

# LDSP- Linear Detection of Selection in Pooled sequence data

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## 1 Introduction

We break up the process into two phases.

**Phase I:** The Intuition is that data at each SNP are binomial counts, which help estimate the frequency of a SNP in a pool, but they don't tell you the frequency exactly, they are noisy. But by combining information across multiple corrected SNPs, you can improve the estimated frequency of the test SNP

**Phase II:** After we estimate the frequency of the putatively selected SNP in each replicate population, we estimate the group effect using a linear model which also allows us to model genetic drift with a normal error term.. The idea is that in the positively selected population, the group effect will be positive while negative in the negatively selected population, and 0 in the neutrally evolving population.

## 2 Phase I

Consider one lineage for now.

Let  $y = (y_1, y_2, \dots, y_p)'$  denote the vector of allele frequencies in the study sample. Let  $E[y_i] = \mu_i$  and the frequency of the test SNP be  $y_t$  and  $M$  denote the  $2m \times p$  panel (i.e.  $2m$  haplotypes and  $p$  SNPs). As in (Wen & Stephens, 2010), we assume

$$\bar{y}|M \sim N_p(\mu, \Sigma) \quad (1)$$

(Wen & Stephens, 2010) derived the estimates for  $\mu$  and  $\Sigma$  from the haplotype copying model presented in (Li & Stephens, 2003).

$$\hat{\mu} = (1 - \theta)f^{panel} + \frac{\theta}{2}1 \quad (2)$$

$$\hat{\Sigma} = (1 - \theta)^2 S + \frac{\theta}{2}(1 - \frac{\theta}{2})I \quad (3)$$

and  $S$  is obtained from  $\Sigma^{panel}$ , specifically,

$$S_{i,j} = \begin{cases} \Sigma_{i,j}^{panel} & i = j \\ e^{-\frac{\rho_{i,j}}{2m}} \Sigma_{i,j}^{panel} & i \neq j \end{cases} \quad (4)$$

and,

$$\theta = \frac{(\sum_{i=1}^{2m-1} \frac{1}{i})^{-1}}{2m + (\sum_{i=1}^{2m-1} \frac{1}{i})^{-1}} \quad (5)$$

## 2.1 Data at SNP $i$

Let  $(n_i^0, n_i^1)$  denote the counts of "0" and "1" alleles at SNP  $i$  and  $n_i = n_i^0 + n_i^1$ . Then

$$n_i^1 \sim \text{Bin}(n_i, X_i) \sim N(n_i X_i, n_i X_i (1 - X_i))$$

where  $X_i$  is the true population frequency of the SNP  $i$  "1" allele.

$$\implies \hat{X}_i | X_i \sim N(X_i, \frac{X_i(1 - X_i)}{n_i}) \quad (6)$$

where  $\hat{X}_i = \frac{n_i^1}{n_i}$

Next we replace  $X_i$  by  $\hat{X}_i$  in the variance for tractability issues. Therefore,

$$\hat{X}_i | X_i \sim N(X_i, \frac{\hat{X}_i(1 - \hat{X}_i)}{n_i}) \quad (7)$$

## 2.2 Incorporating Dispersion

Letting  $y_i^{obs} = \hat{X}_i$  from equation 7, we see that

$$y^{obs} | y^{true} \sim N_p(y^{true}, \text{diag}(\epsilon_1, \dots, \epsilon_p)) \quad (8)$$

where  $\epsilon_i = \frac{y_i^{obs}(1 - y_i^{obs})}{n}$  and  $n$  is the total coverage for SNP  $i$

In the distribution of  $\vec{y}$ , we assumed that the panel and study individuals are from the sample population, and the parameters  $\theta$  and  $\rho$  are estimated without error. Deviations from these assumptions will cause over-dispersion: the true allele frequencies will lie further from their expected values than the model predicts. To allow this, we modify equation 1 by introducing an over-dispersion parameter  $\sigma^2$ .

$$y^{true} | M \sim N_p(\hat{\mu}, \sigma^2 \hat{\Sigma}) \quad (9)$$

Combining both equations, we obtain,

$$y^{obs} | M \sim N_p(\hat{\mu}, \sigma^2 \hat{\Sigma} + \text{diag}(\epsilon_1, \dots, \epsilon_p)) \quad (10)$$

where we can estimate  $\sigma^2$  by maximum likelihood.

We use Bayes theorem to obtain the distribution for the true frequencies conditional on the observed data (as derived in Wen & Stephens).

$$P(y^{true} | y^{obs}) = \frac{P(y^{obs} | y^{true}) P(y^{true})}{P(y^{obs})}$$

## 2.3 Estimating the true frequency at SNP $t$

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### 3 Phase II - estimating $\beta$

Let  $f_{i,k,j}$  denote the frequency of the  $j$ th SNP in population  $i$  and replicate  $k$ . Then,

$$\log\left(\frac{1-f_{i,k,j}}{f_{i,k,j}}\right) = \mu_j + \beta_j g_i + \epsilon \quad (11)$$

where  $\epsilon \sim N(0, \sigma_d^2)$ ,  $\sigma_d^2$  is the variance due to drift,  $\mu_j$  is the frequency of the  $j$ th SNP in the founding population and

$$g_i = \begin{cases} -1 & i = 0 \\ 0 & i = 1 \\ 1 & i = 2 \end{cases}$$

The intuition here is that sites with large  $\beta$  coefficients are under selection.