INTRODUCTION

SeqResults is a meta-data aware system enabling comparison of results across multiple libraries

We have developed SeqResults to enable simple comparison of libraries across experiments. The Galaxy-integrated component captures metadata and results in a relational database. Results are available via a simple web site and Tableau visualizations. SeqResults has recently been extended with RNA-seq features. It aggregates simple metrics like fractions of reads on exons, introns and other genomic regions, average 5'3' coverage and alignment efficiency. However, summary metrics are only part of the story. Accurate representation of transcript levels is important to any RNA-seq experiment. We present a simple interface to compare transcript levels as well as 5'3' coverage profiles of individual transcripts across experiments. SeqResults now contains millions of individual results from 6841 libraries produced during development of NEBNext library preparation reagents.

ARCHITECTURE

Update

Visualize

INPUT

Store

Galaxy Tool Input

Typical Aggregation Workflow

STORE

PER-TRANSKRIT 5'-3' COVERAGE

CONCLUSIONS

SeqResults is an open-source, integrated system of tools to help people find, visualize, and derive meaning from sets of sequence libraries. It has proven valuable for the development of NEBNext library prep reagents spanning RNA, DNA and targeted sequencing methods. Rapid analysis and visualization of detailed results enable the NEBNext team to innovate quickly and produce high quality library preparation reagents.

REFERENCES