16SrRNA Intermediate Bioinformatics Online Course: Int_BT_2019

16S analysis pipeline

QC and ASV picking using the dada2 pipeline

Outline

- Quality Control

- **DADA2 background**

- DADA2 workflow

DADA2 background

Divisive Amplicon Denoising Algorithm 2 (DADA2) is an open source algorithm implemented in R, which uses a statistical inference to correct amplicon errors.

It intends to simplify the study of microbial communities by allowing to reconstruct amplicon-sequenced communities at the highest resolution.

Callahan et al., 2016

DADA2 background

DADA2 implements a complete workflow that takes raw amplicon sequencing data in fastq files as input.

It produces an error-corrected table of the abundances of amplicon sequence variants in each sample (ASV table).

Callahan et al., 2016

Int_BT_2019
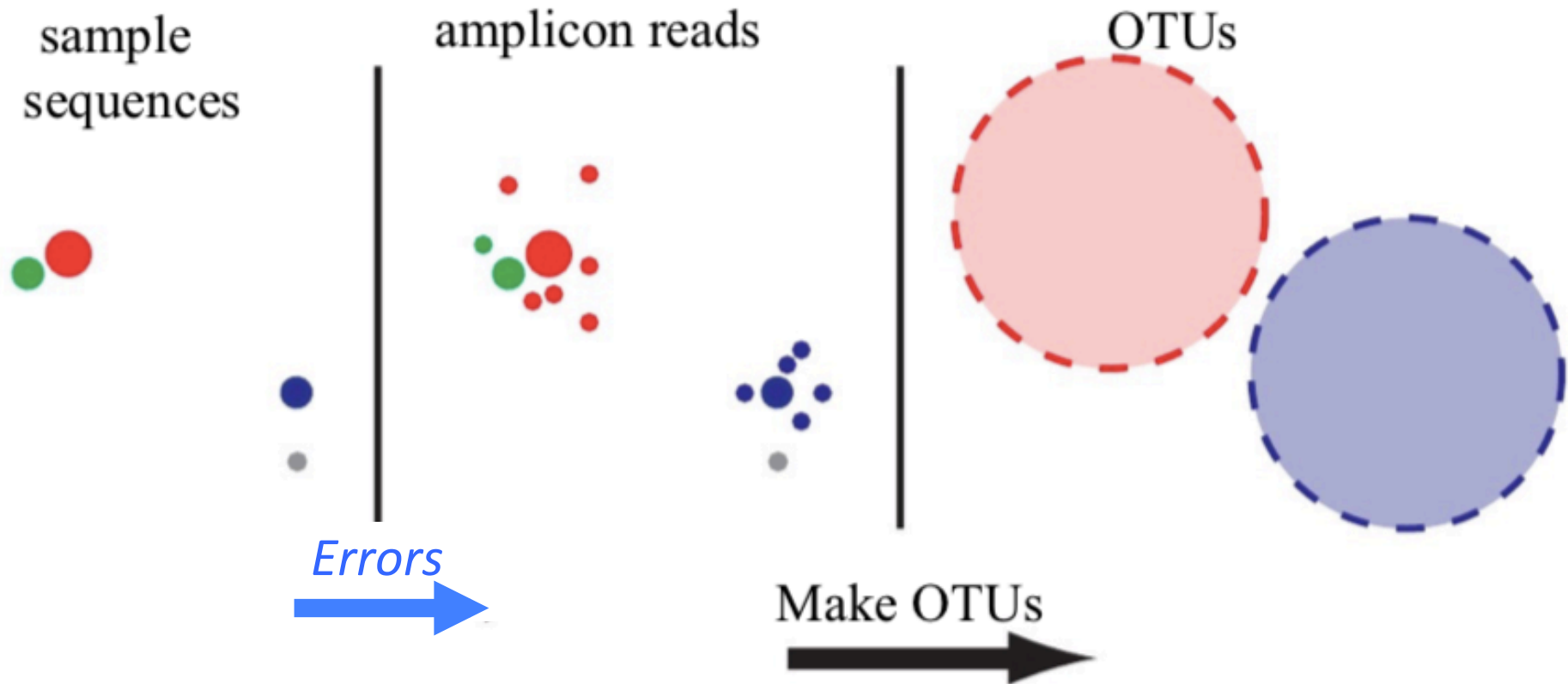Imane Allali

DADA2 background

Benefits to DADA2:

- Compatible with all amplicon types

    16S, 18S, ITS,…

- Works on different next generation sequencing platforms

    Illumina, Ion Torrent, 454 pyrosequencing

- Provides single-nucleotide resolution

- Lower false-positive rate

DADA2 background

- R or RStudio.

- QIIME2
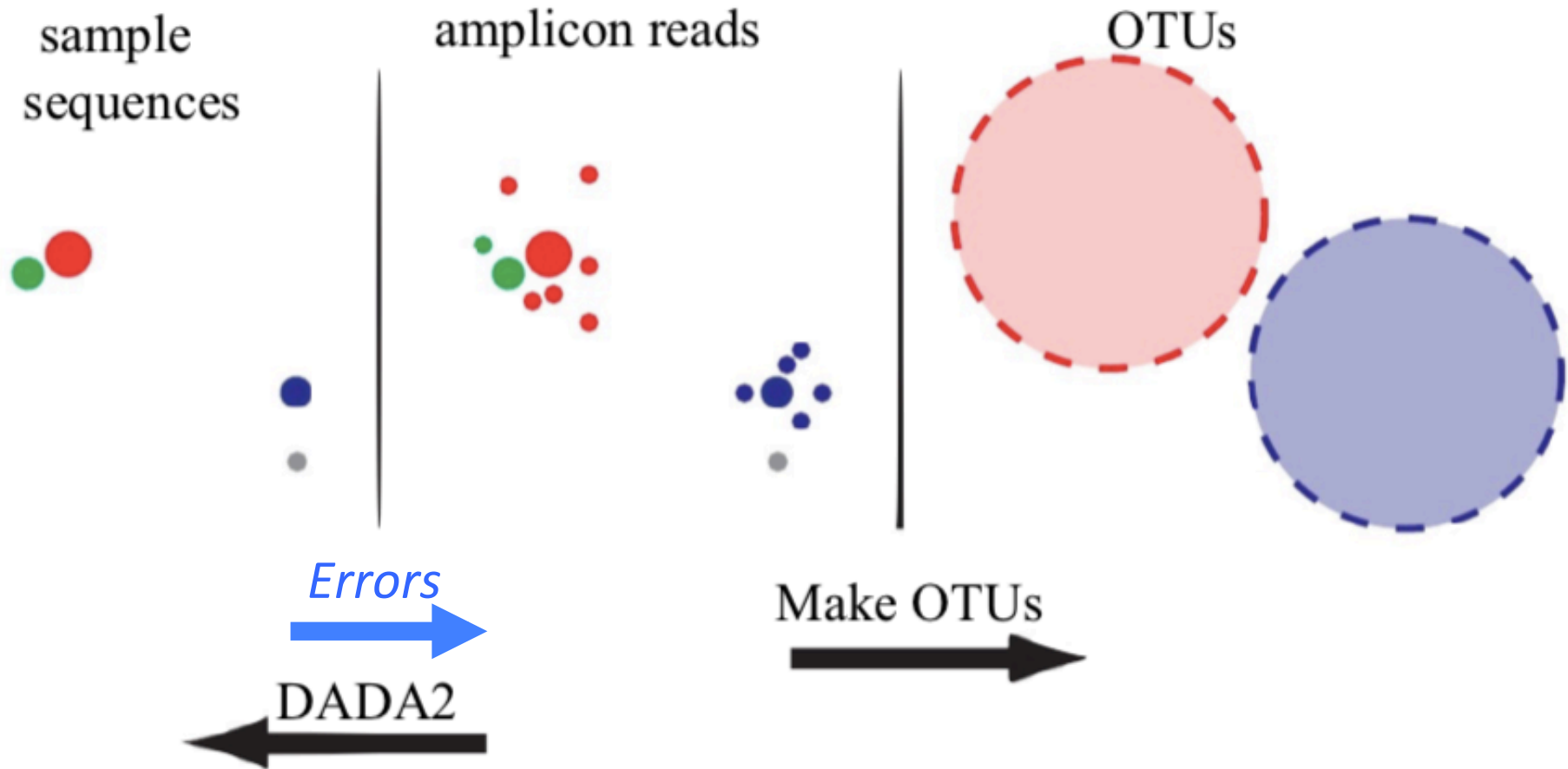 - Simplified and condensed the dada2 workflow

DADA2 background

sample sequences → amplicon reads (Errors) → Make OTUs → OTUs

Benjamin Callahan

DADA2 background

sample sequences

amplicon reads

OTUs

Errors

DADA2

Make OTUs

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