



# H3ABioNet

Pan African Bioinformatics Network for H3Africa

## 16SrRNA Intermediate Bioinformatics Online Course: Int\_BT\_2019

### 16S analysis pipeline

### Taxonomic classification and alignment using the dada2 pipeline

### Practical



**H3ABioNet**

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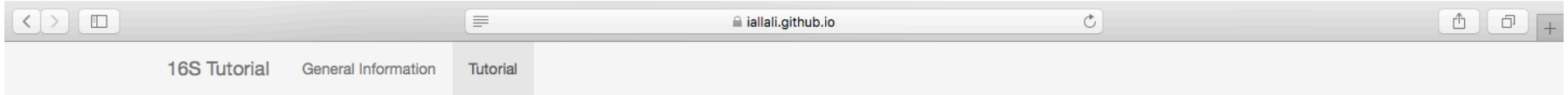


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# Practical

The practical is available here:

[https://iallali.github.io/DADA2\\_pipeline/16SrRNA\\_DADA2\\_pipeline.html](https://iallali.github.io/DADA2_pipeline/16SrRNA_DADA2_pipeline.html)



## 5. Merge the Paired Reads

In this step, we merge the forward and reverse reads to obtain the full sequences.

```
merge.reads <- mergePairs(dadaF, filt.dataF, dadaR, filt.dataR, verbose=TRUE)
```

```
## 76306 paired-reads (in 1153 unique pairings) successfully merged out of 82378 (in 2526 pairings) input.
```

```
## 54948 paired-reads (in 720 unique pairings) successfully merged out of 60139 (in 1811 pairings) input.
```

```
## 83013 paired-reads (in 843 unique pairings) successfully merged out of 89310 (in 2175 pairings) input.
```

```
## 74533 paired-reads (in 1093 unique pairings) successfully merged out of 81135 (in 2674 pairings) input.
```

```
## 67364 paired-reads (in 855 unique pairings) successfully merged out of 71053 (in 1743 pairings) input.
```

```
## 69262 paired-reads (in 1194 unique pairings) successfully merged out of 76778 (in 2891 pairings) input.
```

```
## 97401 paired-reads (in 954 unique pairings) successfully merged out of 106466 (in 2867 pairings) input.
```

```
## 129237 paired-reads (in 1632 unique pairings) successfully merged out of 146610 (in 5263 pairings) input.
```

```
## 111558 paired-reads (in 1143 unique pairings) successfully merged out of 120597 (in 3110 pairings) input.
```

```
## 85319 paired-reads (in 839 unique pairings) successfully merged out of 92957 (in 2348 pairings) input.
```

```
## 68550 paired-reads (in 915 unique pairings) successfully merged out of 74010 (in 2198 pairings) input.
```

```
## 92870 paired-reads (in 1266 unique pairings) successfully merged out of 107043 (in 4252 pairings) input.
```

```
## 101935 paired-reads (in 981 unique pairings) successfully merged out of 108579 (in 2495 pairings) input.
```