

# Statistics for Genomic Data Science: Week 1

---

Jeff Leek

@jtleek

[www.jtleek.com](http://www.jtleek.com)

**This week:**

**Background**

**Exploratory analysis**

## BioC2015

Our our [Annual Conference](#) has just concluded. See you next year!

## About *Bioconductor*

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data.

Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, [1024 software packages](#), and an active user community. Bioconductor is also available as an [AMI](#) (Amazon Machine Image) and a series of [Docker](#) images.

## News

### Install »

Get started with *Bioconductor*

- [Install \*Bioconductor\*](#)
- [Explore packages](#)
- [Get support](#)
- [Latest newsletter](#)
- [Follow us on twitter](#)
- [Install R](#)

### Learn »

Master *Bioconductor* tools

- [Courses](#)
- [Support site](#)
- [Package vignettes](#)
- [Literature citations](#)
- [Common work flows](#)
- [FAQ](#)
- [Community resources](#)
- [Videos](#)

### Use »

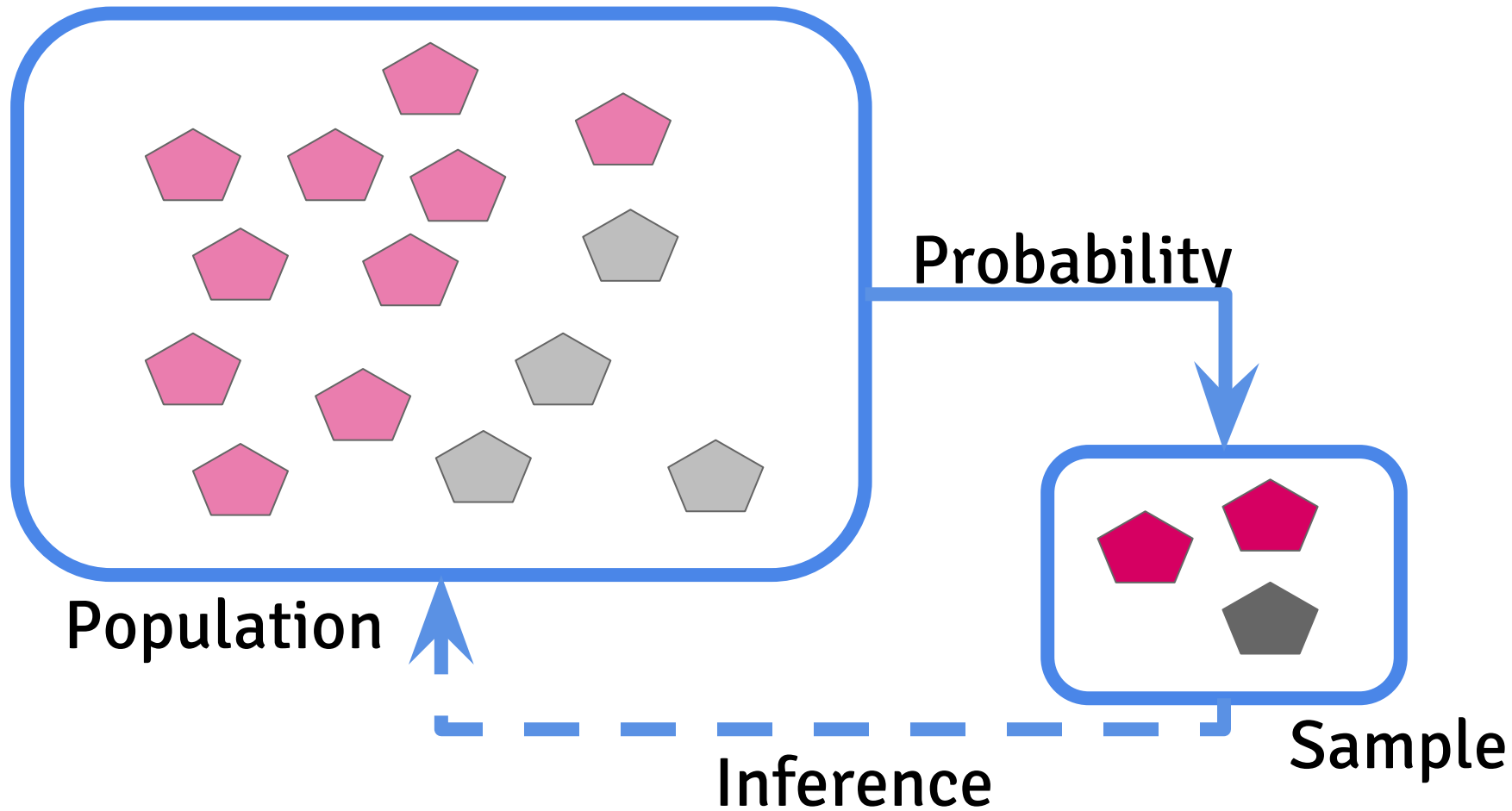
Create bioinformatic solutions with *Bioconductor*

- [Software](#), [Annotation](#), and [Experiment](#) packages
- [Amazon Machine Image](#)

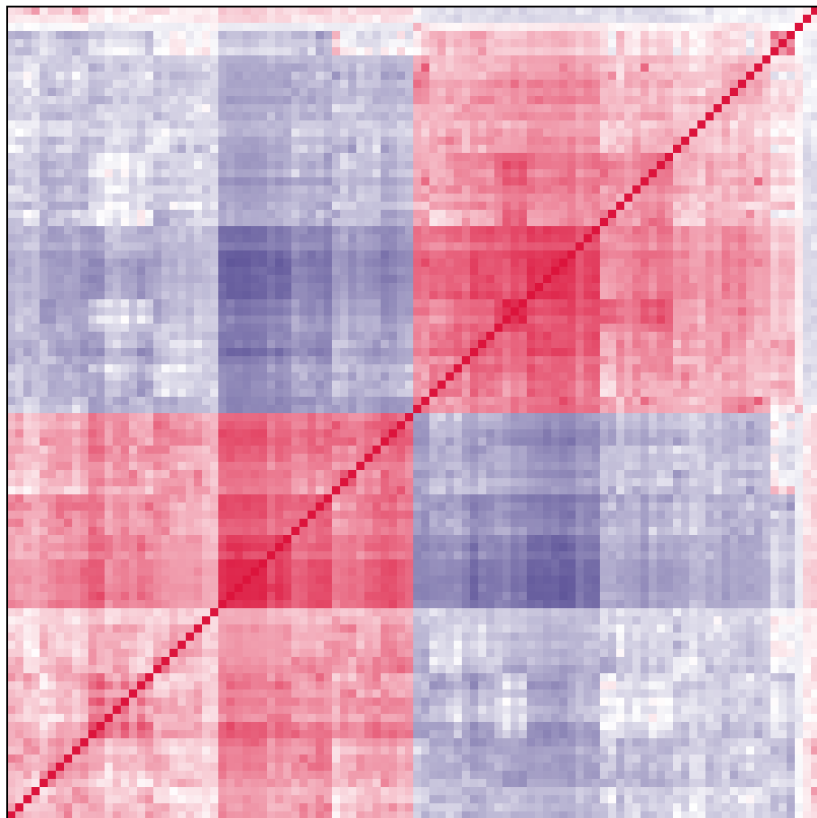
### Develop »

Contribute to *Bioconductor*

- [Use Bioc 'devel'](#)
- 'Devel' [Software](#), [Annotation](#) and [Experiment](#) packages
- [Package guidelines](#)



Correlation matrix



Scatterplot

