



Fast and accurate sample inference from amplicon data with single-nucleotide resolution

DADA2 + PacBio is live in version 1.9.1

High-throughput amplicon sequencing of the full-length 16S rRNA gene with single-nucleotide resolution

Installation

Binaries for the current release version of DADA2 (1.8) are available from Bioconductor. Note that you must have R 3.5.0 or newer, and [Bioconductor version 3.7](#), to install the current release from Bioconductor.

```
## try http:// if https:// URLs are not supported
source("https://bioconductor.org/biocLite.R")
biocLite("dada2")
```

If you wish to install the latest and greatest development version, or to install to earlier versions of R, see our [from-source installation instructions](#).

[Explore the DADA2 website](https://benjjneb.github.io/dada2/)
<https://benjjneb.github.io/dada2/>

Github

- Join if you haven't already.
- Perform some action (star, comments, etc.)
- Explore DADA2 issues:
<https://github.com/benjjneb/dada2/issues>

Start going through the DADA2 tutorial

- Read each step!
- Try function options.
- Use the help (e.g. `?filterAndTrim`).
- Inspect output objects (e.g. `print, class, dim, str`).
- Not a race, we will return to this tomorrow