Manuscript Title

This manuscript ([permalink](#)) was automatically generated from [BiocWrites/bioc_bib_chapter_2023@8acc974](#) on November 2, 2023.

Authors

- **Vincent J. Carey**
  [XXXX-XXXX-XXXX-XXXX](#) · [vjcitn](#)
  Channing Lab, Harvard · Funded by Grant XXXXXXXX

- **Sean Davis** ✉
  [0000-0002-8991-6458](#) · [seandavi](#)
  University of Colorado Anschutz School of Medicine

✉ — Correspondence possible via [GitHub Issues](#) or email to Sean Davis <seandavi@gmail.com>.

Abstract

Introduction

Results

Table 1: Packages described in this review.

Package	Category	Reference
GEOquery	Access NCBI Gene Expression Omnibus	[1]
TCGABioLinks	Access TCGA data	[2]

How Bioconductor enhances cancer data reuse and value

The GEOquery package

Multiassay cancer data integration using Bioconductor (MAE + viz, iSEE)

Copy number variation analysis (Workshop, DNAcopy, PureCN, CNVRanger, Sehyun, Ludwig)

Approaches to providing reproducible, reusable, robust software for cancer data science (VC)

Bioconductor approaches to single-cell and spatially resolved cancer data and analysis (Workshops, Ludwig, Davide)

Pharmacogenomics resources in Bioconductor (Ben HK)

bibliometrics as code (MM) – maybe

References

1. **GEOquery: a bridge between the Gene Expression Omnibus (GEO) and BioConductor.**
   Sean Davis, Paul S Meltzer
   Bioinformatics (Oxford, England) (2007-05-12) https://www.ncbi.nlm.nih.gov/pubmed/17496320
   DOI: 10.1093/bioinformatics/btm254 · PMID: 17496320

2. **TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data.**
   Antonio Colaprico, Tiago C Silva, Catharina Olsen, Luciano Garofano, Claudia Cava, Davide
   Garolini, Thais S Sabedot, Tathiane M Malta, Stefano M Pagnotta, Isabella Castiglioni, … Houtan
   Noushmehr
   Nucleic acids research (2015-12-23) https://www.ncbi.nlm.nih.gov/pubmed/26704973
   DOI: 10.1093/nar/gkv1507 · PMID: 26704973 · PMCID: PMC4856967