

Genome-wide Association Studies

BIOS 770

02/03/2022

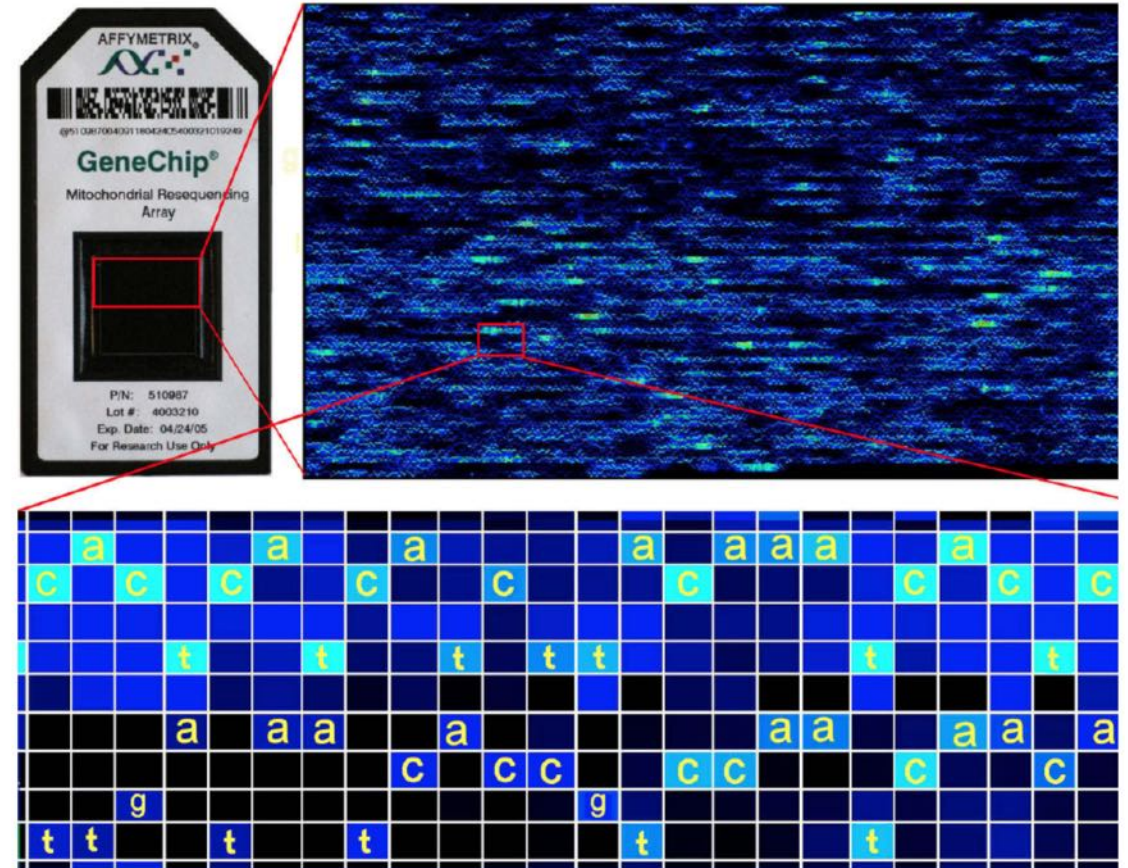
Jingjing Yang (jingjing.yang@emory.edu)

Outline

- Genotype Calling and Imputation
- Single Variant Test (common variants with MAF > 1%)
 - Dichotomous Trait
 - Chi-square test with contingency tables
 - Logistic regression model based test
 - Quantitative Trait
 - General linear regression model based test
- Visualization by Manhattan plot and LocusZoom plot

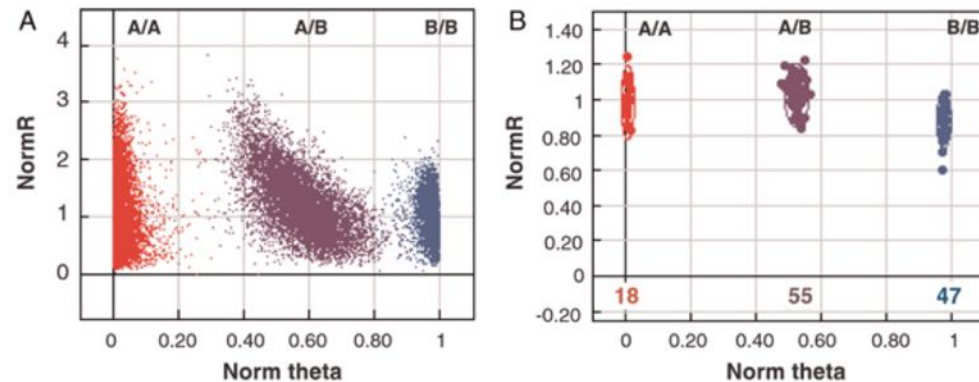
DNA Microarrays

- Old generation of technology (Affymetrix or Illumina)
- Still widely used for cheap cost, ~\$200 / sample
- Can be customized with densely spaced SNPs for target genes
- Genotype 0.5 Million ~ 1 Million SNPs



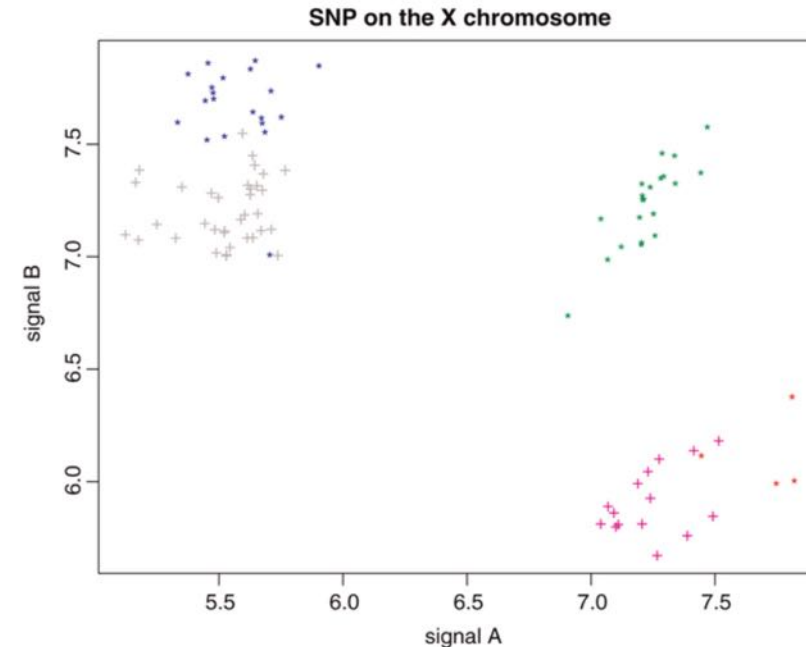
Variant Calling for Microarray Genotyping

- Each SNP has three possible genotypes: AA, BB, AB with two alleles A and B
- Summarize the probe intensities for each allele and SNP, and then make a call based on the summarized intensities



Normalised and summarised allele intensities from the Illumina BeadChip array.

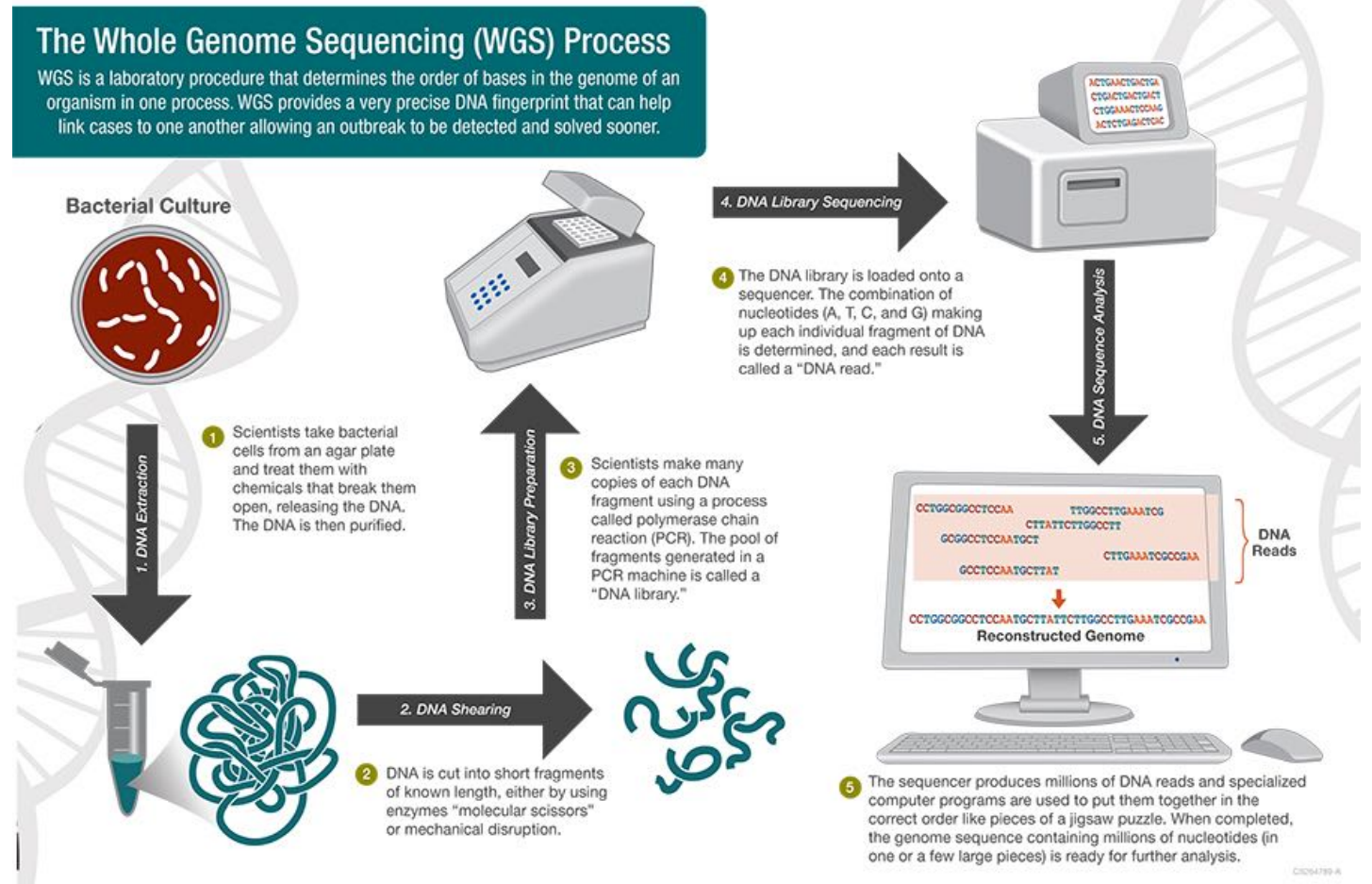
The intensities are shown in transformed polar coordinates: the theta-coordinate represents the angle from the x-axis (the angle from the x-axis to the vector [A, B] of the two allele intensities), and the R-coordinate represents the copy number (the length of the vector). (A) Intensities for a single nucleotide polymorphism (SNP) from 120 arrays, clearly separating the intensities into three groups (A/A, A/B, B/B). (B) Data from 317,000 SNPs (from the same 120 arrays). This plot clearly indicates that signal strength varies considerably with the SNP, a factor that must be taken into account when genotyping individual SNPs and deriving copy numbers. The figure is reproduced with the permission of Gunderson *et al.* [15]



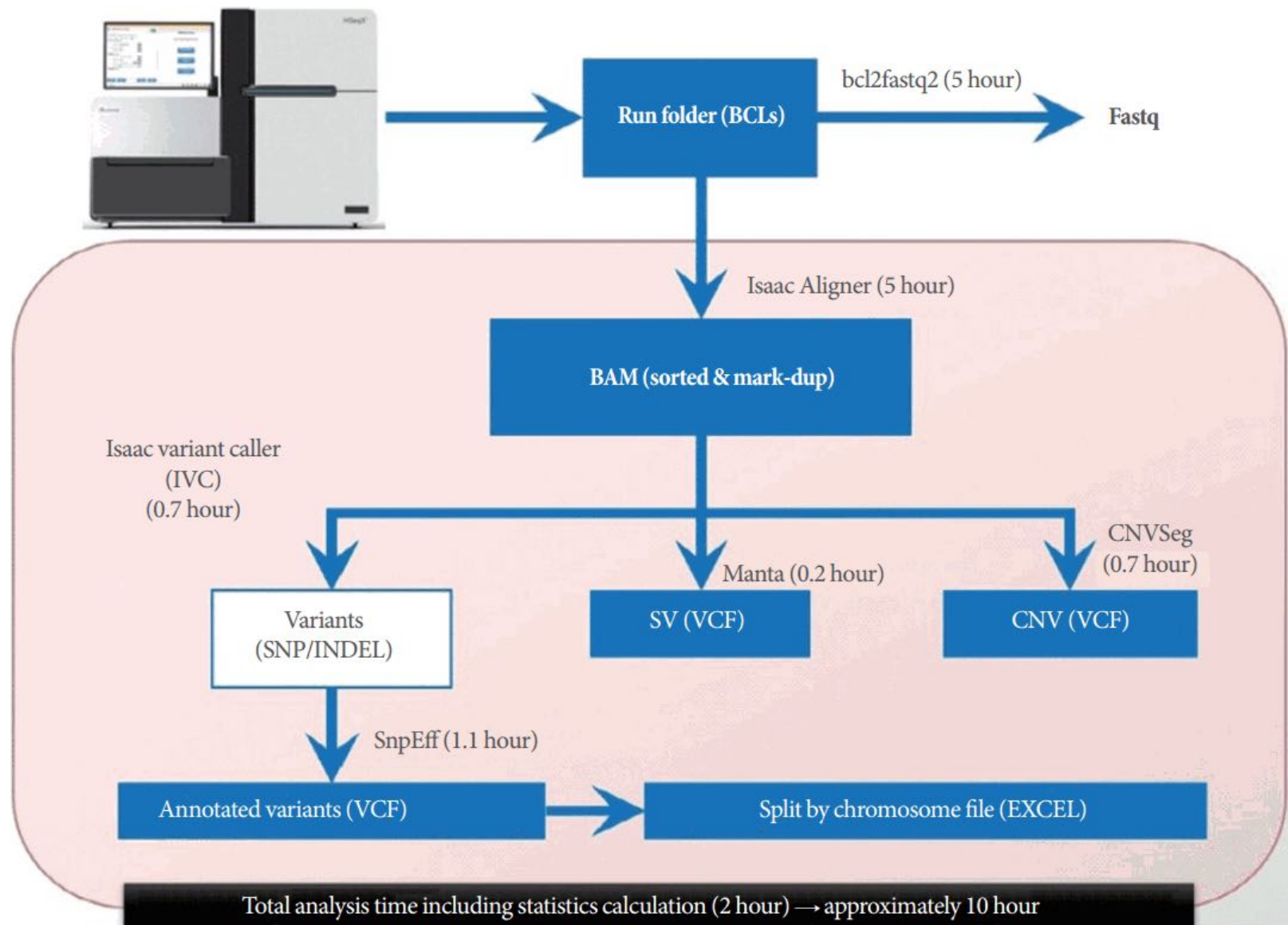
Normalised and summarised allele intensities from the Affymetrix GeneChip array. Each SNP is represented by a pair of intensity values (A, B) for the A and B alleles, respectively (here, on a log-scale). An X chromosome SNP is shown, clearly indicating separation into distinct genotype clusters. The plot also shows that different copy numbers can be distinguished. Males are haploid for the particular SNP (ie either AY or BY) and show up as homozygous but with reduced allele intensity. Grey: BY; blue: BB; green: AB; red: AA; and pink: AY.

Whole Genome Sequencing (WGS)

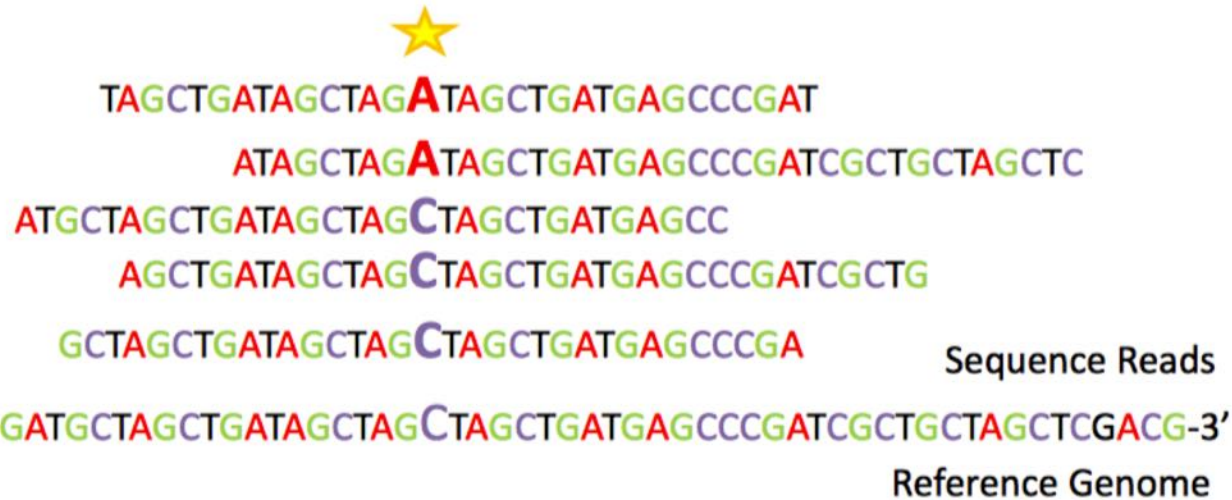
- Next-generation sequencing technology
- Introduction video of Illumina Sequencing technology:
<https://www.youtube.com/watch?v=fCd6B5HRaZ8>
- Cost ~\$2000/sample
- Profile >10M SNPs



WGS Analysis Workflow



Variant Calling for Sequence Genotyping



Ingredients That Go Into Prior

- Most sites don't vary
 - P(non-reference base) ~ 0.001
- When a site does vary, it is usually heterozygous
 - P(non-reference heterozygote) ~ 0.001 * 2/3
 - P(non-reference homozygote) ~ 0.001 * 1/3
- Mutation model
 - Transitions account for most variants (C↔T or A↔G)
 - Transversions account for minority of variants

$$P(\text{Genotype}|\text{reads}) = \frac{P(\text{reads}|\text{Genotype})\text{Prior}(\text{Genotype})}{\sum_G P(\text{reads}|G)\text{Prior}(G)}$$

Combine these likelihoods with a prior incorporating information from other individuals and flanking sites to assign a genotype.

Variant Calling for Sequence Genotyping



- Assume the probability to sequence “C” given “A”, or sequence “A” given “C” is 0.001:
 $P(\text{reads} \mid AA) = \text{dbinom}(3, \text{size} = 5, \text{prob} = 0.001) = 9.98e-9$
 $P(\text{reads} \mid AC) = \text{dbinom}(3, \text{size} = 5, \text{prob} = 0.5) = 0.312$
 $P(\text{reads} \mid CC) = \text{dbinom}(2, \text{size} = 5, \text{prob} = 0.001) = 9.97e-6$
- Assume population based prior with $P(A) = 0.2$
 $\text{Prior}(AA) = 0.04$; $\text{Prior}(AC) = 0.32$; $\text{Prior}(CC) = 0.64$
 $\text{Posterior}(AA) < 0.001$
 $\text{Posterior}(AC) = 0.999$
 $\text{Posterior}(CC) < 0.001$

- Individual Based Prior**
 - Assumes all sites have an equal probability of showing polymorphism
 - Specifically, assumption is that about 1/1000 bases differ from reference
 - If reads were error free and sampling Poisson ...
 - ... 14x coverage would allow for 99.8% genotype accuracy
 - ... 30x coverage of the genome needed to allow for errors and clustering
- Population Based Prior**
 - Uses frequency information obtained from examining other individuals
 - Calling very rare polymorphisms still requires 20-30x coverage of the genome
 - Calling common polymorphisms requires much less data
- Haplotype Based Prior or Imputation Based Analysis**
 - Compares individuals with similar flanking haplotypes
 - Calling very rare polymorphisms still requires 20-30x coverage of the genome
 - Can make accurate genotype calls with 2-4x coverage of the genome
 - Accuracy improves as more individuals are sequenced

Genotype data format

- Single nucleotide polymorphism (SNP) : One reference allele and one alternative allele, e.g., AG, AA, GG
- Variant Call Format (VCF): Text file recording one SNP per row

```
##fileformat=VCFv4.3
##fileDate=20090805
##source=myImputationProgramV3.1
##reference=file:///seq/references/1000GenomesPilot-NCBI36.fasta
##contig=<ID=20,length=62435964,assembly=B36,md5=f126cdf8a6e0c7f379d618ff66beb2da,species="Homo sapiens",taxonomy=x>
##phasing=partial
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##INFO=<ID=AF,Number=A,Type=Float,Description="Allele Frequency">
##INFO=<ID=AA,Number=1,Type=String,Description="Ancestral Allele">
##INFO=<ID=DB,Number=0,Type=Flag,Description="dbSNP membership, build 129">
##INFO=<ID=H2,Number=0,Type=Flag,Description="HapMap2 membership">
##FILTER=<ID=q10,Description="Quality below 10">
##FILTER=<ID=s50,Description="Less than 50% of samples have data">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT NA00001 NA00002 NA00003
20 14370 rs6054257 G A 29 PASS NS=3;DP=14;AF=0.5;DB;H2 GT:GQ:DP:HQ 0|0:48:1:51,51 1|0:48:8:51,51 1/1:43:5:.,.
20 17330 . T A 3 q10 NS=3;DP=11;AF=0.017 GT:GQ:DP:HQ 0|0:49:3:58,50 0|1:3:5:65,3 0/0:41:3
20 1110696 rs6040355 A G,T 67 PASS NS=2;DP=10;AF=0.333,0.667;AA=T;DB GT:GQ:DP:HQ 1|2:21:6:23,27 2|1:2:0:18,2 2/2:35:4
20 1230237 . T . 47 PASS NS=3;DP=13;AA=T GT:GQ:DP:HQ 0|0:54:7:56,60 0|0:48:4:51,51 0/0:61:2
20 1234567 microsat1 GTC G,GTCT 50 PASS NS=3;DP=9;AA=G GT:GQ:DP 0/1:35:4 0/2:17:2 1/1:40:3
```

Human genetic variants and sample sizes over past 20 years

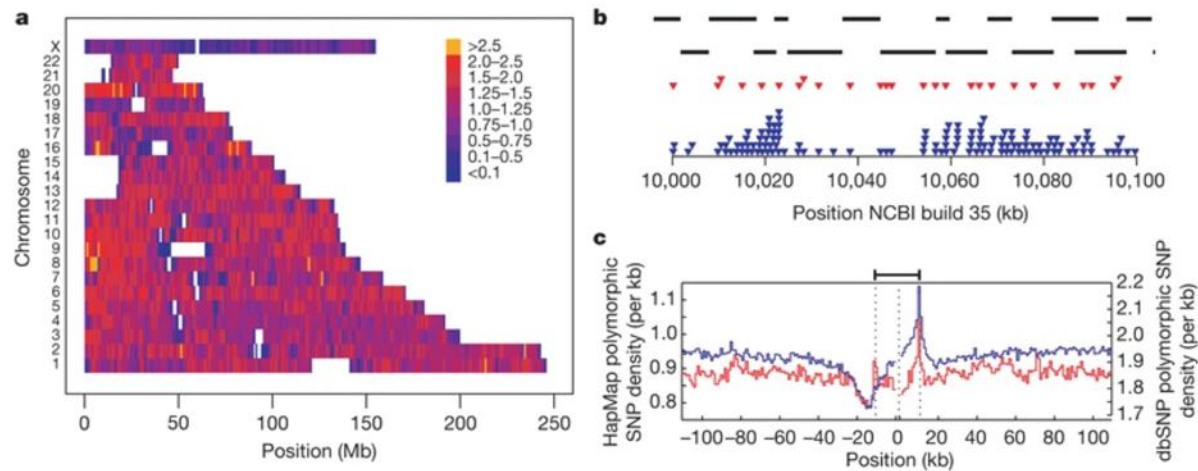
Year	No. of Samples	No. of Markers	Publication
Ongoing	120,000	600 million	NHLBI Precision Medicine Cohorts / TopMed
2016	32,488	40 million	Haplotype Reference Consortium (Nature Genetics)
2015	2,500	80 million	The 1000 Genomes Project (Nature)
2012	1,092	40 million	The 1000 Genomes Project (Nature)
2010	179	16 million	The 1000 Genomes Project (Nature)
2010	100,184	2.5 million	Lipid GWAS (Nature)
2008	8,816	2.5 million	Lipid GWAS (Nature Genetics)
2007	270	3.1 million	HapMap (Nature)
2005	270	1 million	HapMap (Nature)
2003	80	10,000	Chr. 19 Variation Map (Nature Genetics)
2002	218	1,500	Chr. 22 Variation Map (Nature)
2001	800	127	Three Region Variation Map (Am J Hum Genet)
2000	820	26	T-cell receptor variation (Hum Mol Genet)

HapMap Project (2002 - 2010)

- Goal: Develop a haplotype map of the human genome.
- The HapMap is valuable by reducing the number of SNPs required to examine the entire genome for association with a phenotype from the 10 million SNPs that exist to roughly 500,000 tag SNPs.
- **Phase II HapMap** characterizes **>3.1M SNPs (~1.3M from Phase I)** genotyped in **270** individuals from 4 populations, including 25-35% common SNPs (~10M), one per kilobase.
 - 30 trios of Yoruba (**YRI**) in Ibadan, Nigeria : African
 - 30 trios of Centre d'Etude du Polymorphisme Humain (CEPH) collection (**CEU**) living in Utah : European
 - 45 unrelated Han Chinese individuals in Beijing (**CHB**) + 45 unrelated Japanese in Tokyo (**JPT**) : Asian

The International HapMap Consortium. Nature 449, 851-861 (2007).

Figure 1: SNP density in the Phase II HapMap.



a, SNP density across the genome. Colours indicate the number of polymorphic SNPs per kb in the consensus data set. Gaps in the assembly are shown as white. **b**, Example of the fine-scale structure of SNP density for a 100-kb region on chromosome 17 showing Perlegen amplicons (black bars), polymorphic Phase I SNPs in the consensus data set (red triangles) and polymorphic Phase II SNPs in the consensus data set (blue triangles). Note the relatively even spacing of Phase I SNPs. **c**, The distribution of polymorphic SNPs in the consensus Phase II HapMap data (blue line and left-hand axis) around coding regions. Also shown is the density of SNPs in dbSNP release 125 around genes (red line and right-hand axis). Values were calculated separately 5' from the coding start site (the left dotted line) and 3' from the coding end site (right dotted line) and were joined at the median midpoint position of the coding unit (central dotted line).

The International HapMap Consortium. Nature 449, 851-861 (2007).

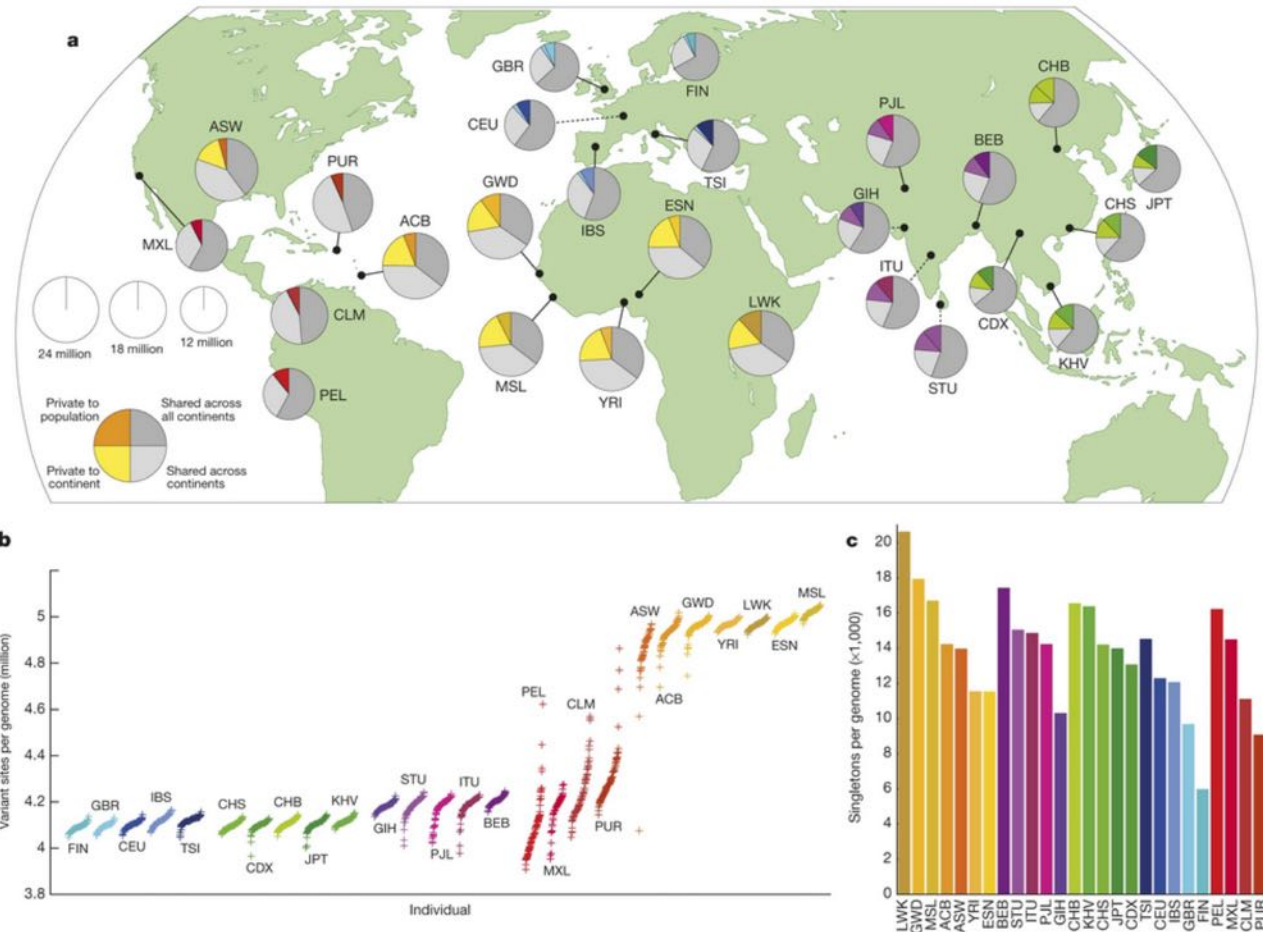
1000 Genome Project (2008 - 2015)

Goal: Find most genetic variants with MAF > 1% in populations across the world.

- First project to sequence (~8X coverage) the genomes of a large number of people (n = 2504)
- Largest public catalogue of human variation and genotype data: <http://www.internationalgenome.org/>
- 26 different populations under 5 super populations:

- **AFR**, African
- **AMR**, Ad Mixed American
- **EAS**, East Asian
- **EUR**, European
- **SAS**, South Asian

The 1000 Genomes Project Consortium. Nature 526, 68-74 (2015).



a, Polymorphic variants within sampled populations. The area of each pie is proportional to the number of polymorphisms within a population. Pies are divided into four slices, representing variants private to a population (darker colour unique to population), private to a continental area (lighter colour shared across continental group), shared across continental areas (light grey), and shared across all continents (dark grey). Dashed lines indicate populations sampled outside of their ancestral continental region. **b**, The number of variant sites per genome. **c**, The average number of singletons per genome.

Table 1. Median autosomal variant sites per genome in 1000 genome project

	AFR		AMR		EAS		EUR		SAS	
Samples	661		347		504		503		489	
Mean coverage	8.2		7.6		7.7		7.4		8.0	
	Var. sites	Singletons	Var. sites	Singletons	Var. sites	Singletons	Var. sites	Singletons	Var. sites	Singletons
SNPs	4.31M	14.5k	3.64M	12.0k	3.55M	14.8k	3.53M	11.4k	3.60M	14.4k
Indels	625k	-	557k	-	546k	-	546k	-	556k	-
Large deletions	1.1k	5	949	5	940	7	939	5	947	5
CNVs	170	1	153	1	158	1	157	1	165	1
MEI (Alu)	1.03k	0	845	0	899	1	919	0	889	0
MEI (L1)	138	0	118	0	130	0	123	0	123	0
MEI (SVA)	52	0	44	0	56	0	53	0	44	0
MEI (MT)	5	0	5	0	4	0	4	0	4	0
Inversions	12	0	9	0	10	0	9	0	11	0
Nonsynon	12.2k	139	10.4k	121	10.2k	144	10.2k	116	10.3k	144
Synon	13.8k	78	11.4k	67	11.2k	79	11.2k	59	11.4k	78
Intron	2.06M	7.33k	1.72M	6.12k	1.68M	7.39k	1.68M	5.68k	1.72M	7.20k
UTR	37.2k	168	30.8k	136	30.0k	169	30.0k	129	30.7k	168
Promoter	102k	430	84.3k	332	81.6k	425	82.2k	336	84.0k	430
Insulator	70.9k	248	59.0k	199	57.7k	252	57.7k	189	59.1k	243
Enhancer	354k	1.32k	295k	1.05k	289k	1.34k	288k	1.02k	295k	1.31k
TFBSs	927	4	759	3	748	4	749	3	765	3
Filtered LoF	182	4	152	3	153	4	149	3	151	3
HGMD-DM	20	0	18	0	16	1	18	2	16	0
GWAS	2.00k	0	2.07k	0	1.99k	0	2.08k	0	2.06k	0
ClinVar	28	0	30	1	24	0	29	1	27	1

The 1000 Genomes Project Consortium. Nature 526, 68-74 (2015).

See [Supplementary Table 1](#) for continental population groupings. CNVs, copy-number variants; HGMD-DM, Human Gene Mutation Database disease mutations; k, thousand; LoF, loss-of-function; M, million; MEI, mobile element insertions.

Impute Microarray Genotype Data

- Using WGS reference panel, e.g., 1000 Genome
- Fill in SNP genotypes for those not genotyped by Microarray
- Genotype imputation has become a standard tool in GWAS
 - Can only impute variants observed in a reference panel. Reference panels with millions of deeply sequenced individuals are available.
 - Result in ~10M imputed common variants
 - Improve GWAS power
 - Facilitating fine-mapping and meta-analysis
 - Facilitating GWAS results interpretation

Genotype Imputation Intuition

- Any two individuals, even if unrelated, can share short stretches of chromosome derived from a distant common ancestor.
- Observed genotypes from Microarray can be used to identify DNA segments shared between the study sample and a reference panel of sequenced genomes.
- A study haplotype can be represented as a mosaic of short segments of related haplotypes found in the reference panel.
- Points where the reference haplotype template changes represent historical recombination events.
- Points where the observed target allele differs from the template allele represent historical mutation events, gene conversion events, genotype error, or erroneously assigned matches.

Observed Genotypes

Observed Genotypes

. . . . **A** **A** **A**
. . . . **G** **C** **A**

Study
Sample

Reference Haplotypes

C G **A** G **A** T C T C C T T C T T C T G T G C
C G **A** G **A** T C T C C C G **A** C C T C **A** T G G
C C **A** **A** G C T C T T T T C T T C T G T G C
C G **A** **A** G C T C T T T T C T T C T G T G C
C G **A** G **A** C T C T C C G **A** C C T T **A** T G C
T G G G **A** T C T C C C G **A** C C T C **A** T G G
C G **A** G **A** T C T C C C G **A** C C T T G T G C
C G **A** G **A** C T C T T T T C T T T T G T **A** C
C G **A** G **A** C T C T C C G **A** C C T C G T G C
C G **A** **A** G C T C T T T T C T T C T G T G C

HapMap

Identify Match Among Reference

Observed Genotypes

. . . . **A** **A** **A**
. . . . **G** **C** **A**

Reference Haplotypes

C	G	A	G	A	T	C	T	C	C	T	T	C	T	T	C	T	G	T	G	C
C	G	A	G	A	T	C	T	C	C	C	G	A	C	C	T	C	A	T	G	G
C	C	A	A	G	C	T	C	T	T	T	T	C	T	T	C	T	G	T	G	C
C	G	A	A	G	C	T	C	T	T	T	T	C	T	T	C	T	G	T	G	C
C	G	A	G	A	C	T	C	T	C	C	G	A	C	C	T	T	A	T	G	C
T	G	G	G	A	T	C	T	C	C	C	G	A	C	C	T	C	A	T	G	G
C	G	A	G	A	T	C	T	C	C	C	G	A	C	C	T	T	G	T	G	C
C	G	A	G	A	C	T	C	T	T	T	T	C	T	T	T	T	G	T	A	C
C	G	A	G	A	C	T	C	T	C	C	G	A	C	C	T	C	G	T	G	C
C	G	A	A	G	C	T	C	T	T	T	T	C	T	T	C	T	G	T	G	C

Phase Chromosome, Impute Missing Genotypes

Observed Genotypes

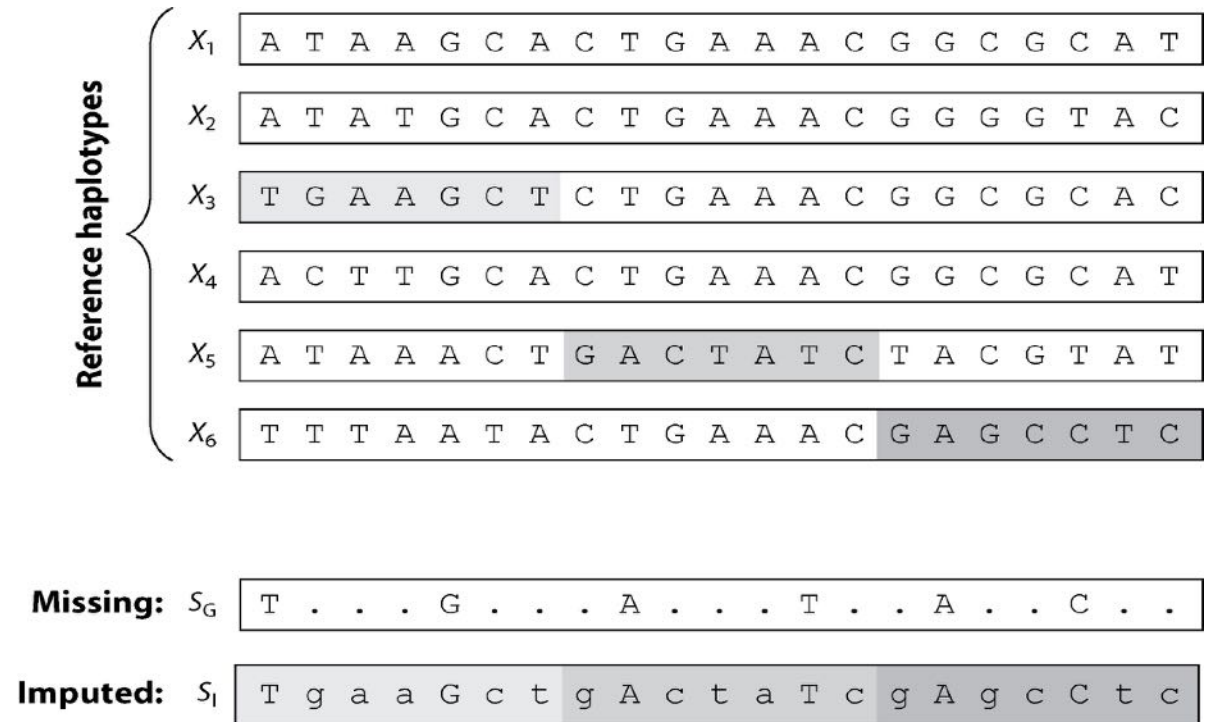
c	g	a	g	A	t	c	t	c	c	c	g	A	c	c	t	c	A	t	g	g
c	g	a	a	G	c	t	c	t	t	t	t	C	t	t	t	c	A	t	g	g

Reference Haplotypes

C	G	A	G	A	T	C	T	C	C	T	T	C	T	T	C	T	G	T	G	C
C	G	A	G	A	T	C	T	C	C	C	G	A	C	C	T	C	A	T	G	G
C	C	A	A	G	C	T	C	T	T	T	T	C	T	T	C	T	G	T	G	C
C	G	A	A	G	C	T	C	T	T	T	T	C	T	T	C	T	G	T	G	C
C	G	A	G	A	C	T	C	T	C	C	G	A	C	C	T	T	A	T	G	C
T	G	G	G	A	T	C	T	C	C	C	G	A	C	C	T	C	A	T	G	G
C	G	A	G	A	T	C	T	C	C	C	G	A	C	C	T	T	G	T	G	C
C	G	A	G	A	C	T	C	T	T	T	T	C	T	T	T	T	G	T	A	C
C	G	A	G	A	C	T	C	T	C	C	G	A	C	C	T	C	G	T	G	C
C	G	A	A	G	C	T	C	T	T	T	T	C	T	T	C	T	G	T	G	C

Li and Stephens Mode

- Hidden Markov Model (HMM)
 - Observed genotypes of unknown phase in a study sample represent the observed data of the HMM.
 - Underlying and unobserved set of phased genotypes represent the hidden states of the HMM.
 - Probability of a template switch between markers is determined by the HMM transition probabilities, related to population recombination rate.
 - Probability that an observed allele differs from the template is determined by the HMM emission probabilities.

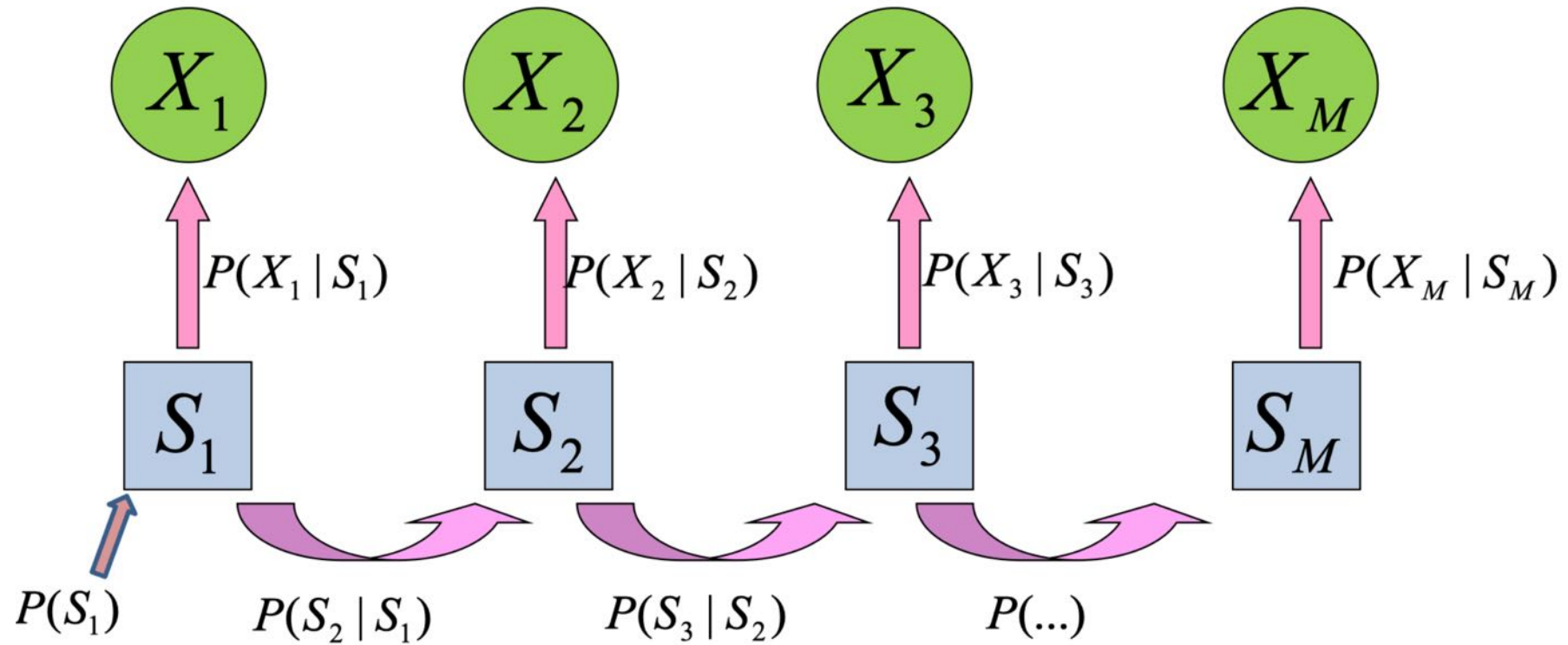


Das S, et al. 2018.
Annu. Rev. Genom. Hum. Genet. 19:73–96

Figure 2

An illustration of genotype imputation, showing the process of imputation for a study haplotype (S_G) genotyped at 6 markers using a reference panel of sequenced haplotypes at 21 markers. The alleles in S_G are used to match short segments from the reference panel. For example, in the first genomic segment, the alleles T and G imply that the corresponding segment might have been copied from haplotype X₃. In the second segment, the alleles A and T imply that haplotype X₅ might have been copied. Proceeding similarly, the study haplotype can be represented as a mosaic of DNA segments from haplotypes X₃, X₅, and X₆. Consequently, the missing sites can be imputed to obtain the final imputed haplotype, S₁.

Markov Model



The final ingredient connects template states along the chromosome ...

Possible States

- A state S selects pair of template haplotypes
 - Consider S_i as vector with two elements $(S_{i,1}, S_{i,2})$
- With H possible haplotypes, H^2 possible states
 - $H(H+1)/2$ of these are distinct
- A recombination rate parameter describes probability of switches between states
 - $P((S_{i,1} = a, S_{i,2} = b) \rightarrow (S_{i+1,1} = a, S_{i+1,2} = b)) \quad (1-\theta)^2$
 - $P((S_{i,1} = a, S_{i,2} = b) \rightarrow (S_{i+1,1} = a^*, S_{i+1,2} = b)) \quad (1-\theta)\theta/H$
 - $P((S_{i,1} = a, S_{i,2} = b) \rightarrow (S_{i+1,1} = a^*, S_{i+1,2} = b^*)) \quad (\theta/H)^2$

Emission Probabilities

- Each value of S implies expected pair of alleles
- Emission probabilities will be higher when observed genotype matches expected alleles
- Emission probabilities will be lower when alleles mismatch
- Let $T(S)$ be a function that provides expected allele pairs for each state S

Emission Probabilities

$$P(G_j|S_j) = \begin{cases} (1-\varepsilon_j)^2 + \varepsilon_j^2, & T(S_j)=G_j \text{ and } G_j \text{ is heterozygote,} \\ 2(1-\varepsilon_j)\varepsilon_j, & T(S_j)\neq G_j \text{ and } G_j \text{ is heterozygote,} \\ (1-\varepsilon_j)^2, & T(S_j)=G_j \text{ and } G_j \text{ is homozygote,} \\ (1-\varepsilon_j)\varepsilon_j, & T(S_j) \text{ is heterozygote and} \\ & G_j \text{ homozygote,} \\ \varepsilon_j^2, & T(S_j) \text{ and } G_j \text{ are opposite} \\ & \text{homozygotes.} \end{cases}$$

HMM

- The probability of each possible unobserved path through the HMM hidden states (reference haplotypes) can be calculated.
 - Penalized when path switches reference haplotypes via HMM transition probability
 - Penalized when reference allele on the path differs from the observed allele via HMM emission probabilities
- Probability that the unobserved path goes through a particular HMM state (state probability per reference haplotype) can be calculated by HMM forward-backward algorithm
- The probability (Z) that the target haplotype (study sample) carries a particular allele is the sum of the state probabilities corresponding to reference haplotypes that carry the allele
 - Z is also the expected number of a particular allele

Phasing

- Pre-phasing genotype data of the study sample greatly reduce computation burden of genotype imputation
 - First pre-phasing (haplotype estimation) of the genotypes of study samples
 - Imputation into the estimated study haplotypes
- Reduce the complexity of the imputation step from quadratic to linear in the number of reference haplotypes
 - Allowing matches to be found by comparing against phased sample haplotypes rather than against all pairs of sample haplotypes
 - Reduce cost for exploring multiple reference panels
 - Benefits from advanced phasing methods

Techniques for Computation Efficiency

- Storing reference data in memory
 - Burrows-Wheeler Transform
 - M3VCF format :exploits local redundancy among haplotypes by only storing unique allele sequences along with a map
 - Reduce >90% computation time compared with using VCF format with >100K reference samples
 - Allowing reference haplotypes to be locally clustered
 - Binary reference format (bref) : Because of the bulk of alleles with low nonmajor allele frequency in reference panel, only store a list of reference haplotypes that carry the minor allele (one list per allele)
 - Searching the lists of haplotypes to find the allele on a given haplotype
 - If haplotype is not found in any list, the haplotype carries the major allele
 - Reduces >30% computation time with >100K reference samples

Techniques for Computation Efficiency

- Clustering identical reference haplotype segments
 - Conduct local clustering ahead for the reference panel
 - Same allele sequence can be carried by many reference haplotypes in short regions
 - Reduce state space for non-boundary regions
- Imputation via linear interpolation
 - HMM state probabilities are calculated for genotyped markers of the study sample
 - HMM state probabilities at imputed markers are estimated by linear interpolation on genetic distance
- One can cluster reference haplotypes that have identical allele sequences between two genotyped markers before linear interpolation

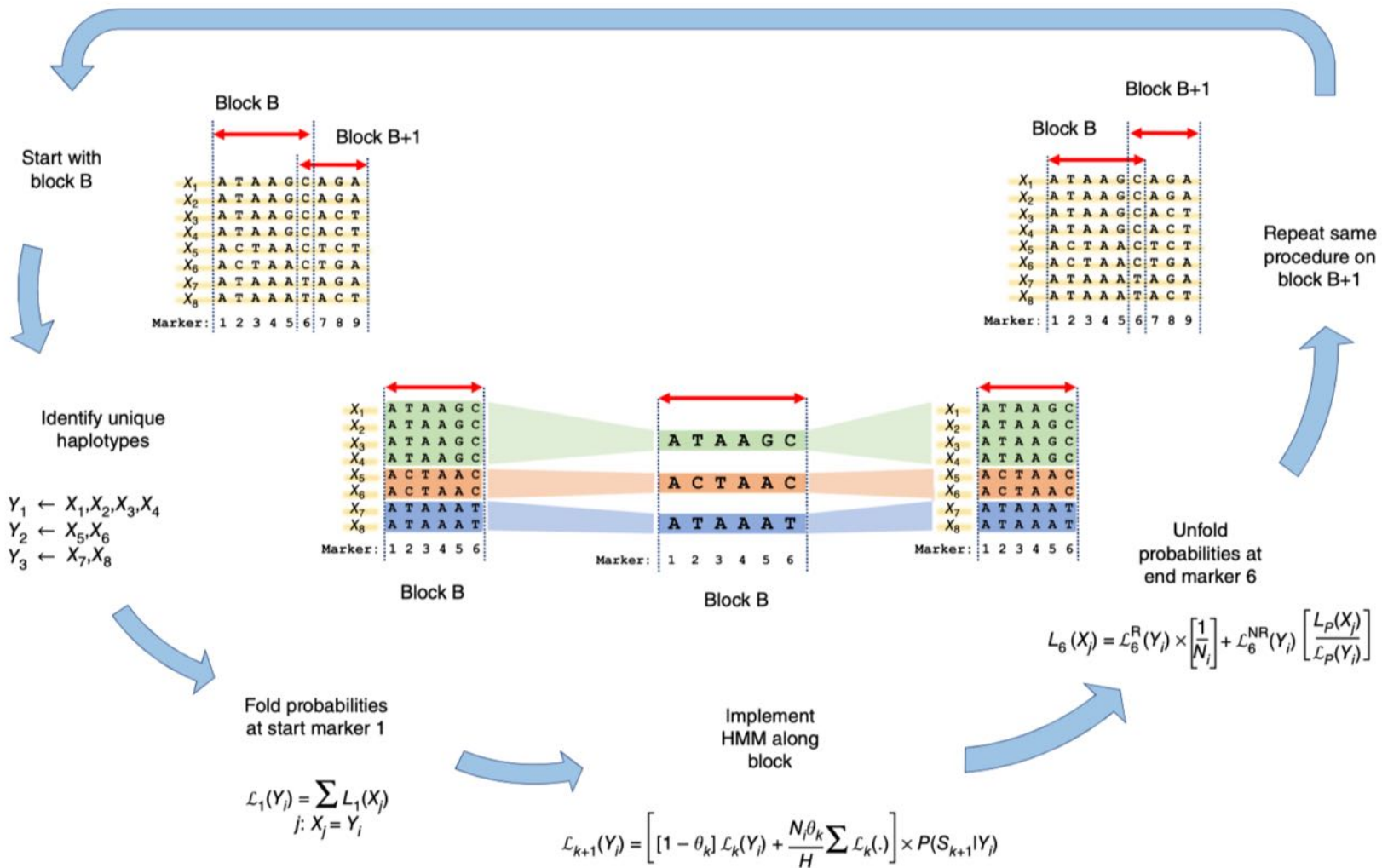


Figure 1 Overview of state space reduction. We consider a chromosome region with $M = 9$ markers and $H = 8$ haplotypes: X_1, X_2, \dots, X_8 . We break the region into consecutive genomic segments (blocks) and start by analyzing block B from marker 1 to marker 6. In block B, we identify $U = 3$ unique haplotypes: Y_1, Y_2 , and Y_3 (colored in green, red, and blue, respectively). Given we know the left probabilities of the original state space at marker 1 (that is, $L_1(X_1), \dots, L_1(X_8)$), we fold them to get the left probabilities of the reduced state space at marker 1: $L_1(Y_1), L_1(Y_2)$, and $L_1(Y_3)$. We implement HMM on the reduced state space (Y_1, Y_2 , and Y_3) from marker 1 to marker 6 to get $L_6(Y_1), L_6(Y_2)$, and $L_6(Y_3)$. We next unfold the left probabilities of the reduced state space at marker 6 to obtain the left probabilities of the original state space: $L_6(X_1), \dots, L_6(X_8)$. We repeat this procedure on the next block, starting with $L_6(X_1), \dots, L_6(X_8)$, to finally obtain $L_9(X_1), \dots, L_9(X_8)$.

Table 1 Genotype imputation tools that employ a hidden Markov model (HMM)

Tool	Year	Description of state space	Computational complexity	HMM parameter functions
FastPHASE	2006	All genotype configurations from a fixed number of localized haplotype clusters	Maximization-step linear in number of haplotypes, quadratic in number of clusters	Depends on recombination and mutation rates; parameters are fit using an expectation-maximization algorithm
IMPUTE	2007	All genotype configurations from all reference haplotypes	Quadratic in number of haplotypes	Depends on a fine-scale recombination map that is fixed and provided internally by the program
Beagle	2007	All genotype configurations from a variable number of localized haplotype clusters	Quadratic in number of haplotypes	Empirical model with no explicit parameter functions
IMPUTE2	2009	All reference haplotypes	Phasing quadratic in number of haplotypes, imputation linear in number of haplotypes	Same as IMPUTE
MaCH	2010	All genotype configurations from all reference haplotypes	Quadratic in number of haplotypes	Depends on recombination rate, mutation rate, and genotyping error; parameters are fit using a Markov chain Monte Carlo or expectation-maximization algorithm
Minimac and Minimac2	2012	All reference haplotypes	Linear in number of haplotypes	Same as MaCH
Minimac3	2016	All unique allele sequences observed in reference data in a small genomic segment	Linear in number of haplotypes	Same as MaCH, but parameter estimates are precalculated and fixed
Beagle 4.1	2016	All reference haplotypes at genotyped markers	Linear in number of haplotypes	Depends on recombination rates and error rates, which are precalculated and fixed
Minimac4	2017	Collapsed allele sequences from reference data that match at genotyped positions in small genomic segments	Linear in number of haplotypes	Same as Minimac3
IMPUTE4 ^a	2017	All possible reference haplotypes	Linear in number of haplotypes	Same as IMPUTE2
Beagle 5.0	2018	A user-specified number of reference haplotypes	Linear in number of haplotypes	Same as Beagle 4.1

This table describes the typical state space and parameter functions used to model the Li and Stephens framework. Minimac and IMPUTE2 were the first tools to use the prephasing approach. Minimac3 and Beagle 4.1 exploit local haplotype redundancy to reduce the size of the state space and hence the computational burden.

^aIMPUTE4 uses the same HMM as IMPUTE2; however, to reduce memory usage and increase speed, it uses compact binary data structures and takes advantage of high correlations between inferred copying states in the HMM to reduce computation.

Measuring Imputation Accuracy

- Imputation methods estimate a probability distribution for the allele carried by each haplotype per imputed marker
- Posterior genotype probabilities can be derived under HWE
- Expected allele dose (dosage) of the imputed genotype is given by the sum of the posterior allele probabilities for each haplotype — used for follow-up GWAS
- Imputation r^2 : squared correlation between the true and estimated dose of an allele across all imputed samples
 - Can be estimated from posterior allele probabilities without knowing the true allele
 - Threshold 0.3 is commonly used

ESTIMATING r^2

One attractive feature of r^2 , the squared correlation between true and imputed allele dose, is that it can be estimated from posterior allele probabilities without knowing the true allele on each chromosome. Here, we derive an estimate of r^2 in terms of the posterior allele probabilities.

Let X be 1 if a chromosome carries the allele of interest and be 0 otherwise, and let Z be the estimated posterior allele probability that $X=1$. Then r^2 is defined to be the squared correlation of X and Z . We say that the posterior allele probabilities are correctly calibrated if $E[X|Z] = Z$. If the posterior allele probabilities are correctly calibrated, we can use the law of total expectation and the fact that $X^2 = X$ to obtain

$$\begin{aligned} E[X^2] &= E[X] = E[E[X|Z]] = E[Z] \\ \text{Var}(X) &= E[X^2] - E[X]^2 \\ &= E[Z] - E[Z]^2 \end{aligned}$$

and

$$\begin{aligned} \text{Cov}(X, Z) &= E[XZ] - E[X]E[Z] \\ &= E[E[XZ|Z]] - E[E[X|Z]] E[Z] \\ &= E[Z^2] - E[Z]E[Z] \\ &= \text{Var}(Z). \end{aligned}$$

Consequently,

$$\begin{aligned} r^2 &= \frac{(\text{Cov}(X, Z))^2}{\text{Var}(X)\text{Var}(Z)} \\ &= \frac{\text{Var}(Z)}{\text{Var}(X)} \\ &= \frac{E[Z^2] - E[Z]^2}{E[Z] - E[Z]^2} \end{aligned}$$

If there are n imputed chromosomes and z_i is the estimated reference allele probability in the i th haplotype, one can estimate $E[Z^k]$ as $E[Z^k] \approx (1/n) \sum z_i^k$ and r^2 as

$$r^2 \approx \frac{n \sum z_i^2 - (\sum z_i)^2}{n \sum z_i - (\sum z_i)^2}.$$

Table 2 The most commonly used public reference panels to date

Reference panel	Number of reference samples	Number of sites (autosomes + X chromosome)	Average sequencing coverage	Ancestry distribution	Publicly available	Indels available	Reference
International HapMap Project phase 3	1,011	1.4 million	NA ^a	Multiethnic	Yes	No	47
1000G phase 1	1,092	28.9 million	2–6×	Multiethnic	Yes	Yes	1
1000G phase 3	2,504	81.7 million	7× genomes, 65× exomes	Multiethnic	Yes	Yes	3
UK10K Project	3,781	42.0 million	7× genomes, 80 × exomes	European	Yes	Yes	89
HRC	32,470	40.4 million	4–8 × ^b	Predominantly European ^c	Partially ^d	No	69
TOPMed	60,039	239.7 million	30×	Multiethnic	Partially ^e	Yes	71

Abbreviations: 1000G, 1000 Genomes Project; HRC, Haplotype Reference Consortium; indel, insertion or deletion; NA, not applicable; TOPMed, Trans-Omics for Precision Medicine.

^aThe International HapMap Project phase 3 data were genotyped on the Illumina Human1M and Affymetrix 6.0 SNP arrays.

^bThe HRC panel was obtained by combining sequencing data across many low-coverage (4–8×) and a few high-coverage sequencing studies.

^cThe only non-European samples in the HRC panel are through the 1000G reference panel (which was a contributing study).

^dMost of the HRC samples (~27,000) are available for download through controlled access from the European Genome-Phenome Archive.

^eSome of the TOPMed samples (~18,000) are available for download through controlled access from the Database of Genotypes and Phenotypes (dbGaP).

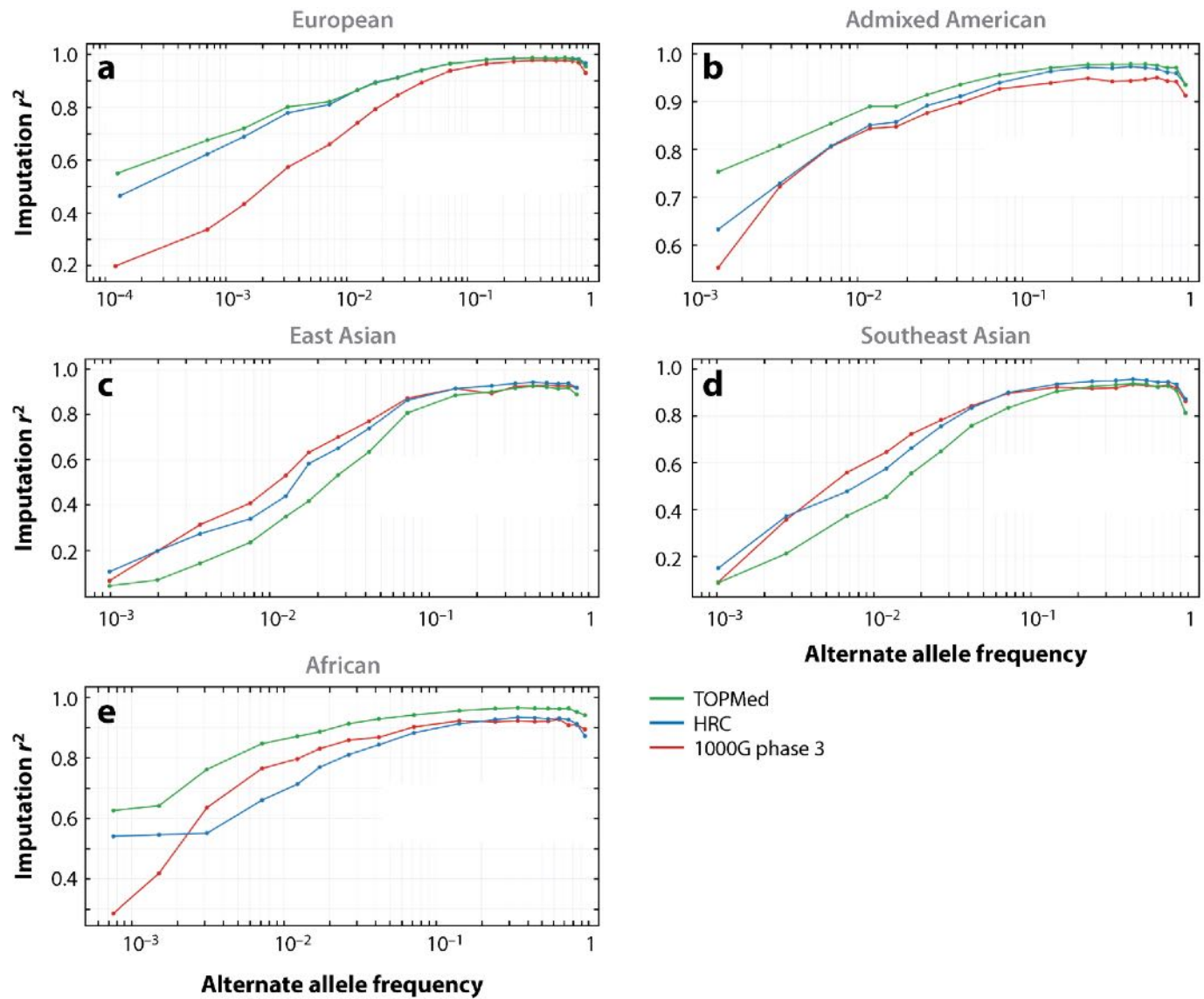


Figure 5 Imputation accuracy for five ancestries: (a) European, (b) admixed American, (c) East Asian, (d) Southeast Asian, and (e) African. We extracted 10 samples from each of these ancestries from the 1000 Genomes Project (1000G) phase 3 data, masked all variants except those on the Illumina 1M chip, and imputed them using the Trans-Omics for Precision Medicine (TOPMed) (with 18,000 samples), Haplotype Reference Consortium (HRC), and 1000G phase 3 (after removing overlaps) reference panels. The aggregate r^2 (measuring the imputation accuracy) is plotted as a function of the alternate allele frequency.

Impute Microarray Genotype Data

- Using WGS reference panel, e.g., 1000 Genome
- Fill in SNP genotypes for those not genotyped by Microarray
- Check imputation r^2 : accept imputed genotypes with $r^2 > \text{e.g., } 0.3$
- Result in $\sim 10\text{M}$ common variants
- Imputed genotype data
 - Dosage format — expected number of minor alleles with domain $[0, 2]$
 - Genotype format — number of minor alleles with values 0, 1, or 2
 - Genotype with the highest estimated probability will be reported

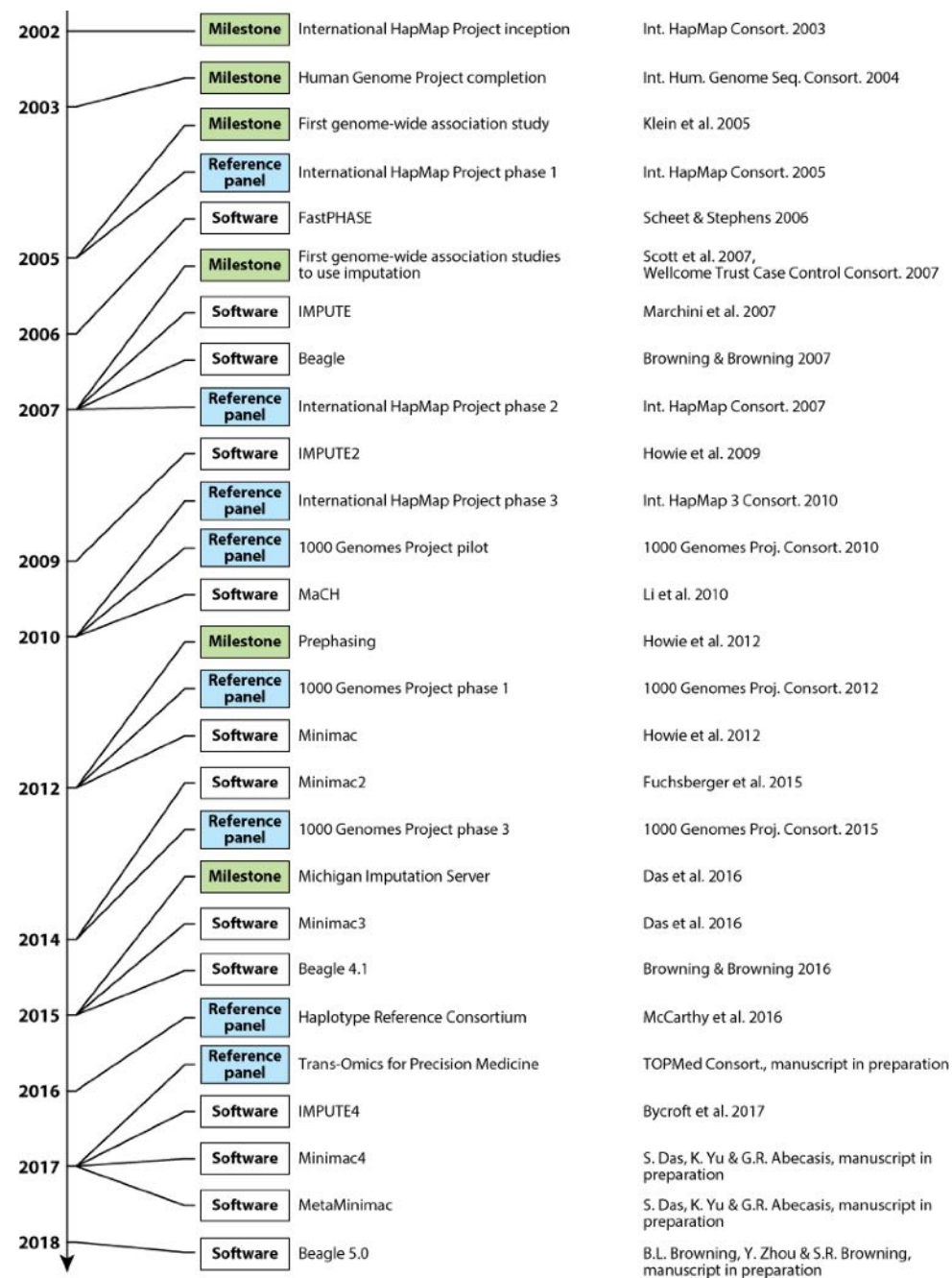


Figure 1 A brief time line summarizing the major developments in genotype imputation. Each major development has been categorized as a milestone (*green*), a reference panel (*blue*), or software (*white*).

Factors Affecting Genotype Imputation Accuracy

- Size of reference panel
- Density of genotyping array
- Minor allele frequency of variant being imputed (in the reference panel)
- Haplotype accuracy in reference and study samples
- Sequencing coverage of reference panel

What is Association Studies?

- Test associations between markers/SNPs/genes and the trait of interest
- Test whether the trait and genotype are independent
- **Population Data**
 - **Contingency table tests (dichotomous trait, e.g., case/control)**
 - **Regression model based tests**
- Family Data

Population-based Association Studies

- Phenotype(s) of interest
 - Dichotomous trait, e.g., case/control
 - Quantitative trait, e.g., Height, BMI, Lipids
 - Mendelian (last lecture) vs. Complex (this lecture)
- Number of markers tested
 - May range from 1 to ~10 million
 - Candidate gene study (often appear as replication study)
 - Genome-wide association study (GWAS)

Phenotype and covariate data

- Phenotype data
 - Dichotomous traits : 0 / 1
 - Quantitative traits : observed continuous quantitative values
- Covariate data
 - Gender
 - Age
 - BMI, etc.

Single Variant GWAS

- Test one SNP per time
- Test genome-wide variants independently
- Suitable for common SNPs with minor allele frequency (MAF) $> 1\%$, or 0.1%

Study Dichotomous Trait

- Compare frequencies of particular alleles, or genotypes, in set of cases and controls
 - Chi-square test using contingency tables
 - Logistic regression model based tests

Chi-Square genotype test with contingency tables

- For example, we observe

	AA	Aa	aa
Control	n_{00}	n_{01}	n_{02}
Case	n_{10}	n_{11}	n_{12}

- Is the observation is significantly different from what we would expect if trait and the genotype are independent?
- H_0 : No association between the trait and the genotype, i.e., sample with genotype AA, Aa, or aa have the same probability to develop disease (to be a Case)

Chi-Square test

- Let O_{ik} denote the count in the i^{th} row and k^{th} column in the contingency table, and E_{ik} denote the corresponding expected count
- Test statistic

$$X^2 = \sum_{i=1}^I \sum_{k=1}^K \frac{(O_{ik} - E_{ik})^2}{E_{ik}} \sim \chi_{(I-1)(K-1)}^2$$

- If study sample size is large, the test statistic follows a chi-squared distribution with degrees of freedom $(I - 1)(K - 1)$ under H_0 , with I rows and K columns in the contingency table.

How to Calculate E_{ik} ?

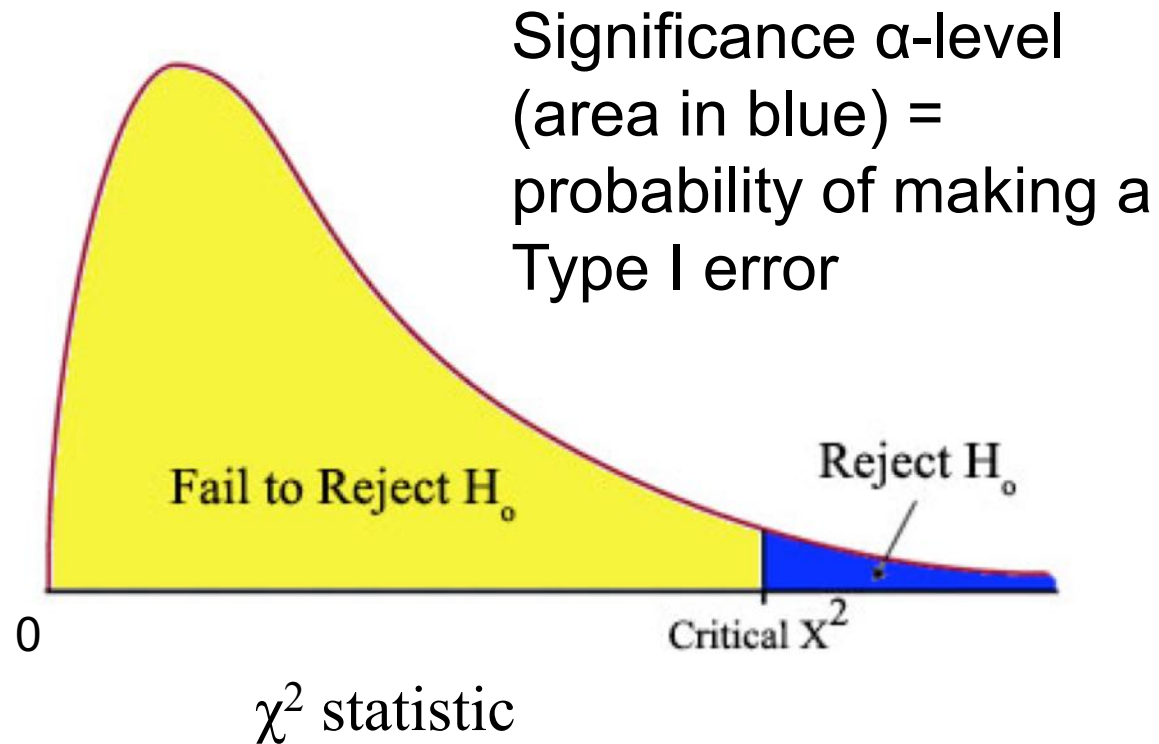
- Contingency table

	AA	Aa	aa	Row Total
Control	n_{00}	n_{01}	n_{02}	$n_{0.}$
Case	n_{10}	n_{11}	n_{12}	$n_{1.}$
Column Total	$n_{.0}$	$n_{.1}$	$n_{.2}$	n

- Observed number of samples per cell: $O_{ik} = n_{ik}$; with disease status (D) $i = 0, 1$; genotype (G) $k = 0, 1, 2$
- Expected number of samples per cell: $E_{ik} = n_{i.} n_{.k} / n$, under independence of disease status and genotype, $np_{D=i}p_{G=k} = n(n_{i.}/n)(n_{.k}/n)$
- Population genotype frequency: $p_{AA} = n_{.0}/n$; $p_{Aa} = n_{.1}/n$; $p_{aa} = n_{.2}/n$
- Expected number of samples per cell: $E_{i0} = n_{i.} p_{AA}$; $E_{i1} = n_{i.} p_{Aa}$; $E_{i2} = n_{i.} p_{aa}$;

Chi-square (χ^2) distribution

Critical value of X^2 chosen to attain desired α -level



Type I error?

p-value?

Example of Genotypic Association Test

- TCF7L2 for Type 2 Diabetes in Finns
- SNP rs12255372 has alleles T and G

	GG	GT	TT	Total
Case	661	255	20	936
Control	724	354	50	1128
Total	1385	609	70	2064

$$X_G^2 = \sum_{i=0,1} \sum_{j=0,1,2} (O_{ij} - E_{ij})^2 / E_{ij}$$

$$X_G^2 = (661 - 628.08)^2 / 628.08 + \dots \approx 14.08 \sim \chi^2, df = 2$$

$$p = .0009$$

Contingency Tables under Dominant (risk allele A) or Recessive (risk allele a) Disease Model

	AA or Aa	aa	Row Total
Control	$n_{00} + n_{01}$	n_{02}	$n_{0.}$
Case	$n_{10} + n_{11}$	n_{12}	$n_{1.}$
Column Total	$n_{.0} + n_{.1}$	$n_{.2}$	n

- H_0 : No association between the trait (to be a Case or Control) and the genotype being AA/Aa or aa
- Chi-square test statistic:

$$X_D^2 = \sum_{i=0,1} \sum_{j=0,1} (O_{ij} - E_{ij})^2 / E_{ij} \sim \chi^2, df = 1$$

Example for Testing Dominant or Recessive Disease Model

- TCF7L2 for Type 2 Diabetes in Finns
- SNP rs12255372 has alleles T and G
- Allele T is dominant to G

	GG	GT+TT	Total
Case	661	255+20=275	936
Control	724	354+50=404	1128
Total	1385	609+70=679	2064

$$X_D^2 = \sum_{i=0,1} \sum_{j=0,1} (O_{ij} - E_{ij})^2 / E_{ij} \sim \chi^2, df = 1$$

$$X_D^2 \approx 9.60 \sim \chi^2, df = 1$$

$$p = .0019$$

Contingency Table for Allelic Association Test

	A	a	Row Total
Control	$n_{0A}=2n_{00}+n_{01}$	$n_{0a}=n_{01}+2n_{02}$	$2n_{0.}$
Case	$n_{1A}=2n_{10}+n_{11}$	$n_{1a}=n_{11}+2n_{12}$	$2n_{1.}$
Column Total	$n_{.A}=2n_{.0}+n_{.1}$	$n_{.a}=n_{.1}+2n_{.2}$	$2n$

- **Assume additive disease model**
- **Assume HWE**
- H_0 : No association between the trait (sample to be a Case or Control) and the number of allele A in the sample genotype

$$X_L^2 = \sum_{i=0,1} \sum_{j=0,1} (O_{ij} - E_{ij})^2 / E_{ij} \sim \chi^2, df = 1$$

Example of Allelic Association Test

- TCF7L2 for Type 2 Diabetes in Finns
- SNP rs12255372 has alleles T and G

	G	T	Total
Case	1577	295	1872
Control	1802	454	2256
Total	3379	749	4128

$$X_L^2 \approx 13.13 \sim \chi^2, df = 1$$

$$p = .0003$$

Measure of Association Strength: Odds Ratio

	Exposed (E)	Not Exposed (\bar{E})
Case (D)	a	b
Control (\bar{D})	c	d

Odds ratio:

$$\begin{aligned} OR &= \frac{P(D|E)/P(\bar{D}|E)}{P(D|\bar{E})/P(\bar{D}|\bar{E})} \\ &= \frac{P(E|D)/P(\bar{E}|D)}{P(E|\bar{D})/P(\bar{E}|\bar{D})} \\ &= ad/bc \end{aligned}$$

- Exposed = carry certain genotype
- Counts pertain to individuals, not alleles.

Odds Ratio

Genotype Model ($\bar{E}=aa$)

	AA	Aa	aa
Case	n_{10}	n_{11}	n_{12}
Control	n_{00}	n_{01}	n_{02}

$$OR_{het} = (n_{11}n_{02})/(n_{01}n_{12})$$

$$OR_{hom} = (n_{10}n_{02})/(n_{00}n_{12})$$

Dominant Model ($\bar{E}=aa$)

	AA or Aa	aa
Case	$n_{10} + n_{11}$	n_{12}
Control	$n_{00} + n_{01}$	n_{02}

$$OR_D = [(n_{10} + n_{11})n_{02}]/[(n_{00} + n_{01})n_{12}]$$

Allele Model ($\bar{E}=a$)

	A	a
Case	$2n_{10} + n_{11}$	$n_{11} + 2n_{12}$
Control	$2n_{00} + n_{01}$	$n_{01} + 2n_{02}$

$$OR_L = [(2n_{10} + n_{11})(n_{01} + 2n_{02})]/[(2n_{00} + n_{01})(n_{11} + 2n_{12})]$$

Confidence Interval for Odds Ratio

In large samples and when OR is estimated from the contingent table, $\log(\widehat{OR})$ is approximately normally distributed, with estimated variance

$$\widehat{\text{Var}}[\log(OR)] \approx \frac{1}{a} + \frac{1}{b} + \frac{1}{c} + \frac{1}{d},$$

where a, b, c, d are the cells contributing to the estimation of OR.

A $(1 - \alpha)100$ th confidence interval for the population OR :

$$\exp^{\log(\widehat{OR}) \pm z_{(1-\alpha/2)} \sqrt{\widehat{\text{Var}}[\log(OR)]}}$$

where $z_{(1-\alpha/2)}$ is the $(1 - \alpha/2)100$ th percentile of the standard normal.

Logistic Regression Model

- Y = dichotomous phenotype
- X = a coding for the genotype

Genotype	Codominant	Dominant	Recessive	Additive
AA	$X = (0, 1)^T$	$X = 1$	$X = 1$	$X = 2$
Aa	$X = (1, 0)^T$	$X = 1$	$X = 0$	$X = 1$
aa	$X = (0, 0)^T$	$X = 0$	$X = 0$	$X = 0$

Assume a logistic regression model:

$$\log \left[\frac{\Pr(Y = 1|X)}{\Pr(Y = 0|X)} \right] = \beta_0 + \alpha C + \beta_1 X$$

where β_0 is the intercept, α is the coefficient for covariates C , and β_1 is the genetic effect-size (i.e., log(Odds-Ratio)).

$$H_0 : \beta_1 = 0$$

$$H_a : \beta_1 \neq 0$$

Test Statistic

- Wald Test: $Z = \frac{\widehat{\beta}_1}{\text{Standard_Error}(\widehat{\beta}_1)} \sim N(0, 1)$ under H_0
- Chi-square Test: $X^2 = \frac{\widehat{\beta}_1^2}{\text{Var}(\widehat{\beta}_1)} \sim \text{Chi_Square}$ with $df=1$ under H_0
- How to obtain p-value?

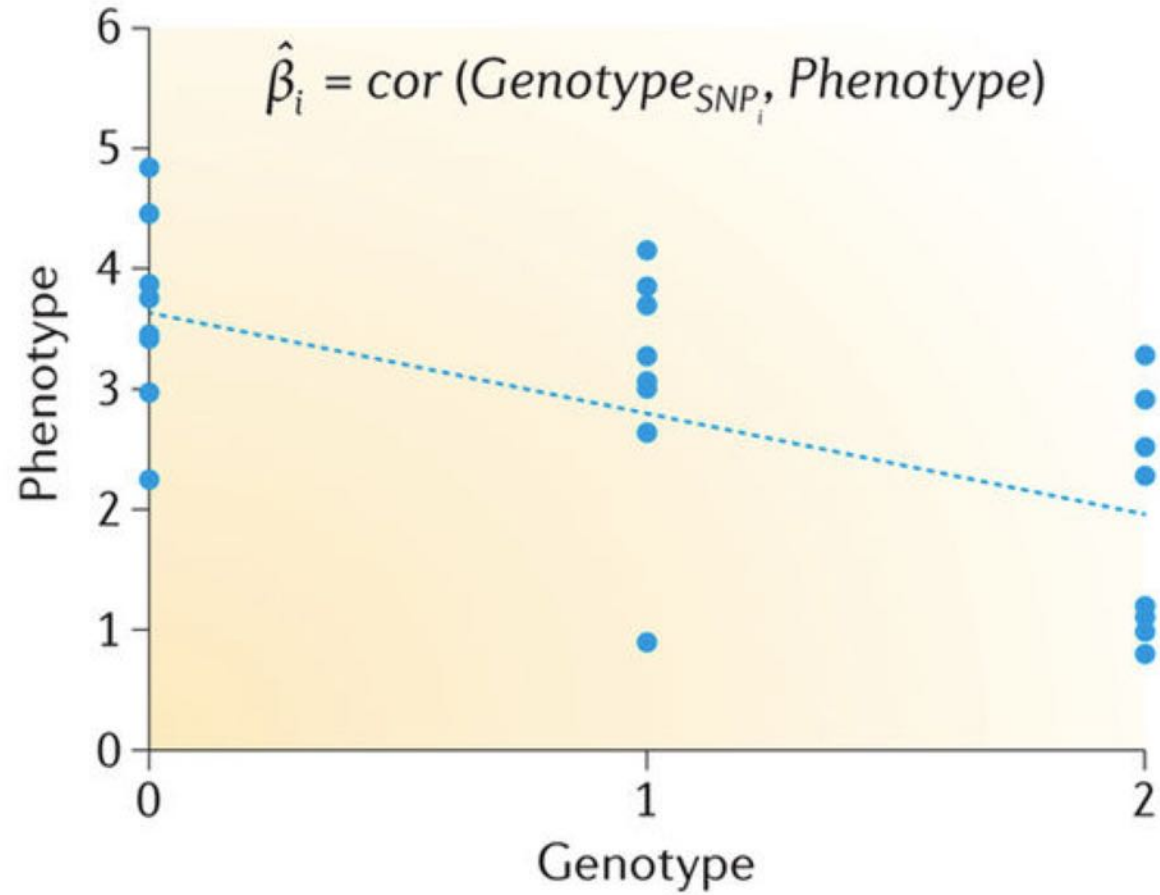
Advantages of Logistic Regression Model

- Account for confounding covariates (C), e.g., age, gender, BMI, smoking
- Flexible for various genetic models
- Flexible for testing multiple markers in the same model (modeling LD)
- Equivalent to the corresponding Chi-square test using contingency tables, if not modeling covariates
- Allow gene-environment interactions
- Without the assumption of HWE

Study Quantitative Trait

- Linear regression model
 - $Y = \beta_0 + \alpha C + \beta_1 X + \epsilon, \epsilon \sim N(0, \sigma^2)$
 - Y represents the quantitative trait values
 - X represents the genotype data (0, 1, 2) for additive genetic model
 - C represents the confounding covariates or other environmental variables
 - ϵ represents the error term, other unknown factors
- $H_0: \beta_1 = 0 ; H_a: \beta_1 \neq 0$
- P-values can be obtained by Wald Test, T-test, Score test, Log likelihood test, etc.

Linear Regression Model



Genome-wide Association Study (GWAS)

GWAS: independent single-variant tests across all genome-wide variants

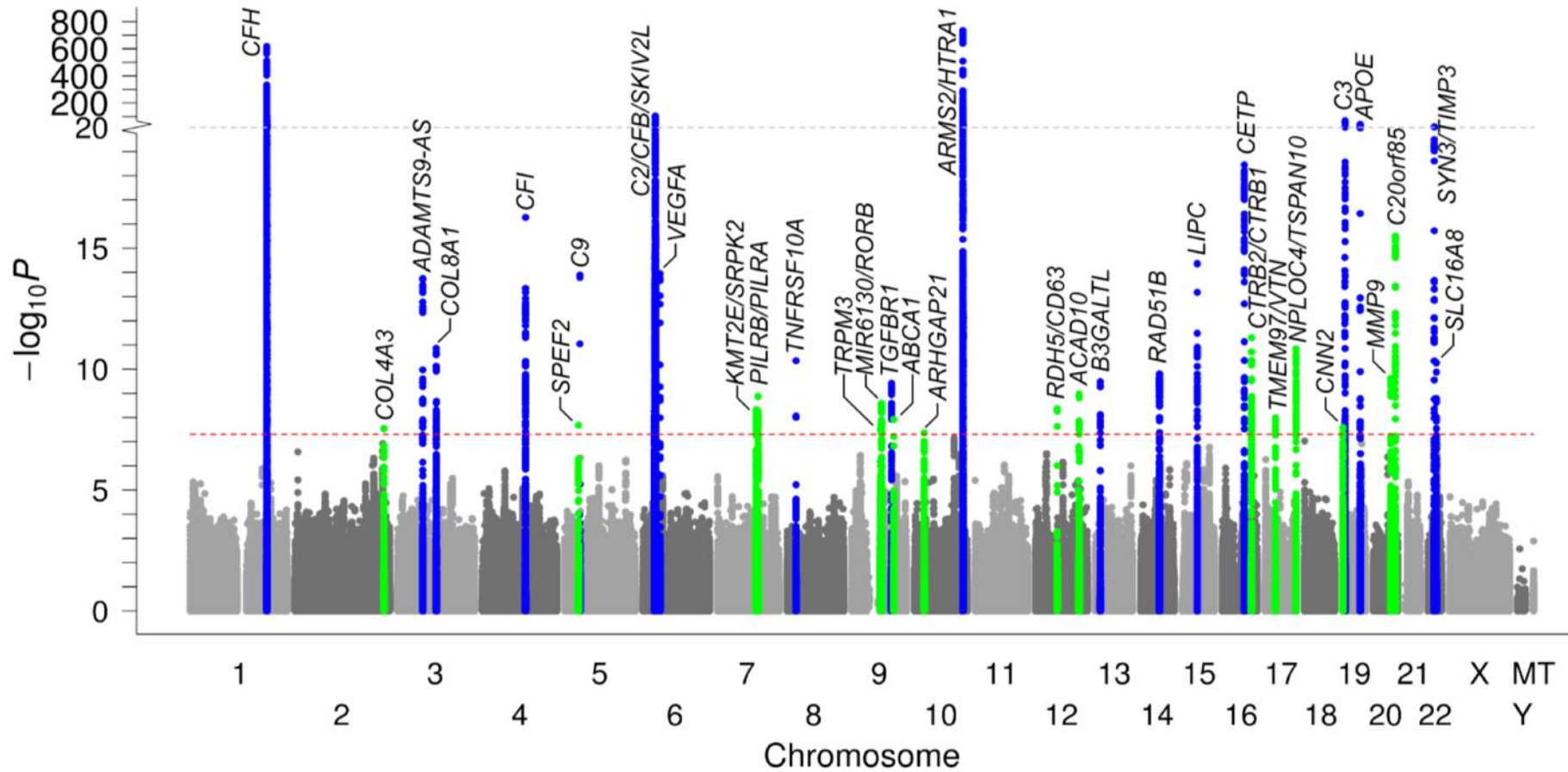
- Quality control (QC) of the study dataset
- Choose a model/test for the phenotype of interest (e.g., linear regression model for quantitative traits, logistic regression model for dichotomous traits, other association tests from previous lecture)
- Significance level $\alpha = 5 \times 10^{-8}$
- Report nearby genes of significant SNPs

Visualize GWAS Results by Manhattan Plot

- Scatter plot of $-\log_{10}(\text{p-values})$ across all genome-wide variants
- Visualize signal peaks



GWAS Results

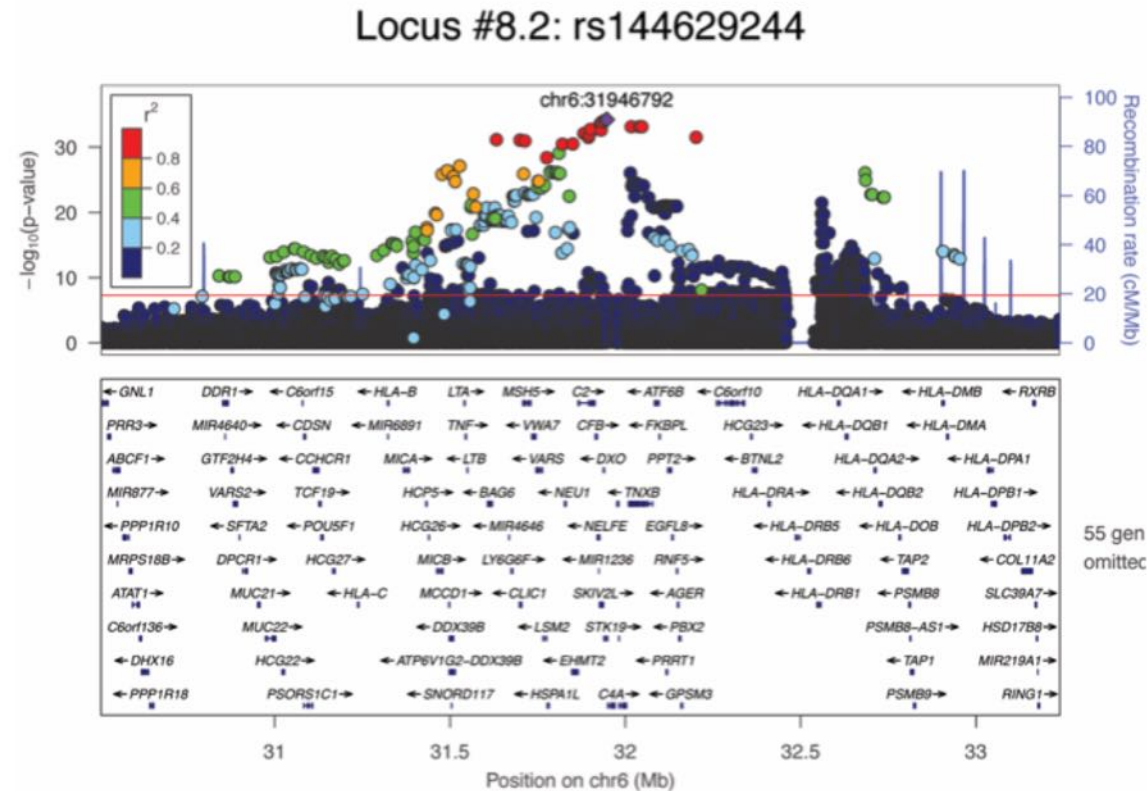


Fritsche L.G.
et al. Nat
Genet, 2016.

18 known AMD loci and 16 novel AMD loci

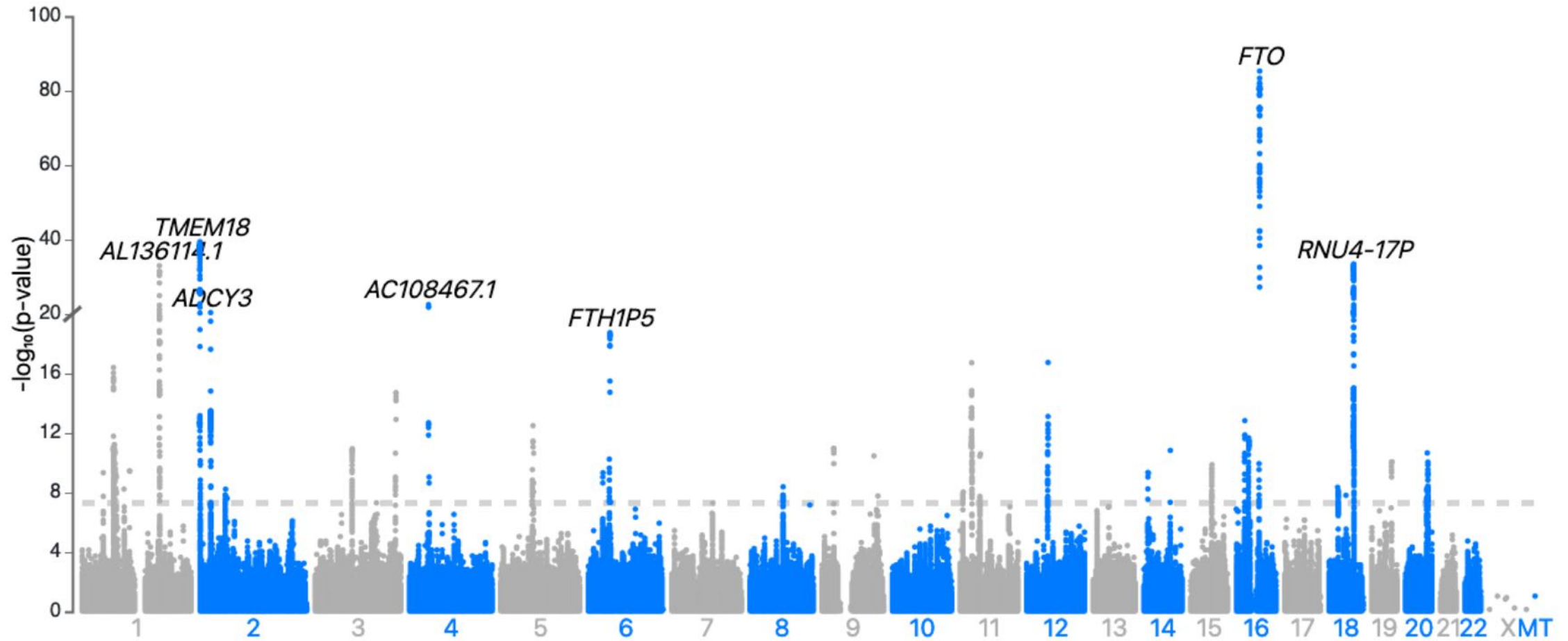
Visualize GWAS Loci by Locus Zoom Plot

- Zoom into the peak region with gene annotations
- Visualize r^2 between the specified significant (purple diamond) signal and its neighbor SNPs
- Visualize recombination rate



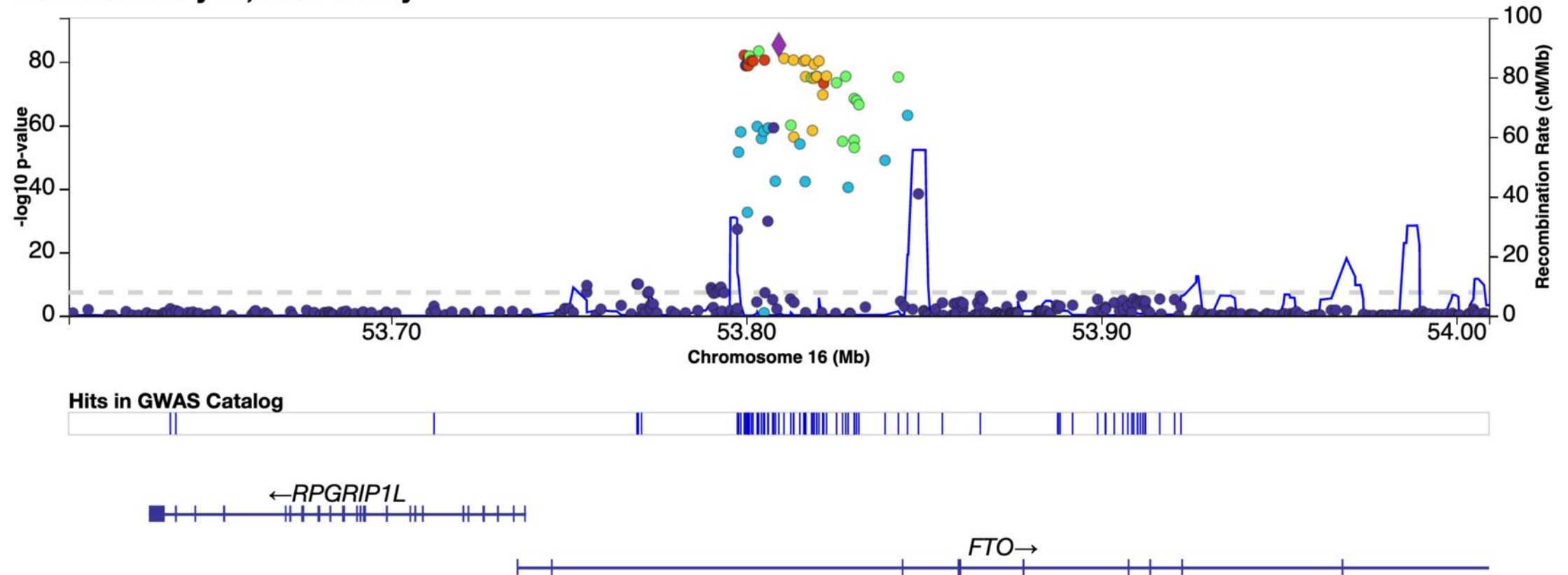
Fritsche L.G.
et al. Nat
Genet, 2016.

LocusZoom Visualization of GWAS of BMI , Women only



LocusZoom Visualization of GWAS of BMI

BMI meta-analysis, women only



Example GWAS Discoveries

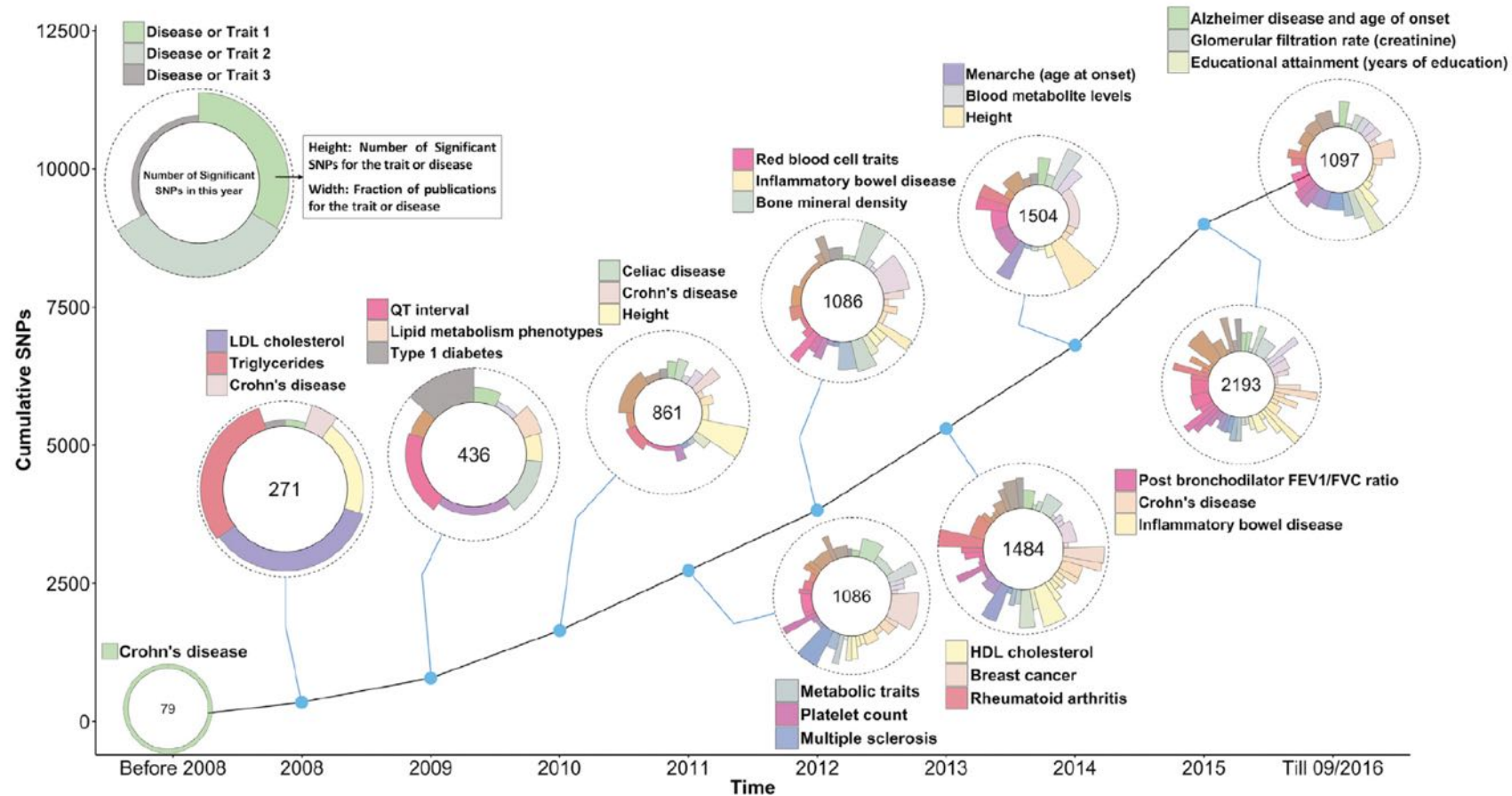
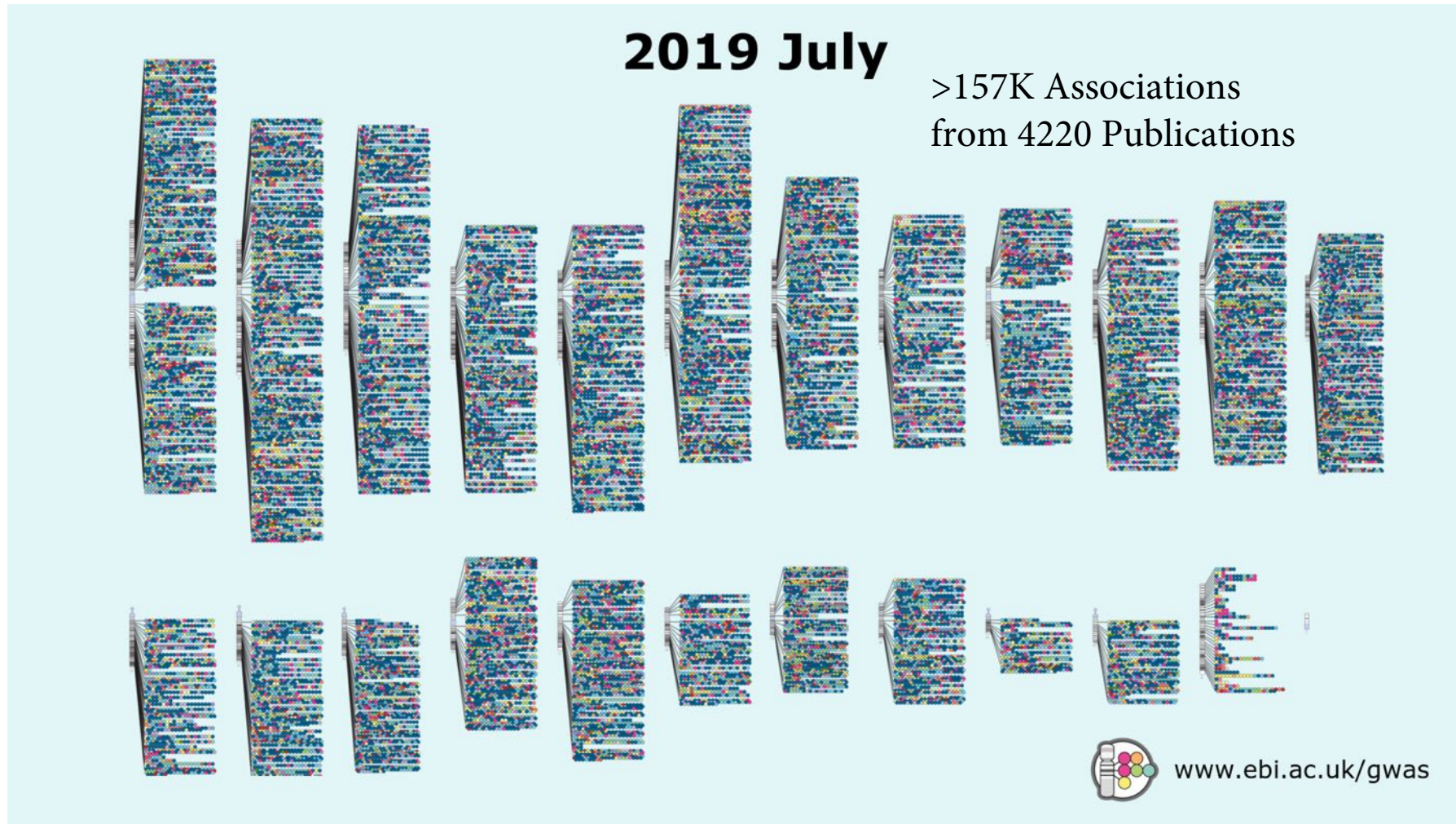


Figure 2. GWAS SNP-Trait Discovery Timeline

Data used for generating the graph were taken from the GWAS Catalogue.¹⁰ SNPs and traits were selected according to the following filters. SNPs were selected with a p value $< 5 \times 10^{-8}$. For each trait with two or more selected SNPs, SNPs were removed if they had an $LD r^2 > 0.5$ (calculated from 1000 Genomes phase 3 data) with another selected SNPs and their p value was larger. For each year of discovery, only the top three traits and diseases with the largest number of SNPs are labeled in the circle.

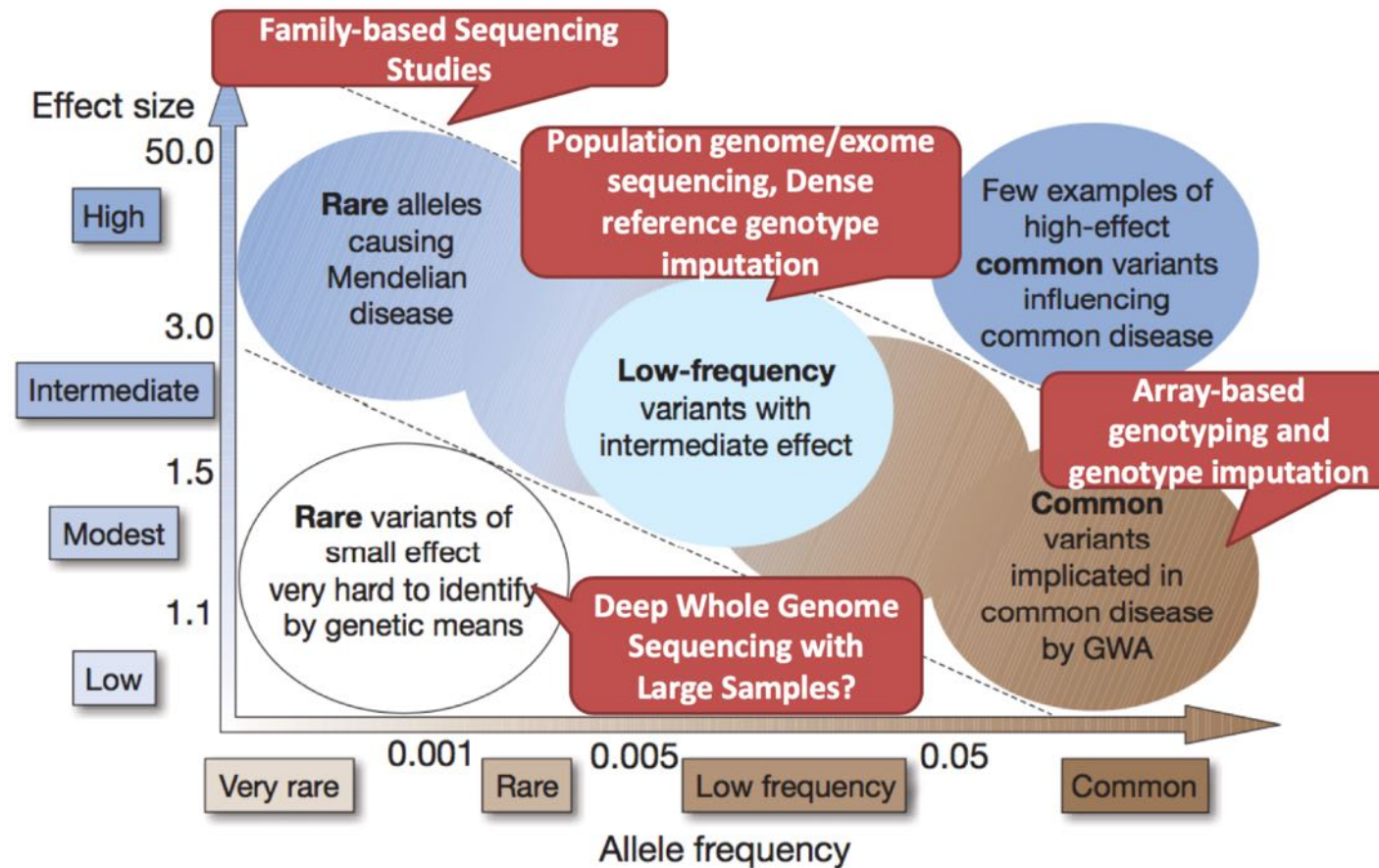
Visscher P.M.
et al. AJHG
2017.

GWAS Catalogue Results

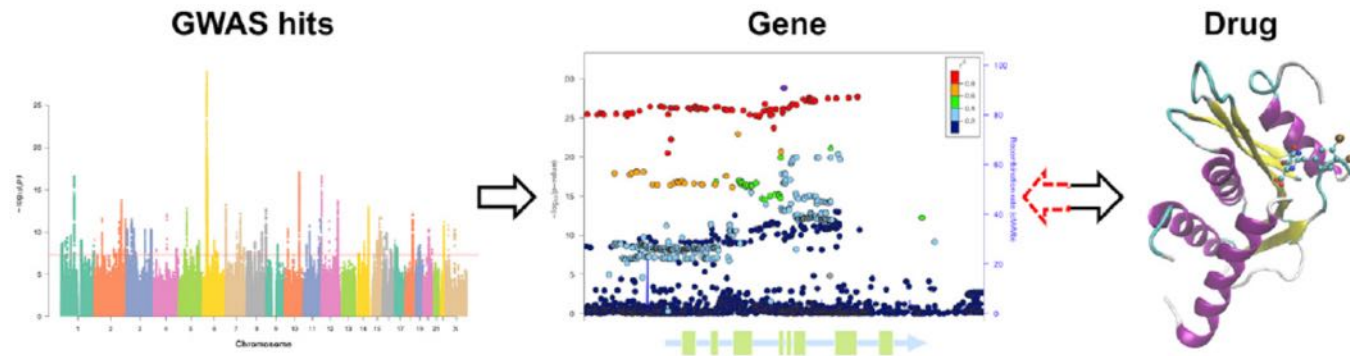


MAF Spectrum and Genetic Effect Sizes

Genetic architecture of complex traits



Example links between GWAS discoveries and drug developments



Trait	Gene with GWAS hits	Known or candidate drug
Type 2 Diabetes	<i>SLC30A8/KCNJ11</i>	ZnT-8 antagonists/Glyburide
Rheumatoid Arthritis	<i>PADI4/IL6R</i>	BB-Cl-amidine/Tocilizumab
Ankylosing Spondylitis(AS)	<i>TNFR1/PTGER4/TYK2</i>	TNF-inhibitors/NSAIDs/fostamatinib
Psoriasis(Ps)	<i>IL23A</i>	Risankizumab
Osteoporosis	<i>RANKL/ESR1</i>	Denosumab/Raloxifene and HRT
Schizophrenia	<i>DRD2</i>	Anti-psychotics
LDL cholesterol	<i>HMGCR</i>	Pravastatin
AS, Ps, Psoriatic Arthritis	<i>IL12B</i>	Ustekinumab

Visscher P.M.
et al. AJHG
2017.

GWAS Tools

- Michigan Imputation Server
 - <https://imputationserver.sph.umich.edu>
- GWAS Tool
 - PLINK: <https://www.cog-genomics.org/plink/>
 - EFACTS: <https://genome.sph.umich.edu/wiki/EFACTS>
- GWAS Results Visualization and Manhattan/LocusZoom Plot Tool
 - <https://my.locuszoom.org/>

Topics for Next Lecture

- Quality Control
- Population Stratification
 - Genomic control factor
 - Genotype principal components
 - Meta-analysis
- Kingship Matrix
- Linear mixed model (LMM)
- Heritability estimation by REML/GCTA