Ecological Genomics Notes

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Info Update:

- Advantages in Seq tech.

- Ranage of applications:

  - WGS (whole genome sequencing)
  - RNAseq (seqencing RNA conveted to cDNA)
  - Targeted caputure seq. (string of probes mixed with sample, pulls immune related genes from organisim and seq just those)
  - Chipseq (chromatin imunoprecipitation seq, recognizezes and antibody and puls out all DNA bound to that portein)

Why one or the other?

Genetic variation

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- phenotypes
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number of samples

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- population
- individual
- comparitive studies
- model or not
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Demographic history

Adaptive geneitc varaitin

gene expression car.

length of reads

number of reads

distribution

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Reads:
- short = 50bp
- long 100 bp, 150 bp, 300 bp (miseq)
- 10,000-60,000bp = SMRT
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Single vs. paired end

- General library Prep. Workflow

  - extraction (DNA, RNA -> to cDNA)
  - fragment sample
  - ligate adaptors (indvidual barcodes)

– add seq. adaptors

Reduced Rep

– RNA -> coding
– GBS/RAD-seq
– near restriciton sites

- Sequencing-by-synthesis (SBS)

    – bridge amp
    – cluster gen.
    – labeled dNTP (ATCG)

- Other Technologies

- Learning Activity

Human Genome Project (2001-2003)

- ABI = Sanger

- 15 years

- 1 geneome (one person)

- $3 billion

Uses PCR and sequences broken by faulty base pairs to work backwards

2014 X-Ten releases

-Hiseq by Illumina (look up video of how it works)
-1 day
-45 whole genomes
-$1000 bucks each

Sheet of glass with 8 lanes with flow cells...(look up)

Take home messages

- Likely using Illumina seq. (just library tech. changes) usually SBS

- adaptors are markers (barcodes) used to identify samples during sequencing

    – first thing that's sample and gives ID barcode = seq adaptor
    – alago is a sequence of DNA that is attatched to plate binds to sample

- Model vs. non Model:

    – short reads (assembly to create long sequnce based on short reads that shift)

    – denavo assembly -> computer program (added variability with mixed sample)

    – 15% error for SMRT can be reduced to less than 1 with repeated passes

    – illumina is much smaller but more accurate (0.05% error)

    – combine the two to have a higher degree of confidnece

Paper Discussion: