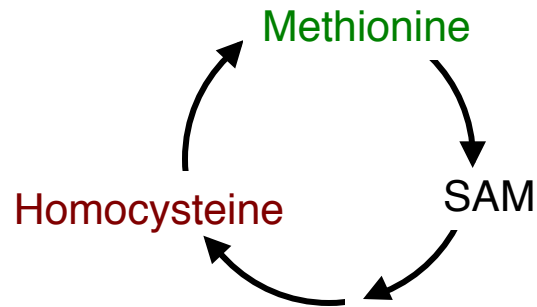
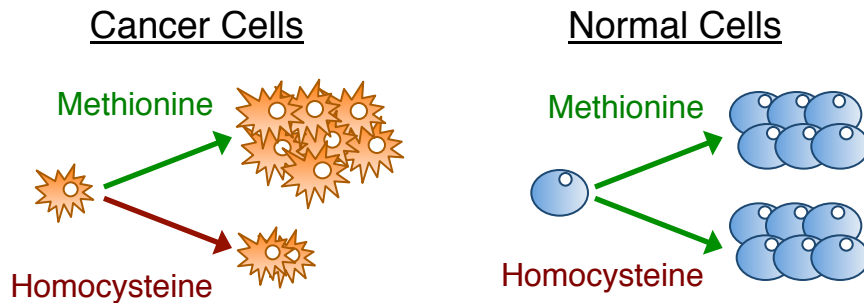




## Metabolism of Nutrients



## Differences between CANCER and NORMAL cells



## Next Generation Sequencing

### RNA-seq

- RNA
- Gene expression, splicing

### ChIP-seq

- DNA
- Genes associated with histone modifications (methylation, acetylation)

### ATAC-seq

- DNA
- Accessibility of specific genes for transcription
- Complementary with RNAseq and ChIPseq data

### Methyl-seq

- DNA
- Methylation on DNA



## Bioinformatics Support Group

- Help introduce the UCI HPC and linux environment
- Introduce different types of NGS analyses
  - RNA-seq
  - ChIP-seq
  - Metagenomics
- Provide useful tools
  - Regular expressions
  - Task arrays
  - BioLinux with UCI RCIC

## Why am I Here?

To learn about computing systems to be more:

- Efficient
  - parallelization
- Effective
  - learn more tools to improve analysis
- Aware of how to troubleshoot linux and cluster issues

