Manuscript Title

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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