

# RNAseq Analysis

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# RNAseq Analysis

Anthony Hall already gave an Adjective introduction to RNA-seq, so I will only Verb - Base Form

a brief review. RNA-seq refers to the Noun of using Adjective parallel

sequencing to obtain global information on an RNA component from an Noun. This

could be poly(A) RNA (representing mRNA), total RNA, Adjective RNA, or some other

fraction. Here we Verb - Base Form on analysis of poly(A) RNA.

There are many questions that can be answered from RNA-seq data. RNA-seq data

can be used to:

Determine which Noun of a genome are expressed

Annotate a Noun

Find splice or alternative splice sites

Examine Noun - Plural in expressed genes

Use de novo assembly in organisms with no Noun to assemble a set of

cDNAs.

Find genes that are Adverb expressed between treatments, Noun,

timepoints, etc.

This lab will Verb - Base Form on differential expression and on polymorphism discovery.

Verb - Present ends in ING RNA-seq data is an evolving field and there are no truly plug-and-play

Noun - Plural. The basic steps are to:

Perform a quality control analysis of the \_\_\_\_\_ Noun

Filter reads to remove:

o Reads of \_\_\_\_\_ Adjective quality

o Adapter contamination

o rRNA or other \_\_\_\_\_ Noun

\_\_\_\_\_ Verb - Base Form reads to a reference genome or cDNA set.

Normalize read counts between \_\_\_\_\_ Noun - Plural

Fit a statistical \_\_\_\_\_ Noun to \_\_\_\_\_ Verb - Base Form for genes that are significantly \_\_\_\_\_ Adjective  
expressed.