Extending PPGtk

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Contents

1	Program organization		1	
	1.1	Model namespaces and classes	1	
	1.2	Metropolis-Hastings algorithm	1	
2	Inb	reeding	1	
	2.1	The likelihood	2	
	2.2	Metropolis-Hastings algorithm	2	
3 B	Beta	Beta mixture model		
	3.1	The likelihood	2	
	3.2	Metropolis-Hastings algorithm	2	
4	Pop	ulation admixture model	2	
	4.1	The likelihood	2	
	4.2	Metropolis-Hastings algorithm	2	

1 Program organization

1.1 Model namespaces and classes

The likelihood of an individuals' read data given the population allele frequency can be computed by summing over the possible genotypes:

$$\mathcal{L}_{i}(p) = P(r_{i}|p) = \sum_{a=0}^{m_{i}} P(r_{i}|a)P(a|p),$$
 (S1)

where $P(r_i|a)$ is the genotype likelihood for genotype $a = 0, ..., m_i$ (e.g., calculated using GATK), and

$$P(a|p) = \binom{m_i}{a} p^a (1-p)^{m_i-a}.$$

For multiple samples, we take the product of the individual likelihoods:

$$\mathcal{L}(p) = \prod_{i} \mathcal{L}_{i}(p) = \prod_{i} \left(\sum_{a=0}^{m_{i}} P(r_{i}|a) P(a|p) \right). \tag{S2}$$

Taking the natural log gives us the log likelihood of the population allele frequency at a single site:

$$\ell(p) = \log \mathcal{L}(p) = \sum_{i} \log \left(\sum_{a=0}^{m_i} P(r_i|a) P(a|p) \right). \tag{S3}$$

1.2 Metropolis-Hastings algorithm

$$P(p) \sim \text{beta}(\alpha = 0.5, \beta = 0.5).$$
 (S4)

$$P(p|r) \propto P(r|p)P(p) = \left(\sum_{a} P(r|a)P(a|p)\right)P(p)$$
 (S5)

$$\alpha = \min\left\{1, \frac{P(r|p^*)P(p^*)}{P(r|p)P(p)}\right\}$$
 (S6)

2 Inbreeding

We introduce another parameter, ϕ , that is related to the inbreeding coefficient (F) through the following equation:

$$F = \frac{1}{1+\phi} \tag{S7}$$

2.1 The likelihood

$$\mathcal{L}_i(p,\phi) = P(r_i|p,\phi) = \sum_{a=0}^{m_i} P(r_i|a)P(a|p,\phi)$$
 (S8)

where $P(r_i|a)$ is the genotype likelihood for genotype $a=0,\ldots,m_i$ (e.g., calculated using GATK), and

$$P(a|p,\phi) = \binom{m_i}{a} \frac{\mathcal{B}(a+\phi p, m_i - a + (1-\phi)p)}{\mathcal{B}(\phi p, (1-\phi)p)},$$

which is the probability density function for the beta-binomial distribution with $\alpha = \phi p$ and $\beta = (1 - \phi)p$. Here, $\mathcal{B}(\cdot)$ is the beta function.

2.2 Metropolis-Hastings algorithm

3 Beta mixture model

- 3.1 The likelihood
- 3.2 Metropolis-Hastings algorithm

4 Population admixture model

- 4.1 The likelihood
- 4.2 Metropolis-Hastings algorithm