HIGH-THROUGHPUT GENOTYPING:
RADSEQ/GENOTYPING BY SEQUENCING
DATA ANALYSIS

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Texas A&M System, Texas, and the World

“How do I start a new sequencing project?”

Questions related to your samples, or the submission process
OUTLINE

- What is RADseq/Genotyping By Sequencing (GBS)
- Examples of RADseq/GBS applications
  - 1. For genome-wide variation discovery;
  - 2. Genetic Maps, QTL mapping
  - 3. Genome wide association study (GWAS), Genomic Selection (GS)
  - 3. Population genetics study
- Data analysis
  - general approach for NGS data analysis
  - Several GBS pipelines
- Hands on exercises
APPROACHES FOR HIGH-THROUGHPUT GENOTYPING:

- Whole-genome re-sequencing
- Exome Capture + Sequencing
- Genotyping SNP assay: *infinium* 90K, Axiom 400K
- Reduced representation: RADseq, Genotyping By Sequencing
WHY REDUCED REPRESENTATION?
Restriction Associated DNA Sequencing, RADSeq
Genotyping By Sequencing, GBS
REDUCED REPRESENTATION GENOME SEQUENCING: RADSEQ/GBS

- More even coverage than random shearing
- Requires less data
- Multiplexing, economically feasible
RADSEQ/GENOTYPING BY SEQUENCING

➤ History
➤ 2007, RAD markers
  ➤ Miller et al. Rapid and cost-effective polymorphism identification and genotyping using restriction site associated DNA (RAD) markers: RAD tags with microarray
  ➤ Van et al. Complexity Reduction of Polymorphic Sequences: RAD tags sequencing with 454 sequencer. Genotyping using Keygene SNPWave (patent application)
➤ 2008, RADseq
➤ GBS, ddRAD, 2-b RAD, bsRADseq
  ➤ Elshire et al. A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species.
  ➤ Peterson et al. Double digest RADseq: an inexpensive method for de novo SNP discovery and genotyping in model and non-model species
  ➤ Wang et al. 2b-RAD: a simple and flexible method for genome-wide genotyping
➤ ....
RADSEQ/GBS PROTOCOLS:

**Original RAD**
1. Digest (one enzyme)
2. Ligate adaptors
3. Multiplex
4. Shear
5. Size select
6. End repair
7. A-tailing
8. Ligate Y-adaptors
9. PCR

**2bRAD**
1. Digest (one IIb enzyme)
2. Ligate adaptors
3. PCR
4. Multiplex

*Nature Reviews Genetics 17, 81–92 (2016) doi:10.1038/nrg.2015.28*
Genomic DNA

Adapter | 100bp |
-------|------|

Sequencer

barcode

Sample 1
Sample 2
Sample 3
Sample ....
RADSEQ/GBS EXPERIMENT DESIGN

➤ Choose the protocol
   ➤ Pick the most suitable restriction enzyme(s) for the targeting genome
      ➤ Methylation-sensitive restriction enzymes
      ➤ Double digestion
### In Silico digestion genome coverage for fragment between 100-600 bp

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</table>
RADSEQ/GBS APPLICATION EXAMPLES

➤ Variation discovery

➤ Single-nucleotide polymorphism discovery by high-throughput sequencing in sorghum. BMC Genomics. 2011

➤ Sequencing from libraries constructed to limit sequencing to start at defined restriction sites led to genotyping 10-fold more SNPs.

Haplotype sharing patterns
RADSEQ/GBS APPLICATION EXAMPLES

➤ Genetic Mapping

➤ Exploiting genotyping by sequencing to characterize the genomic structure of the American cranberry through high-density linkage mapping, BMC Genomics. 2016

➤ 10842 SNPs in total; 4849 markers were mapped.
RADSEQ/GBS APPLICATION EXAMPLES

➤ QTL Mapping

➤ An evaluation of genotyping by sequencing (GBS) to map the Breviaristatum-e (ari-e) locus in cultivated barley, BMC Genomics, 2014

➤ In total, 461M categorized reads from the GPMx mapping population were mapped.... Using these highly conservative criteria, we identified an initial set of 1,949 co-dominant SNPs with robust allele calls across the population.
RADSEQ/GBS APPLICATION EXAMPLES

- Genomic Selection (GS)
  - GS uses genomewide molecular markers to predict complex, quantitative traits in animal and plant breeding.
  - Is GBS suitable for this task?

Jesse Poland, et al, 2012
RADSEQ/GBS APPLICATION EXAMPLES

- Phylogenetic inference

RAD-seq-based phylogeny of the 12 Drosophila species, based on 100-bp-long RAD-seq reads, inferred by maximum likelihood using PhyML 3.0.
SUMMARY

➤ Many protocols to be chosen from
➤ *In silico* digestion helps to pick the restriction enzymes
➤ Feasible for large-scale genomics studies
What kind of data being generated?

Sequence by Synthesis, Anderson and Schrijver, 2010
RADSEQ/GBS DATA ANALYSIS

➤ What kind of data being generated?
  ➤ fastq format
  ➤ each read represented by 4 lines
What kind of data being generated?

- fastq format
What kind of data being generated?

fastq format
What kind of data being generated?

- **fastq format**

A quality score $Q$ is an integer mapping of $p$ (the probability that the base casting is wrong).

$$Q_{sanger} = -10 \log_{10} p$$
RADSEQ/GBS DATA ANALYSIS

➤ What kind of data being generated?
  ➤ fastq format
  ➤ A typical GBS read
Mainly two types of pipeline

- Alignment-based
  - Treat GBS/RADseq data as usual NGS data

- Clustering-based
  - Cluster the reads that are from the same loci, then discover variations within clusters (i.e. multiple sequence alignment)
## ALIGNMENT APPROACH

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CLUSTERING BASED APPROACH

Clustering based on similarity

Tag1
ATA
TTT
ATA

Tag2


Tag3


.
RADSEQ/GBS DATA ANALYSIS

➤ Features of the two types of pipelines
  ➤ Alignment-based
    ➤ require reference
    ➤ compute intensive
    ➤ More accurate
    ➤ Imputation might be easier
  ➤ Clustering-based
    ➤ reference not required
    ➤ Reduce the computation cost by clustering
    ➤ Might lead to large false positive, or removing too many variation with stringent filtering criteria
Reference genome available?

Yes
- Polyploidy?
  Yes
  Alignment-based Pipeline
  No
  Clustering-based Pipeline

No
- Polyploidy?
  Yes
  Build a reference from the reads
  No
  Either would work well

Distant related individuals?

Alignment-based Pipeline

Clustering-based Pipeline
General NGS analysis workflow for variation discovery

Raw reads → QC → Alignment → Processing/Filtering → Calling variations → Filtering → De novo assembly
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<th>Pipeline/Program</th>
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Stacks

- Designed to work with short read (max 1024bp)
- Uniform length of reads
  - Ideal for Illumina
  - For Ion Torrent platform, reads would need to be truncated to a particular length
- Deal with most of the RADseq/GSB protocols
- *Stacks* is designed to process data that *stacks* together:
  - In the case of double-digest RAD, both the single-end and paired-end read are anchored by a restriction enzyme and can be assembled as independent loci;
  - In cases such as with the RAD protocol, where the molecules are sheared and the paired-end therefore does not stack-up, cannot be directly used.
WHY CLUSTERING OR STACKING REDUCE THE COST OF COMPUTATION

TASSEL-GBS:

Instead of trying to map eight reads separately, we may just take one as representative.
Stacks 2 workflow
# Major Parameters

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<th><code>denovo_map.pl</code> Parameter</th>
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1. MINIMUM STACK DEPTH -m 3

If set to a value of 3 then three or more identical reads must be found to consider those reads a stack. If a stack is formed with only two reads, then those reads are set aside and a stack is not constructed.

If this parameter is set too low, then reads with convergent sequencing errors are likely to be erroneously labeled as stacks.

If this parameter is too high, then true alleles will not be recorded and will drop out of the analysis.

If you have low sequencing depth for your samples, you will have to set this parameter to a relatively low value. Conversely, if you have very high sequencing coverage, you will want to increase this parameter.

If you have a high error rate in your sequencing lane, then you are likely to see convergent sequencing or PCR errors (errors that occur independently at the same nucleotide position in the same read) and should increase the minimum stack depth.
1. MINIMUM STACK DEPTH

1. If set to a value of 3 then three or more identical reads must be found to consider those reads a stack. If a stack is formed with only two reads, then those reads are set aside (**secondary reads**) and a stack is not constructed.

2. If this parameter is set too low, then reads with convergent sequencing errors are likely to be erroneously labeled as stacks.

3. If this parameter is too high, then true alleles will not be recorded and will drop out of the analysis.

4. If you have low sequencing depth for your samples, you will have to set this parameter to a relatively low value. Conversely, if you have very high sequencing coverage, you will want to increase this parameter.

5. If you have a high error rate in your sequencing lane, then you are likely to see convergent sequencing or PCR errors (errors that occur independently at the same nucleotide position in the same read) and should increase the minimum stack depth.
2. DISTANCE ALLOWED BETWEEN STACKS

Stack 1
Stack 2
Stack 3
... Stack X

D I C T I O N A R Y

Locus 1
Locus 2
... Locus X
2. DISTANCE ALLOWED BETWEEN STACKS

1. If you set this parameter too low, then some loci will fail to be reconstructed. This means the SNPs contained in that locus will not be identified and this locus will appear as two loci to the remainder of the pipeline.

2. Setting this parameter too high will allow repetitive sequence to chain together into large, nonsensical loci. For example, if stack A is one nucleotide apart from stack B, which is one nucleotide apart from stack C, which is one nucleotide apart from stack D, then A, B, C, and D will be merged into a locus despite A and D being four nucleotides apart. These loci are not useful to the pipeline and at several points the pipeline will try to detect these and set them aside.

3. You will want to experiment with several different values of this parameter to see how many polymorphic loci you can construct.
3. DISTANCE BETWEEN CATALOG LOCI

SAMPLE1

SAMPLE2

SAMPLEX

CATALOG

Locus 1
Haplotypes: C A

Locus 2
Haplotypes: AC CT

Locus 3
Haplotypes: Consensus

Locus X
Haplotypes: AA GG
3. DISTANCE BETWEEN CATALOG LOCI

1 If you set this parameter too low, then some loci will fail to be reconstructed. This means the SNPs contained in that locus will not be identified and this locus will appear as two loci to the remainder of the pipeline.

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3 You will want to experiment with several different values of this parameter to see how many polymorphic loci you can construct.
How to optimize the parameters for my project?

Simulation

- With reference genome available, simulate RADseq/GBS reads from the reference genome with predefined SNPs;
- Call SNPs with different set of parameters, pick the one with the lowest FP and high TP.
- Generate SNPs for multiple sets of parameters, then check the SNP accuracy
DDocent relies almost entirely on third party software to complete every step of the analysis pipeline.

<table>
<thead>
<tr>
<th>Software</th>
<th>Website</th>
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<tbody>
<tr>
<td>FreeBayes</td>
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</tbody>
</table>
DDOCENT PIPELINE

Raw reads → QC reads → filtered reads → de novo assembly

TrimGalore
remove low coverage reads
rainbow cdhit

reference → BWA-mem

BAMs → FreeBayes GATK

Raw variations → VCFtools

Filtered variations
Simulated pairwise population comparisons ordered by expected $F_{ST}$
Any questions?
Let’s give it a try!
DEMO OF GBS DATA ANALYSIS USING STACKS ON HPRC

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**Login to ada:** ssh your-tamu-netid@ada.tamu.edu

**Create a folder:** mkdir stacks_tutorial && cd stacks_tutorial

**Get the tutorial data:** git clone https://github.com/swang8/workshop

**Create working directory:**

```bash
cd workshop/material/tutorial_data/
mkdir RAD && cd RAD
tar xvf ../rad_test.tar
ls -l
```

**Run jobs on working nodes interactively:**

https://portal.hprc.tamu.edu/