基礎生物学研究所 ゲノムインフォマティクス・トレーニングコース2016年8 - 9月

RNA-seq 入門

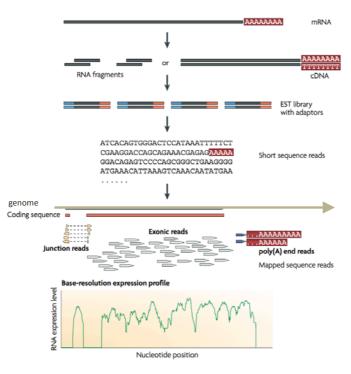
NGS の基礎から de novo 解析まで 準備編・実践編

~概論~

September 8-9, 2016 @ NIBB (Okazaki)

• サポートWiki https://github.com/nibb-gitc/gitc2016sep-rnaseq/wiki

RNA-seq



(Wang 2009 with modifications)

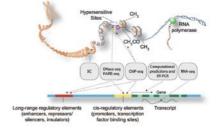
RNA-seq is unraveling complexities of eukaryotic transcriptomes in model and non-model organisms

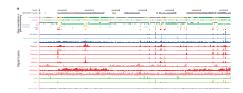
- Gene expression analysis
- Novel gene discovery (model org.)
 - Coding and non-coding genes
- Gene cataloguing (non-model org.)
- Anti-sense transcripts
- RNA editing
- Novel splicing variants & fusion genes
- Allele-specific expression

Beyond transcriptome

- DB for proteome analysis
- SNP finding
- and more ...







Two major goals

- Gene cataloguing
- Gene expression analysis

RNA-seq analysis pipeline for DE

<u>Differential</u> <u>Expression</u> analysis

Millions of short reads



Reads aligned to reference



count by unit
(gene, transcript, exon)

Table of counts



normalization DE testing

List of DE gene

systems biology

- GO enrichment
- multivariate analysis
- network analysis

Biological insights

Biologist が身に付けるべき 6つの informatics スキル

- •初級)UNIXの基礎
- 初級) 統計的な考え方と技術
- 初級) 業界標準のツール
- 初級) データ可視化
- 中級) 初歩的なプログラミング
- ・中級) データベース