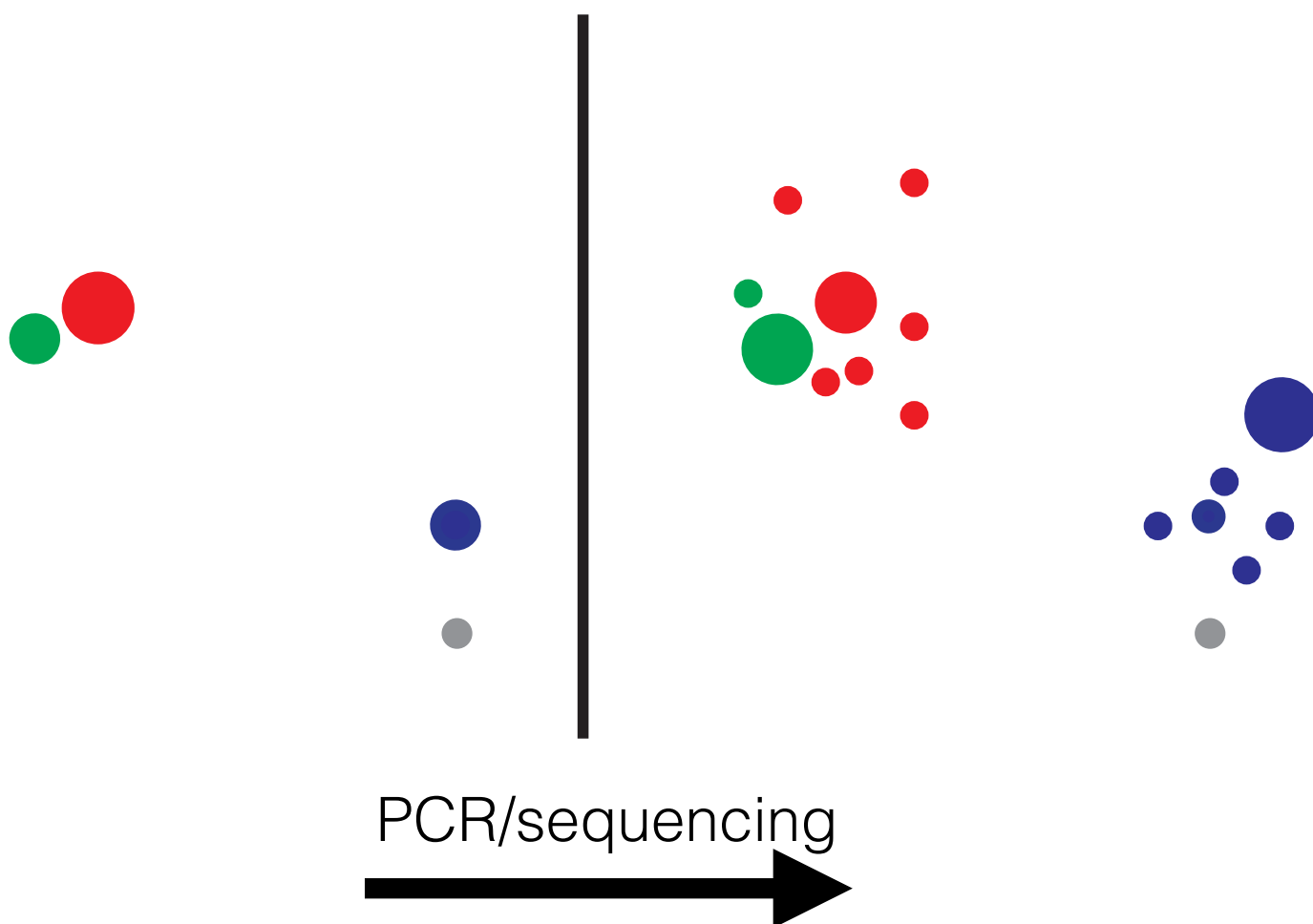


PCR/sequencing



**Sample  
Sequences**

**Amplicon  
Reads**

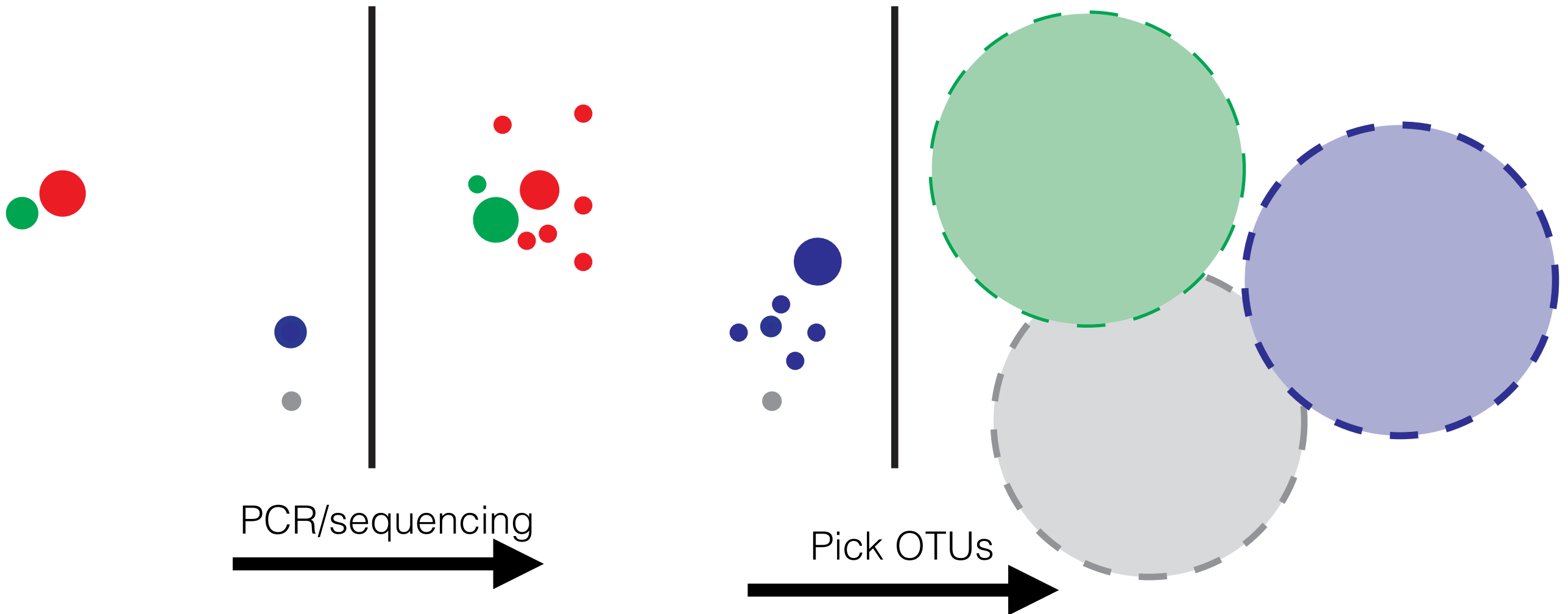




**Sample  
Sequences**

**Amplicon  
Reads**

**Different Operational  
Taxonomic Units**



**Uh oh!**

# Exact Sequence Variants...

OTU85 is ***not a consistent label***

OTU85 is *predictive of a disease?* **Not in future data!**

OTU85 is *associated w/ X and Y?* **Can't be tested!**

OTU85 is *in this community?* **OTUs don't exist in nature!**

OPEN

The ISME Journal (2017), 1–5

[www.nature.com/ismej](http://www.nature.com/ismej)

## PERSPECTIVE

# Exact sequence variants should replace operational taxonomic units in marker-gene data analysis

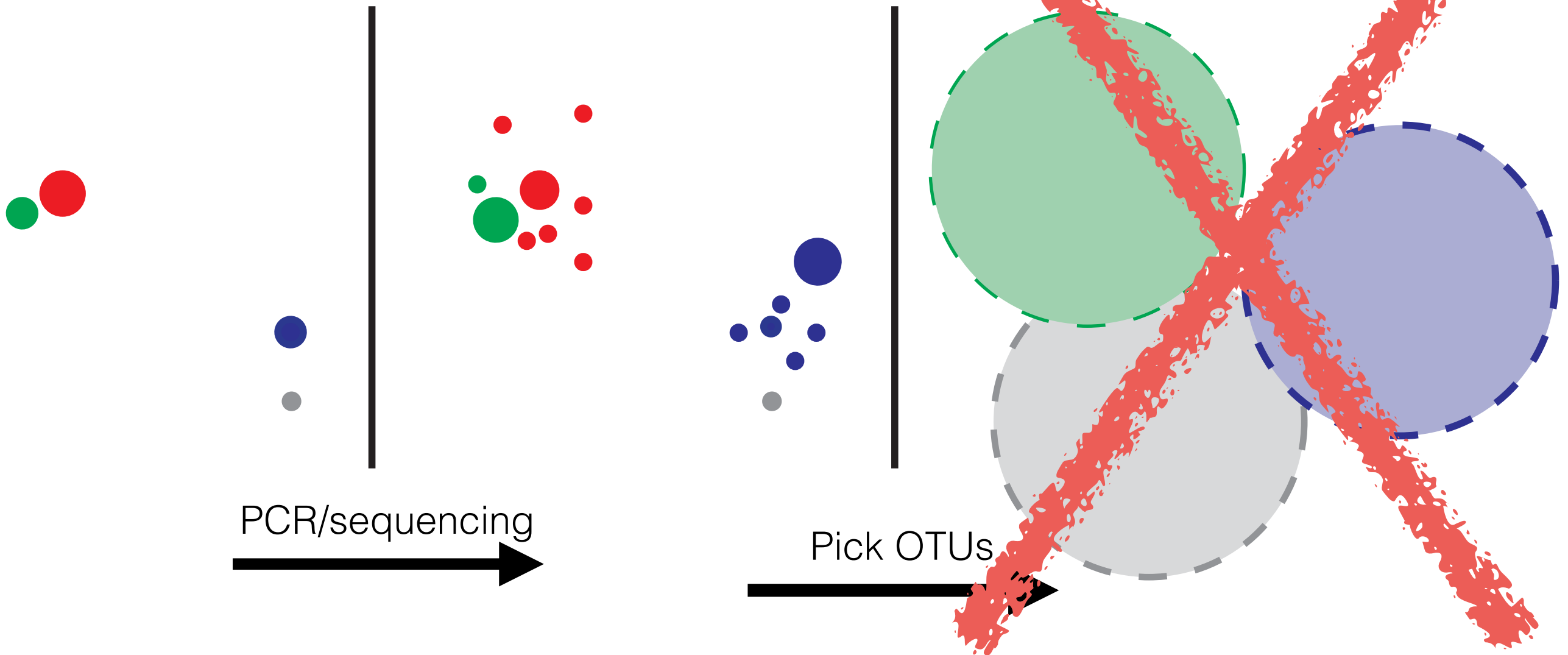
Benjamin J Callahan<sup>1</sup>, Paul J McMurdie<sup>2</sup> and Susan P Holmes<sup>3</sup>

<sup>1</sup>*Department of Population Health and Pathobiology, NC State University, Raleigh NC, USA;* <sup>2</sup>*Whole Biome Inc, San Francisco CA, USA and* <sup>3</sup>*Department of Statistics, Stanford University, Stanford CA, USA*

**Sample  
Sequences**

**Amplicon  
Reads**

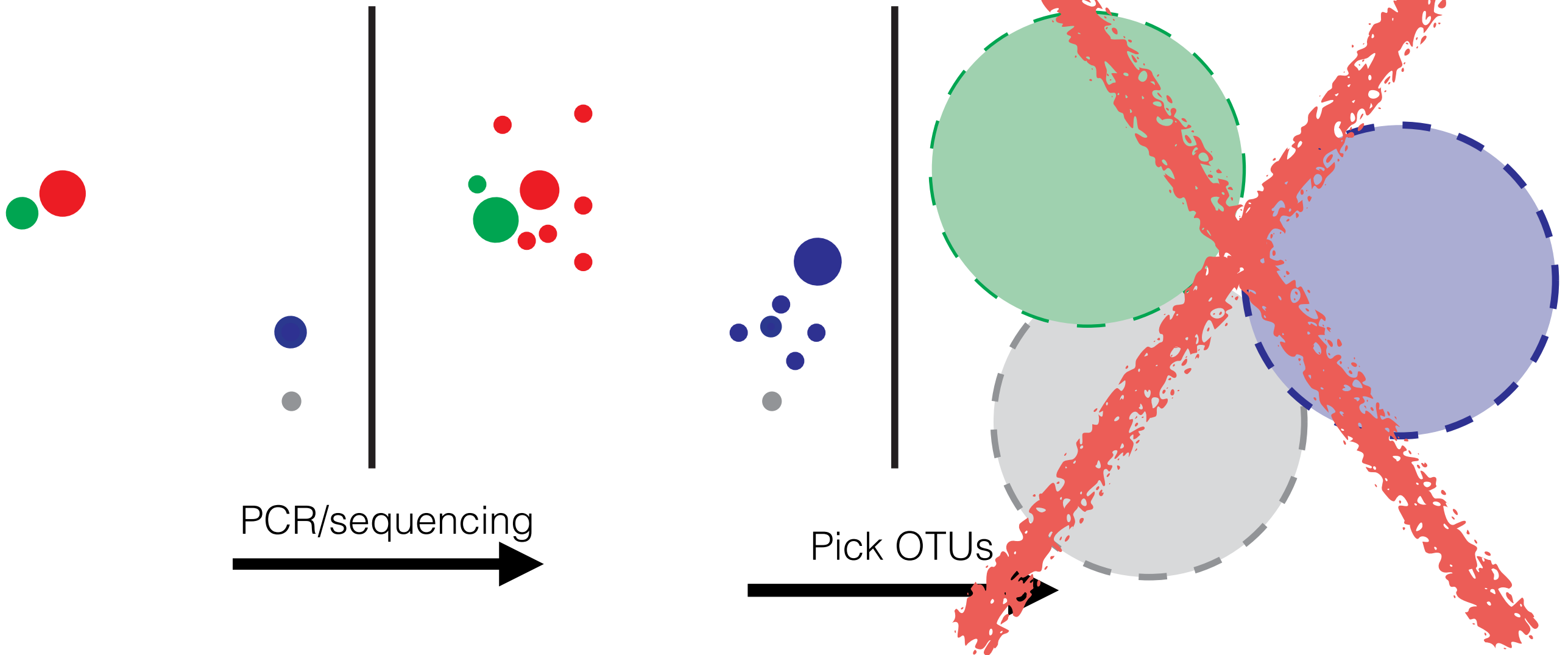
**Different Operational  
Taxonomic Units**



**Sample  
Sequences**

**Amplicon  
Reads**

**Different Operational  
Taxonomic Units**



PCR/sequencing

Pick OTUs

**Infer Sample Sequences**

# Exact Sequence Variants...

OTU85 is **not** a consistent label, but...

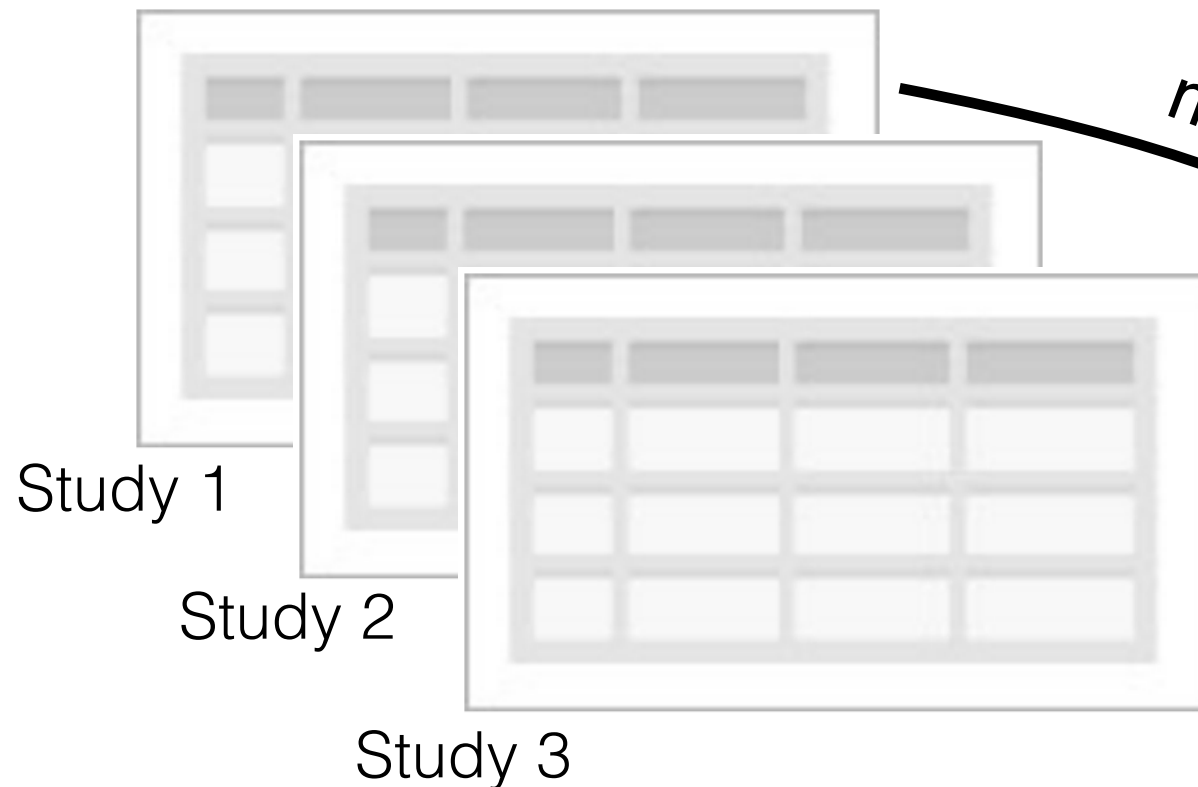
ATTAAACGAGATTATAACCCAGAGTACGAATA...

***is consistent!***



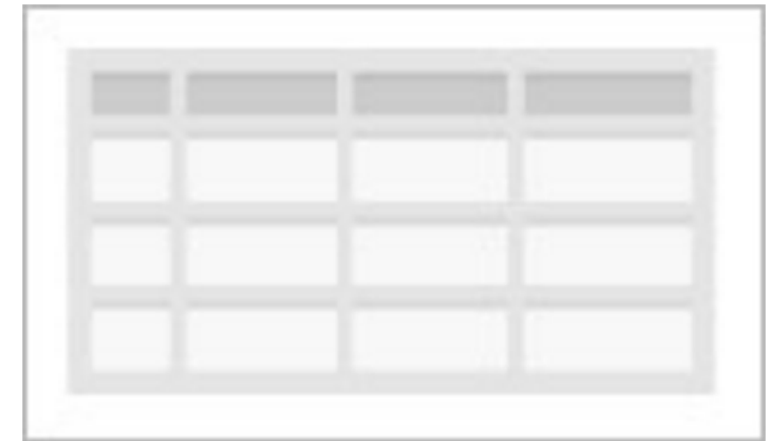
# ...the sequence is the label

## Sequence Tables



merge

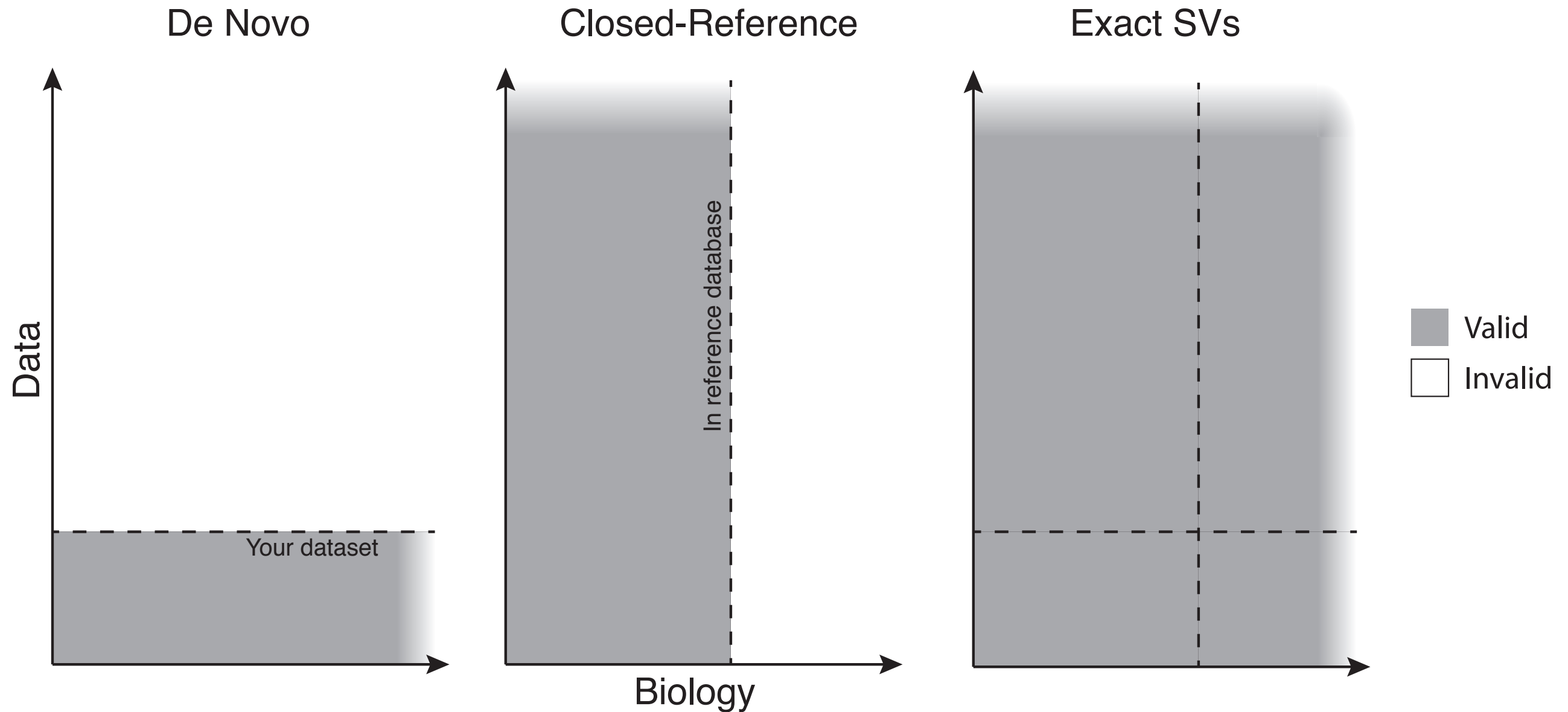
## Cross-study comparison



Eliminates need for joint reprocessing of raw data.  
**Continuous data integration. Unlimited dataset size.**



# ...the sequence is the label



*“Replacing OTUs with ASVs makes marker-gene sequencing more precise, reusable, reproducible and comprehensive.”*