DMPTool   **DMP ID:** 10.48321/D1D046   **Version:** 21 Apr 2023

This page describes a data management plan written for the Civil
Aerospace Medical Institute (faa.gov) using the DMPTool.

Assessment of RNA-seq Sample Preparation Methodology

Contributors to this project

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Project details

Research domain: Biological sciences

Project Start: March 01, 2020

Project End: September 29, 2023

Created: December 22, 2022

Modified: April 21, 2023

Ethical issues related to data that this DMP describes? no

Citation

When citing this DMP use:
Susan Munster. (2022). "Assessment of RNA-seq Sample Preparation
Methodology" [Data Management Plan]. DMPHub.
https://doi.org/10.48321/D1D046

**When connecting to this DMP to related project outputs (such as
datasets) use the ID:**
https://doi.org/10.48321/D1D046

Funding status and sources for this project

Status: Planned

Funder: Federal Aviation Administration (faa.gov)

Grant: unspecified

Project description

This study was designed to designed to address concerns regarding effects of lab processing techniques on downstream results and also to determine an optimal combination of software programs to use to align genetic data and assess differential expression. Homogeneous lab samples were tested using two different purification methods and compared to unpurified samples to determine if either purification method had any impact on differential expression. Genetic data was also simulated with a known rate of differential expression. All samples were aligned and analyzed for differential expression using combinations of seven different alignment programs and nine different differential expression programs. Results were compared to determine which alignment program(s) and which differential expression program(s) provided optimal results in terms of accuracy, time required for processing and data storage footprint.

Planned outputs

Assessment of RNA-Seq Sample Preparation Methodology

56 .fastq genetic sequence data files derived from pooled blood samples and 20 .fastq genetic sequence simulated data files based on chromosome 22.

Format: Dataset

Anticipated volume: 6 GB

Release timeline: January 31, 2023

Intended repository: NCBI dbGaP

An Evaluation of the Downstream Effects of Purification Methods on RNA-Seq Differential Expression

RNA-Seq is a commonly used technique to determine genetic sequences. It requires samples which are both concentrated and in very small volumes. There are common purification techniques which are used to increase concentration and/or reduce volumes for samples. It is not known if either of these techniques has any impact on downstream differential expression analyses, which is vital to biomarker discovery.

https://doi.org/10.21949/1524442

Format: Data Paper

Release timeline: January 31, 2023

RNA-Seq Alignment and Differential Expression Software Comparison

RNA-Seq is a widely used tool to determine genetic sequences. Alignment of genetic sequences to reference genomes can be accomplished by a large selection of software programs. Data analysis of alignments, to determine differential expression (differences in expression) between comparison groups can also be evaluated by a wide variety of software packages. There is not a general consensus as to which combination of alignment program and differential expression package will provide the greatest accuracy while also taking into account computational time and memory storage footprint. This study's aims is to determine which combination(s) of alignment programs(s) and differential expression package(s) provide optimal results.

https://doi.org/10.21949/1524443

Format: Data Paper

Release timeline: January 31, 2023

TBD

Peer-reviewed publication based on the data presented in *RNA-Seq Alignment and Differential Expression Software Comparison*.

Format: Data Paper

Other works associated with this research project