Landscape of DNA and RNA Methylation

Specific Aims: DNA to RNA

- DNA transcription → RNA modification → Protein

- #1 – Genome-wide epigenetic profiles of DNA methylation changes
- #2 – A comprehensive catalog of coding and noncoding, small and large RNA
- #3 – Transcriptome-wide maps of RNA methylation sites

Implications of the Research for Space & Earth

Space: (1) Establish the genetic networks and expression patterns activated by space travel, (2) trace clonality of epigenetic changes, (3) examine the methylation of RNA

Earth: Aid research on aging, cancer, RNA biology, and circadian rhythm, all of which show differences at the (epi)genome & (epi)transcriptome

Δ in Epigenetics: Loci, regions, and clones

Δ in Transcriptome: Genes, Isoform, Edits, Allele, SNVs, ncRNAs, Fusions, & Methylation

Sequencing Data

RNA-seq gives many views of biology. We use r-make.

Viruses/Bacteria/Other

Use: BLAST, MetaPhAN

Predict polyA sites & gain/loss of miRNA binding sites

Algorithms: r-make, BAGET, AlexaSeq, TargetScan

Gene fusion detection

Algorithms: r-make, Snowshoes

Find ncRNAs and new genes

Algorithms: r-make, Aceview

Differential expression by gene, exon, splice isoform, allele, & transcript

Algorithms: STAR, r-make, ASE, Lmna-voom, RSEM

Genetic variation (SNVs and Indels)

Algorithms: STAR/GATK, r-make

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