

Supplementary Materials

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1 Human Genomic Data

1.1 YRI Samples

In order to try to ensure accurate estimation of pairwise diversity, which is a ratio estimator that is sensitivity to its denominator, we use the complete per-basepair genotype calls (gVCF) produced by Illumina’s DRAGEN pipeline (Illumina, Inc. 2020). The original samples were from 178 Yoruban individuals sequenced to 30x by the New York Genome Center (Byrska-Bishop et al. 2022). This allows for filtering to be applied to the entire genome at once, rather than just variants, so the denominator does not need to be estimated separately.

The full list of samples is available in TSV format in the GitHub repository (`data/h1kg/yri_samples.tsv`).

1.2 Filtering gVCFs

gVCFs were filtered using a custom Python tool, `gvcf2counts.py` (in `tools/gvcf2counts.py`), which reads the gVCFs, filters them according to the criteria below, and outputs a Numpy `.npz` file of reference and alternative allele counts for each chromosome (hereafter, “allele counts matrices”).

Genotypes are included in the allele count if and only if:

1. The variant call is set to `PASS` in the VCF.
2. The `QUAL > 50`.
3. The `GQ > 30` (or `RGQ > 30` for invariant sites).

Because the data underlying the counts files are per-basepair resolution gVCFs, each chromosome’s allele counts matrix is of size $l \times 2$, where l is the total chromosome length. Basepairs that fail these filtering requirements lead to a row of zero counts, e.g. no observed reference and alternative allele counts, and thus do not effect the data that goes into the binomial likelihood or π estimates used in figures.

1.3 Site-based Filtering of Counts

The allele counts matrices include many basepairs that may have allele counts that pass the genotype call filters, but are still need to be filtered out because the region of the genome may produce unreliable estimates. The following filters are applied based on masking regions:

1. **Non-accessible regions:** masks out centromeres (`acen` entries in `cytoBand.txt`), with 5Mbp padding on either side. The file of passing masks is `data/annotation/no_centro.bed`.
2. **Reference masking:** soft and hard-masked regions in the human GRCh38 reference genome are also masked.
3. **Non-“putatively” neutral regions:** Additionally, for fitting our likelihood and estimating observed pairwise diversity, we only consider . This masks out phastCons regions (from `phastConsElements100way.bed.gz`) and Ensembl gene regions (from annotation file `Homo_sapiens.GRCh38.107.chr.gff3.gz`). While introns are possibly under some weak selection, they collectively make up nearly 40% of the human genome and are included so genome-wide diversity can be estimated more precisely (possibly at the expense of some bias).

These files are all produced by the Snakemake file `data/annotation/Snakefile`.

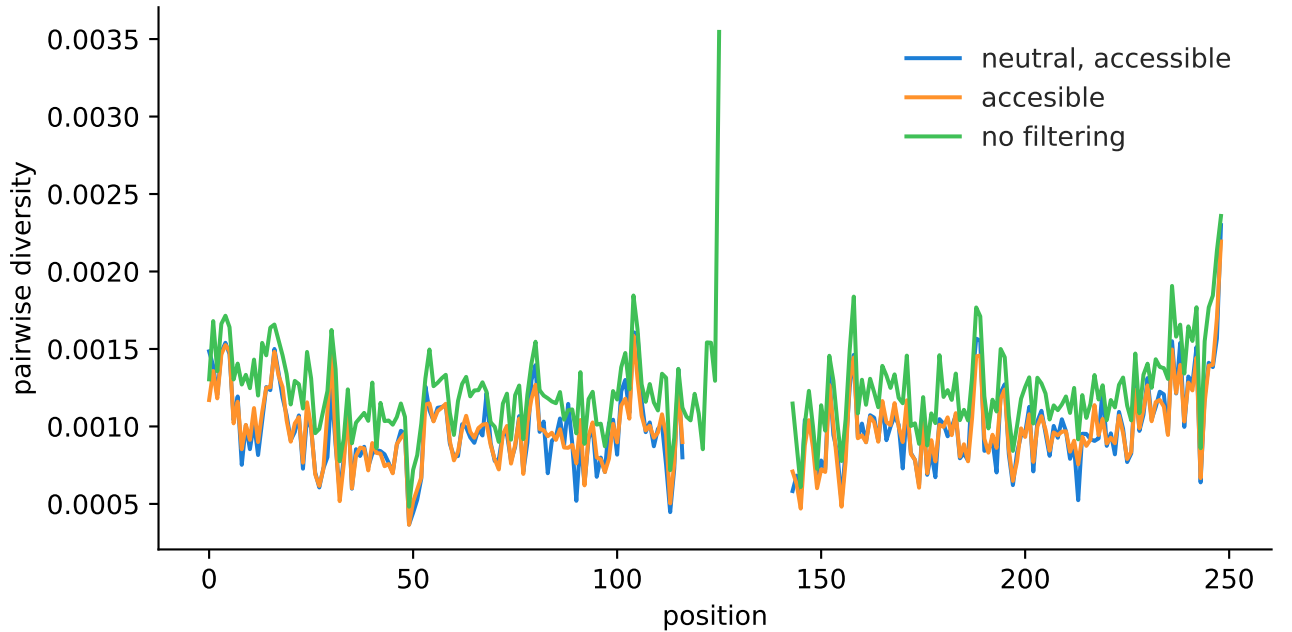


Figure 1: Estimates of chromosome 1 YRI diversity in non-overlapping megabase windows, under different filtering criteria. The filtering criteria are, (1) “neutral, accessible” which includes only putatively neutral sites, and ignores regions masked as inaccessible, (2) “accessible” which only ignores sites masked as inaccessible, and (3) “no filtering” which uses all available data. Note that filtering changes the absolute level of diversity, but has more minor effects on regional patterns of diversity at the megabase scale.

1.4 Data Summary Matrices

Our underlying data for all likelihood and pairwise diversity estimates is the allele count matrix \mathbf{C} with dimensions $L \times 2$, where L is the chromosome length. This is transformed to a pairwise

chrom	accessible	neutral	both
chr1	42.4	64.4	22.9
chr2	46.8	58.7	23.7
chr3	44.1	62.9	24.8
chr4	44.0	59.3	21.5
chr5	44.1	58.0	21.4
chr6	45.0	58.0	22.1
chr7	44.4	65.8	26.4
chr8	43.8	61.2	23.1
chr9	39.2	64.5	20.3
chr10	44.6	62.8	25.3
chr11	42.7	63.5	23.4
chr12	41.7	62.7	22.7
chr13	39.7	62.0	18.3
chr14	37.6	65.4	19.0
chr15	37.0	69.4	20.3
chr16	39.4	63.8	20.9
chr17	40.4	64.0	22.3
chr18	40.9	59.8	19.8
chr19	30.9	69.8	18.0
chr20	36.9	61.6	19.8
chr21	31.6	68.6	18.2
chr22	26.9	75.0	16.4

summary matrix with identical dimensions, \mathbf{Y} . The first column of \mathbf{Y} is the number of pairwise comparisons between chromosomes that are identical, and the second column is the number that are different. Both of these columns are combinatoric summaries of the raw allele counts matrix needed for the binomial likelihood and pairwise diversity estimates. Let $[c_1, c_2]$ be a row of \mathbf{C} for basepair l (the l index is omitted for clarity), and $n = c_1 + c_2$. Then, the (1) total number of pairwise combinations of chromosomes n_T , (2) the number of pairwise with identical alleles n_S , and (3) the number of pairwise combinations with differing alleles n_D are respectively,

$$\begin{aligned} n_T &= \frac{n(n-1)}{2} \\ n_S &= \binom{c_1}{2} + \binom{c_2}{2} \\ n_D &= n_T - n_S \end{aligned}$$

which would be stored in row $\mathbf{Y}_l = [n_S, n_D]$. Note that the per-site \mathbf{Y} handles non-polymorphic sites and missing data. Non-polymorphic sites have $n_S = \binom{n}{2}$ and $n_D = 0$, and missing data has $n_S = n_D = 0$.

1.5 Pairwise Diversity Estimates

The pairwise diversity at site l across the n sampled chromosomes can be calculated from the \mathbf{Y} matrix as follows,

$$\pi(l) = \frac{n_D}{n_T} \tag{1}$$

which is identical to the more common expression of this estimator,

$$\pi(l) = \frac{2}{n(n-1)} \sum_{i < j}^n k_{i,j} \tag{2}$$

where $k_{i,j}$ is 1 if the alleles at this site differ, and 0 otherwise. Note that for sites with missing data, $c_1 = c_2 = 0$ and thus $n_T = 0$ and the division is invalid. Such cases were marked as missing with floating point values NaNs. Binned summaries of data are weighed by the number of complete cases, e.g. rows with $c_1 + c_2 > 0$.

This per-basepair diversity is then averaged over all callable bases, to give a genome-wide or window estimate of diversity of accessible bases in the set \mathcal{A} ,

$$\bar{\pi}(\mathcal{A}) = \frac{\sum_{l \in \mathcal{A}} \pi(l)}{L_{\mathcal{A}}}.$$

where $L_{\mathcal{A}} = |\mathcal{A}|$ is the number of accessible bases. Note that the sum in the numerator is random over the sample of chromosomes sampled from the population. Estimates of pairwise diversity often condition on the accessible bases, and thus treat this as fixed. However, the number of accessible bases varies across the chromosome; this can lead to a source of apparent bias during block-bootstrap estimates of uncertainty. In this case, pairwise diversity is a ratio estimator, and is thus biased, since by Jensen's inequality $\mathbb{E}(y/x) \geq \mathbb{E}(y)/\mathbb{E}(x)$ for random variables x and y .

The genome-wide $\bar{\pi}$ can also be estimated by summing the columns of \mathbf{Y} , and calculating n_D/n_T .

1.6 Window-based Summaries and filtering

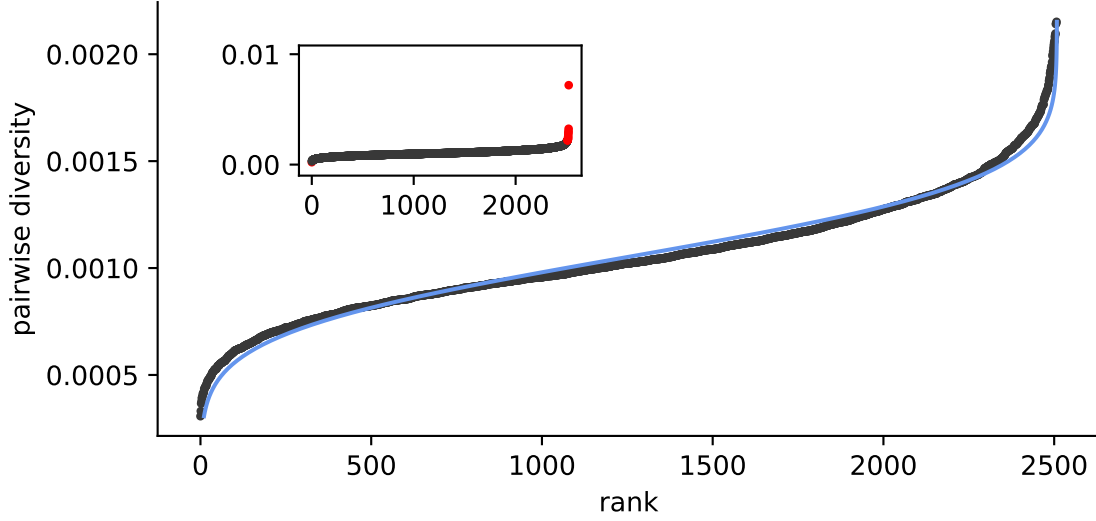


Figure 2: The distribution of diversity across the genome at the megabase scale, with outliers trimmed. The blue line is the normal CDF, fit with MLE parameters XXX. The inset figure is the untrimmed data, with trimmed points shown in red.

The likelihood method is fit to non-overlapping binned summaries of the allele counts matrix. Based on exploratory data analyses, some bins were outliers and excluded (XXX).

1. **Fraction of inaccessible sites per window.** `mask_inaccessible_bins_frac`
2. **Outliers:** Based on exploratory analysis, there were some regions with very high diversity. The 0.05% right tail was excluded.

Likelihood

Our model is essentially a generalized nonlinear model with a binomial link function. This is the form used by Elyashiv et al. (2016) and Murphy et al. (2022). These models fit the observed number of pairwise nucleotide differences in genomic windows to the expected pairwise diversity under some evolutionary model. We only consider BGS models here, so the mean function for position x is the product of the proportion by which BGS reduces diversity at position x , $B(x)$, and genome-wide neutral diversity π_0 ,

$$\pi(x) = B(x, \Phi) \pi_0 \quad (3)$$

Φ is the set of BGS parameters (i.e. the DFE for each feature type and mutation rate), and π_0 is determined by the drift-effective population size, set by only reproductive and demographic processes.

Our statistical models use a binomial likelihood for the observed data summarized at some physical genomic scale. The evolutionary processes that impact $\pi(x)$ do so on different spatial scales, and genomic evolutionary model selection also includes determining the scale at which data fits best. The likelihood considers the probability of observing $n_{D,i}$ pairwise differences in window i given $n_{T,i}$ total possible pairwise comparison, and that the probability of observing a pairwise difference is given by π_i

$$n_{D,i} \sim \text{Binom}(\pi_i, n_{T,i}). \quad (4)$$

This assumes infinite sites, since π_i is assumed to be the probability of

Note that this makes the approximation that the average number of pairwise differences π_x is small, such that the probability of heterozygosity is equal to the

, which links the mean function above with the probability of observing sampling process by which individuals are sampled from the population

putatively neutral site, the observed number of pairwise differences at site i is modeled as, use observed count data summarized at some pre-specified scale

$$\log \mathcal{L}(\theta) = \sum_{v \in \mathcal{V}} \sum_{i \neq j \in \mathcal{S}} \log(P(O_{i,j}(v)|\theta)) \quad (5)$$

where \mathcal{V} is the set of putatively neutral sites, \mathcal{S} is the set of samples, and θ are the BGS parameters. The indicator variable $O_{i,j}(v)$ is 1 if samples i and j are different at site v , and zero otherwise. Thus as they specify in the paper,

$$P(O_{i,j}(v)|\theta) = \begin{cases} \pi(v|\theta), & O_{i,j}(v) = 1 \\ 1 - \pi(v|\theta), & O_{i,j}(v) = 0 \end{cases}. \quad (6)$$

The total size of the set of samples \mathcal{S} is $n_{\mathcal{S}} = |\mathcal{S}|$. Assuming all sites are biallelic, we can simplify the inner summation by counting the number of possible same and different pairwise combinations. If a site v 's vector of allele counts is $[c_1, c_2]$, the total number of pairwise combinations with the same alleles is

$$n_s(v) = \binom{c_1}{2} + \binom{c_2}{2} \quad (7)$$

and the number of different pairwise combinations is

$$n_d(v) = n_T - n_s(v) \quad (8)$$

where $n_T = n_{\mathcal{S}}(n_{\mathcal{S}} - 1)/2$ is the total number of pairwise combinations across the sample set \mathcal{S} . Note that these site-specific counts allow us to use allelic counts directly, and can vary across sites. Our log-likelihood is then,

$$\ell(\theta) = \sum_{v \in \mathcal{V}} [\log(\pi(v|\theta))n_D(v) + \log(1 - \pi(v|\theta))n_S(v)]. \quad (9)$$

In practice, we calculate these values across bins. For each bin, we treat $\pi(v|\theta)$ as fixed, assuming that at this scale, the variation in expected diversity across sites is minimal. For a particular chromosome, we have two classes of sites: those included in the diversity calculation and those ignored. The former sites are all putatively neutral and have reliably called genotypes, and the other sites are possibly non-neutral or do have reliably called genotypes. The total log-likelihood is the sum of bin likelihoods, $\ell(b)$

$$\ell(\theta) = \sum_b \ell(b|\theta) \quad (10)$$

The likelihood within a bin is then,

$$\ell(b|\theta) = \log(\bar{\pi}(b|\theta)) \sum_{v \in \mathcal{V}_b} n_D(v) + \log(1 - \bar{\pi}(b|\theta)) \sum_{v \in \mathcal{V}_b} n_S(v) \quad (11)$$

$$= \log(\bar{\pi}(b|\theta))Y_D(b) + \log(1 - \bar{\pi}(b|\theta))Y_S(b) \quad (12)$$

where the two sum terms as $Y_D(b)$ and $Y_S(b)$ are data reductions at the bin level.

If the data are such that only polymorphic sites are considered, we can adapt this by partitioning the set \mathcal{V} of neutral sites into polymorphic (\mathcal{P}) and fixed sites (\mathcal{F}), i.e. $\mathcal{V} = \mathcal{P} \cup \mathcal{F}$ and $\mathcal{P} \cap \mathcal{F} = \emptyset$. For all $v \in \mathcal{F}$, $n_d(v) = 0$ and $n_s(v) = n_T$.

Then,

$$\ell(\theta) = \sum_{v \in \mathcal{V}} [\log(\pi(v|\theta))n_D(v) + \log(1 - \pi(v|\theta))n_S(v)] \quad (13)$$

$$= \sum_{v \in \mathcal{P}} [\log(\pi(v|\theta))n_D(v) + \log(1 - \pi(v|\theta))n_S(v)] + \sum_{v \in \mathcal{F}} \log(1 - \pi(v|\theta))n_T(v) \quad (14)$$

$$(15)$$

$$\ell(b|\theta) = \log(\bar{\pi}(b|\theta)) \sum_{v \in \mathcal{P}_b} n_D(v) + \log(1 - \bar{\pi}(b|\theta)) \left(\sum_{v \in \mathcal{P}_b} n_S(v) + \sum_{v \in \mathcal{F}_b} n_T(v) \right). \quad (16)$$

Note that if we assume that the total number of combinations at each fixed site is constant, e.g. $n_T = n_T(v)$ for all v , then we can use $\sum_v n_T(v) = n_T|\mathcal{F}_b|$.

The

The core parts of our likelihood are,

$$\ell(\theta) = \sum_b [\log(\bar{\pi}(b|\theta))Y_D(b) + \log(1 - \bar{\pi}(b|\theta))Y_S(b)] \quad (17)$$

where,

$$\bar{\pi}(b|\theta) = \pi_0(b)\bar{B}(b|\theta). \quad (18)$$

Here, $\bar{B}(b|\theta)$ is the predicted reduction in diversity due to BGS in window b , given background selection parameters θ . In practice, this is site-specific. We can write the reduction at any neutral site v in the genome as the product of B s across all segments,

$$B(v|\theta) = \exp \left(- \sum_g \int f(\mu(\mathcal{A}(g)), s, S_g) w(s|\mathcal{A}(g)) ds \right) \quad (19)$$

where S_g is exogenous genomic data about the segment, $S_g = \{L_g, r_g, \rho(|v - p_g|)\}$, where L_g is the segment's length, r_g is the recombination rate per basepair in the segment, and $\rho(|v - p_g|)$ is the recombination distance between the focal site v and the segment position p_g (we approximate, and use the nearest end position to the neutral site). Additionally, $w(s|\mathcal{A}(g))$ is the distribution of selection coefficients for segment g , if segment g is a member of annotation class $\mathcal{A}(g)$.

We can think about the DFE as the conditional distribution of a particular selection coefficient given a mutation occurs, for a particular annotation class. The BGS function $f(\cdot)$ only depends on μ through the introduction of deleterious alleles with selection coefficient s at rate $\omega(s|\mathcal{A}(g)) = \mu(\mathcal{A}(g))w(s|\mathcal{A}(g))$. Thus, we can write,

$$B(v|\theta) = \exp \left(- \sum_g \int f(\omega(s|\mathcal{A}(g)), s, S_g) ds \right) \quad (20)$$

which we can discretize as,

$$B(v|\theta) = \exp \left(- \sum_g \sum_s f(\omega(s|\mathcal{A}(g)), s, S_g) \right). \quad (21)$$

Next, note that there are a finite number of annotation classes, $\mathcal{A} \rightarrow \{a_1, a_2, \dots, a_k\}$, so we can further partition this as

$$B(v|\theta) = \exp \left(- \sum_{\{g: \mathcal{A}(g)=a_1\}} \sum_s f(\omega(s|a_1), s, S_g) + \sum_{\{g: \mathcal{A}(g)=a_2\}} \sum_s f(\omega(s|a_2), s, S_g) + \dots \right) \quad (22)$$

Let us define the $d_\omega \times d_s \times d_g$ multidimensional array \mathbf{F} , and the $d_g \times d_a$ feature classification matrix \mathbf{A} .

2 Calculation of B Maps

Each B map is determined by the annotation track of putatively conserved segments, which includes (1) the segment positions and lengths, (2) the type of feature of each segment (e.g. exons, UTRs, phastcons conserved elements, etc.), as well as (3) the recombination map, and (3) the deleterious selection coefficient $s(i)$ and mutation rate at which these deleterious enter the population for feature type i .

The B maps are computed at fixed, evenly spaced sites.

3 Ratchet Rate Prediction

$$R = \int \tag{23}$$

References

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