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 Biocondcutor version 3.7, to install the current release from Bioconductor.

```r
## 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/
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