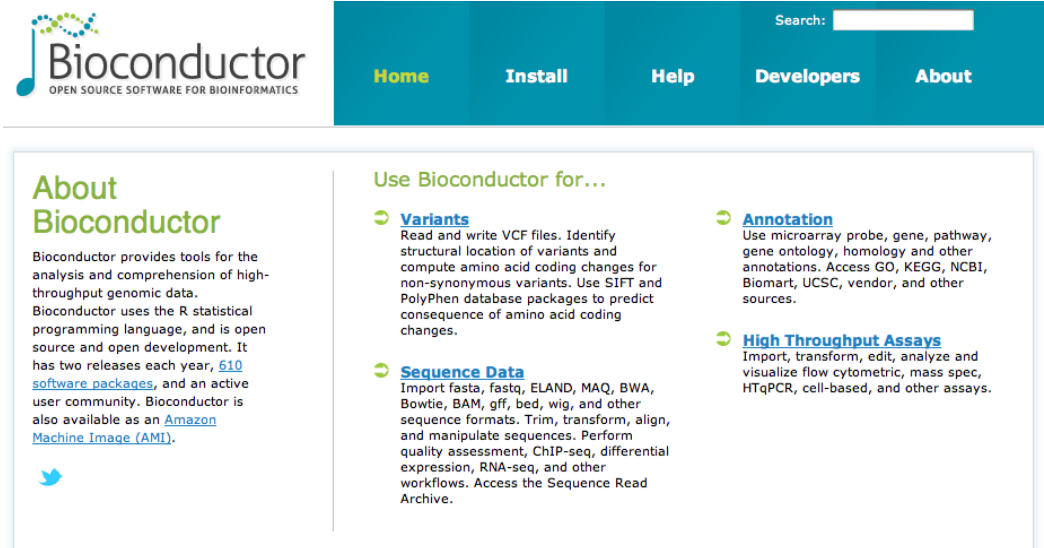


Bioconductor project

Open source software project for the analysis and comprehension of high-throughput genomic data

Packages written in [R](#)
Primarily for Microarray
and Sequence data

Started in 2001 by
Robert Gentleman et al



Bioconductor: Open software development for computational biology and bioinformatics R. Gentleman, V. J. Carey, D. M. Bates, B. Bolstad, M. Dettling, S. Dudoit, B. Ellis, L. Gautier, Y. Ge, and others 2004, [Genome Biology, Vol. 5, R80](#)

Bioconductor goals



The broad goals of the project are to:

Enable sound and powerful statistical analyses in genomics

Provide a computing platform that allows the rapid design and deployment of high-quality software

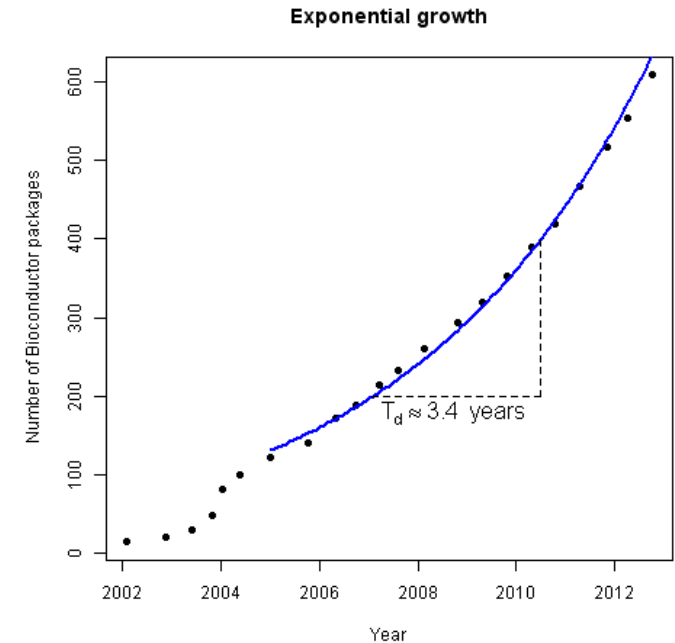
Develop a computing environment for both biologists and statisticians

Promote high-quality dynamic documentation and reproducible research (pdf's and vignettes)

Project growth

Number of contributed packages each bi-annual software release

Release	N	Release	N	Release	N
2002 1.0	15	2006 1.8	172	2010 2.6	389
1.1	20	1.9	188	2.7	419
2003 1.2	30	2007 2.0	214	2011 2.8	467
1.3	49	2.1	233	2.9	517
2004 1.4	81	2008 2.2	260	2012 2.10	554
1.5	100	2.3	294		
2005 1.6	123	2009 2.4	320		
1.7	141	2.5	352		



Bioconductor mailing list statistics

Year	Posts per month	Authors per month	Year	Posts per month	Authors per month
2002	59	13	2008	424	83
2003	231	47	2009	450	86
2004	320	60	2010	504	170
2005	353	61	2011	467	166
2006	348	59	2012	605	196
2007	432	75			

Journal Citations

Pubmed searches for Bioconductor 2003-2011

Year	N	Year	N	Year	N
2003	7	2007	44	2011	68
2004	13	2008	52	2012	48 ³
2005	19	2009	62		
2006	30	2010	52		

Google Scholar citations for Bioconductor packages

Package	Citation	N	Package	Citation	N
limma	Smyth (2005)	1249	DESeq	20979621	230
vsn	12169536	1106	edgeR	19910308	204
affy	14960456	907	eisa	12689096	198
xcms	16448051	546	MassSpecWavelet	16820428	166
globaltest	14693814	421	beadarray	17586828	119
G0stats	17098774	335	cellHTS2	16869968	107
affycomp	14960458	283	affylmGUI	16455752	104
limmaGUI	15297296	279	altcdfenvs	15310390	84
lumi	18467348	268	tilingArray	16787969	88
aCGH	16159913	232	made4	15797915	83
biomaRt	16082012	231			

Installing Bioconductor

Installing packages on the R terminal *using http://*

Set the repository

options(repos="http://cran.stat.auckland.ac.nz")

Download biocLite() from the internet

source("http://bioconductor.org/biocLite.R")

Install core packages

biocLite()

Install a specific package

biocLite("limma")

Install several packages

biocLite(c("GenomicFeatures", "AnnotationDbi"))

Using biocLite() auto magically resolves packages and their dependences from both [Bioconductor](#) and [CRAN](#)

Installing Bioconductor...

Automatically install a package if it cannot be loaded on a machine

```
## Package 'getopt' is in CRAN, 'limma' is in Bioconductor
```

```
packages <- c("getopt","limma")
```

```
## Load or install and load required packages
```

```
for (pck in packages){
```

```
  if (suppressPackageStartupMessages(!require(pck,character.only=TRUE)) ){
```

```
    ## Install biocLite the first time only
```

```
    if(.Platform$OS.type == "windows") setInternet2(TRUE)
```

```
    if(match(pck, packages) == 1) source("http://www.bioconductor.org/biocLite.R")
```

```
    biocLite(pck, suppressUpdates = TRUE)
```

```
    suppressPackageStartupMessages(require(pck,character.only=TRUE))
```

```
  }
```

```
}
```

Getting started using Bioconductor

Vignette documentation

List of help documentation
vignette()

Mailing lists

<http://www.bioconductor.org/help/mailling-list/>

Workshop course material from many previous events

<http://www.bioconductor.org/help/course-materials/>

HT Sequence Analysis with R and Bioconductor

<http://manuals.bioinformatics.ucr.edu/home/ht-seq>

