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# A new penalized criterion for variable selection and clustering using genotypic data

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## Abstract

We consider the problem of estimating the number of components and the relevant variables in a mixture model for multilocus genotypic data. A new penalized maximum likelihood criterion is proposed, and a non-asymptotic oracle inequality is obtained. Further, under weak assumptions on the true probability underlying the observations, the selected model is asymptotically consistent. On a practical aspect, the shape of our proposed penalty function is defined up to a multiplicative constant which is calibrated thanks to the slope heuristics, in an automatic data-driven procedure. Using simulated data, we found that this procedure improves the performances of the selection procedure with respect to classical criteria such as **BIC** and **AIC**. The new criterion gives an answer to the question “Which criterion for which sample size?”.

*Keywords:* Variables selection, Penalized Likelihood, Slope heuristics, Mixture multinomial models, Population genetics.

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## 1. Introduction

This article is concerned with a problem of variable selection and estimation of the number of populations for unsupervised classification. We deal with multilocus genotypic data from  $n$  diploid individuals for which there is no knowledge about the population they come from. The data consist of a sample of genotypes at a certain number  $L$  of loci (variables) that may be large. The individuals of the sample are clustered into a certain unknown number  $K$  of genetically homogeneous populations on the basis of their genotypes. It may happen that only a subset  $S$  of variables are relevant for clustering purposes, and the others are just noise. Thus, in addition to the number  $K$  of populations and the allelic frequencies, we are also interested in the subset  $S$ , which may have significance for biologists.

A number of clustering methods using multilocus data have been proposed in recent years (see [1, 2, 3]). But the problem of variable selection for cluster-

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ing using such data was first addressed in [4], where the question is regarded as a model selection problem in a density estimation framework. Using simulated data, that article shows that the variable selection procedure based on the Bayesian Information Criterion (**BIC**) significantly improves clustering and prediction capacities in our framework. It also gives a theoretical consistency result: when the true density  $P_0$  underlying the observations belongs to one of the competing models, then there exists a smallest model  $\mathcal{M}_{(K_0, S_0)}$  containing  $P_0$ ; further, the **BIC** type criteria select  $\mathcal{M}_{(K_0, S_0)}$  with probability tending to one as the sample size  $n$  goes to infinity. This consistency approach may require large sample sizes which may be difficult to obtain. The knowledge of the “optimal” model, aside the allelic frequencies, is an important information for biologists.

In the present paper we focus on density estimation. The approach we follow does not aim at choosing the true model underlying the data, even if our procedure performs well also for that. The resulting criteria are rather designed to minimize some risk function of the estimated density with respect to the true density. In this context simpler models can be preferred to  $\mathcal{M}_{(K_0, S_0)}$ , in which too many parameters can entail estimators with a too big variance. Further, in this approach there is no need to assume that  $P_0$  belongs to one of the competing models  $\mathcal{M}_{(K,S)}$ .

**BIC**, as well as Akaike Information Criterion (**AIC**), relies on a strong asymptotic assumption, and can thus be inappropriate for small sample sizes. In this article, we propose a non asymptotic penalized criterion based on the metric entropy theory of Massart [5]. It leads to a non asymptotic oracle inequality, which compares the risk of the selected estimator to the risk of the estimator associated with the unknown best model (see Theorem 1). There exists a large literature on model selection via penalization from a non asymptotic perspective. This literature is still in development with the appearance of sophisticated tools of probability such as concentration and deviations inequalities (see [5] and the references therein).

However, our proposed penalty function presents a drawback: it is defined up to an unknown multiplicative constant, and is not directly usable in practice. In fact, our main result mainly suggests the shape of the penalty function:

$$\text{pen}_n(m) = \lambda D_m/n,$$

where  $D_m$  is the dimension of model  $m$ , and  $\lambda$  an unknown constant depending on the sample size and the complexity of the collection of models under competition, which has to be calibrated. A calibration of  $\lambda$  with the so-called slope heuristics has been proposed in [6] for the calibration of a multiplicative constant in such a case. We propose a modified version based on a sliding window of this calibration method. The resulting criterion does not require ad-hoc choice of the penalty parameters and adapts automatically to the data. Although the full theoretical validation of slope heuristics is provided only in the Gaussian homoscedastic and heteroscedastic regression frameworks [6, 7], they have been implemented in several other frameworks (see [8, 9, 10, 11] for applications in density estimation, genomic, etc.). The simulations performed in Subsection 4.3 illustrate that our criterion behaves well with respect to more classical criteria as **BIC** and **AIC**, both to estimate the density, even when  $n$  is relatively small, and to retrieve the true model.

The paper is organized as follows. Section 2 is devoted to the presentation of the mixture models framework and to the model selection paradigm. In Section 3 we state and prove our main result, the oracle inequality. Section 4 is devoted to the practical aspect of our procedure which has been implemented in the stand alone software **MixMoGenD** (Mixture Model using Genotypic Data) (see [4]). Results on simulated experiments are also presented: we compare our proposed criterion to classical **BIC** and **AIC**, in both points of view of the selection of the true model and of density estimation. Eventually, the Appendices contain several technical results used in the main analysis.

## 2. Model and methods

### 2.1. Framework

We suppose we deal with independent and identically distributed (iid) realizations of a random vector  $X = (X^l)_{1 \leq l \leq L}$ , representing the genotype of an individual at  $L$  loci. Each genotype  $X^l$  consists in a (non ordered) set  $\{X^{l,1}, X^{l,2}\}$  of two (that may be equal) alleles taking their values in the same set  $\{1, \dots, A_l\}$ . The numbers  $A_l$  of alleles are supposed to be known, and to verify  $A_l \geq 2$ : a locus with a single allele state is useless for clustering purposes.

We consider a model-based clustering, which means that the sample is a finite mixture of an unknown number  $K$  of populations (clusters) characterized by their allelic frequencies. Let denote by  $Z$  the (unobserved) population an individual comes from. Variable  $Z$  takes its values in the set  $\{1, \dots, K\}$  of the labels of the different clusters. Its distribution is given by the vector  $\pi = (\pi_k)_{1 \leq k \leq K}$ , where  $\pi_k = P(Z = k)$ . Conditionally to  $Z$ , the loci  $X^1, \dots, X^L$  are supposed to be independent, and the alleles  $X^{l,1}$  and  $X^{l,2}$  at any locus  $l$  are also supposed to be independent. The preceding two assumptions are what biologists call *Linkage Equilibrium* (LE) and *Hardy-Weinberg Equilibrium* (HWE) respectively. According to these assumptions, the probability distribution of a genotype  $x = (x^l)_{1 \leq l \leq L}$  in a population  $k$  is given in the following equations

$$P(x | Z = k) = \prod_{l=1}^L P(x^l | Z = k) \quad (1)$$

$$P(x^l | Z = k) = (2 - \mathbb{1}_{x^{l,1} = x^{l,2}}) \alpha_{k,l,x^{l,1}} \alpha_{k,l,x^{l,2}}, \quad (2)$$

where  $\alpha_{k,l,j} := P(X^{l,1} = j | Z = k) = P(X^{l,2} = j | Z = k)$  is the probability of allele  $j$  at locus  $l$  in population  $k$ . The mixing proportions  $\pi_k$  and the allelic probabilities  $\alpha_{k,l,j}$  will be treated as parameters.

Although Hardy-Weinberg and linkage equilibria models are based on several simplifying assumptions that can seem unrealistic, they have still proven to be useful in describing many population genetics attributes and serve as a base model in the development of more realistic models of microevolution. The choice of estimators derived from the maximum likelihood estimator (MLE) responds to the wish of biologists to group the sample into clusters minimizing the Hardy-Weinberg and linkage disequilibria, and this brings some robustness to our modeling (see [12] and references therein).

It may happen that the structure of interest is contained in only a subset  $S$  of the  $L$  available loci, the others been useless or even harmful to detect a

reasonable clustering into statistically different populations. For the loci in  $S$ , the allelic frequencies of at least two populations are different: we will call them clustering loci. For the other loci, the alleles are equally distributed across the clusters. We denote by  $\beta_{l,j}$  the allelic frequency of allele  $j$  at locus  $l$  in the whole population:

$$\beta_{l,j} = \alpha_{1,l,j} = \dots = \alpha_{k,l,j} \dots = \alpha_{K,l,j} \text{ for any } l \notin S \text{ and } 1 \leq j \leq A_l. \quad (3)$$

Obviously,  $S = \emptyset$  if  $K = 1$ , otherwise  $S$  belongs to  $\mathcal{P}^*(L)$ , the set of all non empty subsets of  $\{1, \dots, L\}$ .

Summarizing all these assumptions, we can write down the likelihood of a genotype  $x = (x^l)_{1 \leq l \leq L}$ :

$$P_{(K,S)}(x|\theta) = \left[ \sum_{k=1}^K \pi_k \prod_{l \in S} (2 - \mathbb{1}_{x^{l,1}=x^{l,2}}) \alpha_{k,l,x^{l,1}} \times \alpha_{k,l,x^{l,2}} \right] \times \prod_{l \notin S} (2 - \mathbb{1}_{x^{l,1}=x^{l,2}}) \beta_{l,x^{l,1}} \beta_{l,x^{l,2}} \quad (4)$$

where  $\theta = (\pi, \alpha, \beta)$  is a multidimensional parameter, with

$$\alpha = (\alpha_{k,l,j})_{1 \leq k \leq K; l \in S; 1 \leq j \leq A_l}$$

$$\beta = (\beta_{l,j})_{l \notin S; 1 \leq j \leq A_l}.$$

For a given  $K$  and  $S$ ,  $\theta = \theta_{(K,S)}$  ranges in the set

$$\Theta_{(K,S)} = \mathbb{S}_{K-1} \times \left[ \prod_{l \in S} \mathbb{S}_{A_l-1} \right]^K \times \prod_{l \notin S} \mathbb{S}_{A_l-1}, \quad (5)$$

where  $\mathbb{S}_{r-1} = \left\{ p = (p_1, p_2, \dots, p_r) \in [0, 1]^r : \sum_{j=1}^r p_j = 1 \right\}$  is the  $(r-1)$ -dimensional simplex.

Then we consider the collection of all parametric models

$$\mathcal{M}_{(K,S)} = \{ P_{(K,S)}(\cdot | \theta_{(K,S)}); \theta_{(K,S)} \in \Theta_{(K,S)} \} \quad (6)$$

with  $(K, S) \in \mathbb{M} := \{(1, \emptyset)\} \cup (\mathbb{N} \setminus \{0, 1\}) \times \mathcal{P}^*(L)$ . To alleviate notations, we will often use the single index  $m \in \mathbb{M}$  instead of  $(K, S)$ .

Each model  $\mathcal{M}_{(K,S)}$  corresponds to a particular structure situation with  $K$  clusters and a clustering relevant variable subset  $S$ . Thus the choice of a model  $(K, S)$  among the collection  $\mathbb{M}$  includes an estimate of the subset of clustering variables and the number of clusters. Inferring  $K$  and  $S$  becomes a model selection problem in a density estimation framework. It also leads to a data clustering, via the estimation of the parameter  $\theta_{(K,S)}$  and the prediction of the  $z_i$ 's, which can be performed by the Maximum A Posteriori (MAP) method.

## 2.2. Model selection via penalization

A common method to solve model selection problems consists in the minimization of a penalized maximum likelihood criterion. In each model  $\mathcal{M}_{(K,S)}$ ,

consider the maximum likelihood estimator (MLE)  $\widehat{P}_{(K,S)} = P_{(K,S)}(\cdot|\widehat{\theta})$ , which minimizes the log-likelihood contrast

$$\gamma_n(P) = -\frac{1}{n} \sum_{i=1}^n \ln P(X_i) \quad (7)$$

where  $X_i = (X_i^l)_{1 \leq l \leq L}$  denotes the multilocus genotype of individual  $i$ . Then a data driven selected model  $\mathcal{M}_{(\widehat{K}_n, \widehat{S}_n)}$  is chosen, where  $(\widehat{K}_n, \widehat{S}_n)$  minimizes a penalized maximum likelihood criterion of the form

$$\mathbf{crit}(K, S) = \gamma_n(\widehat{P}_{(K,S)}) + \mathbf{pen}_n(K, S), \quad (8)$$

where  $\mathbf{pen}_n : \mathbb{M} \rightarrow \mathbb{R}_+$  is the penalty function. Eventually the selected estimator is  $\widehat{P}_{(\widehat{K}_n, \widehat{S}_n)}$ .

The penalty function is designed to avoid overfit problems. Classical penalties, such as the ones used in **AIC** and **BIC** criteria, are based on the dimension of the model. In the following, we will refer to the number of free parameters

$$D_{(K,S)} = K - 1 + K \sum_{l \in S} (A_l - 1) + \sum_{l \notin S} (A_l - 1) \quad (9)$$

as the dimension of the model  $\mathcal{M}_{(K,S)}$ .

Our work is centered on the MLE estimator  $\widehat{P}_{(K,S)}$ , but this last one presents a drawback. For the sake of density estimation, we would like to use the Kullback-Leibler divergence **KL** as a risk function to measure the quality of an estimator. Unfortunately, when an allele is not present in the sample, the MLE estimator assigns to it a zero probability. As a consequence, the Kullback risk  $\mathbb{E}_{P_0} \left[ \mathbf{KL} \left( P_0, \widehat{P}_{(K,S)} \right) \right]$  is infinite.

The Hellinger distance offers an alternative to the Kullback-Leibler divergence. Let us consider two probability distribution  $P$  and  $Q$ , admitting respectively  $s$  and  $t$  as density functions with respect to a common  $\sigma$ -finite measure  $\mu$ . We call Hellinger distance between  $P$  and  $Q$  the quantity  $\mathbf{h}(P, Q)$  defined by

$$\mathbf{h}(P, Q)^2 = \int \left( \sqrt{s(x)} - \sqrt{t(x)} \right)^2 d\mu(x). \quad (10)$$

Let  $(K^*, S^*)$  a minimizer in  $(K, S)$  of the Hellinger risk of the MLE estimator

$$R_{(K,S)} = \mathbb{E}_{P_0} \left[ \mathbf{h}^2 \left( P_0, \widehat{P}_{(K,S)} \right) \right]. \quad (11)$$

The density  $\widehat{P}_{(K^*, S^*)}$  is called oracle for the Hellinger risk. It is not an estimator, since it depends on the true density  $P_0$ . However it can be used as a benchmark to quantify the quality of our model selection procedure: in the simulation performed in paragraph 4.3.2, we compare the Hellinger risk of the selected estimator  $\widehat{P}_{(\widehat{K}_n, \widehat{S}_n)}$  to the oracle risk.

### 3. New criteria and non asymptotic risk bounds

#### 3.1. Main result

Our main theorem provides an oracle inequality. It links the Hellinger risk of the selected estimator to the Kullback-Leibler divergence **KL** between the

true density and each model in the models collection. Unlike **KL** which is not a metric, the Hellinger distance  $\mathbf{h}$  permits to take advantage of the metric properties (metric entropy) of the models.

**Theorem 1.** *We consider the collection  $\mathbb{M}$  of models defined above, and a corresponding collection of  $\rho$ -MLEs  $(\hat{P}_{(K,S)})_{(K,S) \in \mathbb{M}}$ , which means that for every  $(K, S) \in \mathbb{M}$*

$$\gamma_n(\hat{P}_{(K,S)}) \leq \inf_{Q \in \mathcal{M}_{(K,S)}} \gamma_n(Q) + \rho.$$

Let  $M = \sup_{1 \leq l \leq L} A_l$  and  $\xi = \frac{4\sqrt{ML}}{2(1+3\sqrt{2})^L - 1}$ . Assume that  $\xi < 1$  or  $n > \xi^2 K$ .

There exists absolute constants  $\kappa$  and  $C$  such that whenever

$$\mathbf{pen}_n(K, S) \geq \kappa \left( 5 + \sqrt{\max\left(\frac{1}{2} \ln n + \frac{1}{2} \ln L, \frac{\ln 2}{2} + \ln L\right)} \right)^2 \frac{D_{(K,S)}}{n} \quad (12)$$

for every  $(K, S) \in \mathbb{M}$ , then the model  $\mathcal{M}_{(\hat{K}_n, \hat{S}_n)}$  where  $(\hat{K}_n, \hat{S}_n)$  minimizes

$$\mathbf{crit}(K, S) = \gamma_n(\hat{P}_{(K,S)}) + \mathbf{pen}_n(K, S)$$

over  $\mathbb{M}$  exists and moreover, whatever the underlying probability  $P_0$ ,

$$\begin{aligned} & \mathbb{E}_{P_0} \left[ \mathbf{h}^2 \left( P_0, \hat{P}_{(\hat{K}_n, \hat{S}_n)} \right) \right] \\ & \leq C \left( \inf_{(K,S) \in \mathbb{M}} (\mathbf{KL}(P_0, \mathcal{M}_{(K,S)}) + \mathbf{pen}_n(K, S)) + \rho + \frac{(3/4)^L}{n} \right) \end{aligned}$$

where, for every  $(K, S) \in \mathbb{M}$ ,  $\mathbf{KL}(P_0, \mathcal{M}_{(K,S)}) = \inf_{Q \in \mathcal{M}_{(K,S)}} \mathbf{KL}(P_0, Q)$ .

The condition  $\xi < 1$  is used in the proof to avoid more complicated calculations. In practice,  $\xi$  is very likely to be smaller than 1 for  $L$  not too small.

Note that as soon as  $n \geq 2L$ , (12) is simplified in the following way

$$\mathbf{pen}_n(K, S) \geq \kappa \left( 5 + \sqrt{\frac{1}{2} \ln n + \frac{1}{2} \ln L} \right)^2 \frac{D_{(K,S)}}{n}.$$

The leading term for large  $n$  is  $\frac{\ln n}{2} \frac{D_{(K,S)}}{n}$ , which is the penalty function of **BIC**. As a consequence, we can apply Theorem 2 from [4]: when the underlying distribution  $P_0$  belongs to one of the competing models, the smallest model  $(K_0, S_0)$  containing  $P_0$  is selected with probability tending to 1 as  $n$  goes to infinity.

Such a penalty is not surprising in our context: it is in fact very similar to the one obtained in [8] in a Gaussian mixture framework.

Sharp estimates of  $\kappa$  are not available. Further, Theorem 1 is too conservative in practice, and leads to an over-penalized criterion which is outperformed by smaller penalties. So it is mainly used to suggest the shape of the penalty function

$$\mathbf{pen}_n(K, S) = \lambda \frac{D_{(K,S)}}{n} \quad (13)$$

where  $\lambda$  is a parameter to be chosen depending on  $n$  and the collection  $\mathbb{M}$  — but not on  $(K, S)$ . Slope heuristics [6, 7] can be used in practice to calibrate  $\lambda$ : this is done in Section 4, where we use change-point detection [9] in relation to slope heuristics.

Since  $\mathbf{h}^2$  is upper bounded by 2, the non-asymptotic feature of Theorem 1 is interesting when  $n$  is large enough with respect to  $D_{(K,S)}$ . However, even with small values of  $n$ , the simulations performed in Subsection 4.3 show that the penalized criterion calibrated using the slope heuristics keep good behaviors.

### 3.2. A general tool for model selection

Theorem 1 is obtained from [5, Theorem 7.11]. This last result deals with model selection problems by proposing penalty functions related to geometrical properties of the models, namely metric entropy with bracketing for Hellinger distance.

The framework here is the following. We consider some measurable space  $(A, \mathcal{A})$ , and  $\mu$  a  $\sigma$ -finite positive measure on  $A$ . A collection of models  $(\mathcal{M}_m)_{m \in \mathbb{M}}$  is given, where each model  $\mathcal{M}_m$  is a set of probability density functions  $s$  with respect to  $\mu$ . The following relation permits us to extend the definition of  $\mathbf{h}$  to positive functions  $s$  or  $t$  whose integral is finite but not necessary 1. Denoting  $\sqrt{s}$  the function defined by  $\sqrt{s}(x) = \sqrt{s(x)}$ , and by  $\|\cdot\|_2$  the usual norm in  $\mathbb{L}^2(\mu)$ , then

$$\mathbf{h}(s, t) = \|\sqrt{s} - \sqrt{t}\|_2.$$

Let us now recall the definition of metric entropy with bracketing. Consider some collection  $F$  of measurable functions on  $A$ , and  $d$  one of the following metrics on  $F$ :  $\mathbf{h}$ ,  $\|\cdot\|_1$ , or  $\|\cdot\|_2$ . A bracket  $[l, u]$  is the collection of all measurable functions  $f$  such that  $l \leq f \leq u$ . Its  $d$ -diameter is the distance  $d(u, l)$ . Then, for every positive number  $\varepsilon$ , we denote by  $N_{[\cdot]}(\varepsilon, F, d)$  the minimal number of brackets with  $d$ -diameter not larger than  $\varepsilon$  which are needed to cover  $F$ . The  $d$ -entropy with bracketing of  $F$  is defined as the logarithm of  $N_{[\cdot]}(\varepsilon, F, d)$ , and is denoted by  $H_{[\cdot]}(\varepsilon, F, d)$ .

We assume that for each model  $\mathcal{M}_m$  the square entropy with bracketing  $\sqrt{H_{[\cdot]}(\varepsilon, \mathcal{M}_m, \mathbf{h})}$  is integrable at 0. Let us consider some function  $\phi_m$  on  $\mathbb{R}_+$  with the following properties

- (I).  $\phi_m$  is nondecreasing,  $x \mapsto \phi_m(x)/x$  is non-increasing on  $(0, +\infty)$  and for every  $\sigma \in \mathbb{R}_+$  and every  $u \in \mathcal{M}_m$

$$\int_0^\sigma \sqrt{H_{[\cdot]}(x, S_m(u, \sigma), \mathbf{h})} dx \leq \phi_m(\sigma),$$

where  $S_m(u, \sigma) = \{t \in \mathcal{M}_m : \|\sqrt{t} - \sqrt{u}\|_2 \leq \sigma\}$ .

- (I) is verified in particular with  $\phi_m(\sigma) = \int_0^\sigma \sqrt{H_{[\cdot]}(x, \mathcal{M}_m, \mathbf{h})} dx$ .

In order to avoid measurability problems, we suppose that for each  $m \in \mathbb{M}$ , the following separability condition is verified for  $\mathcal{M}_m$ :

- (M). There exists some countable subset  $\mathcal{M}'_m$  of  $\mathcal{M}_m$  and a set  $A' \subset A$  with  $\mu(A') = \mu(A)$  such that for every  $t \in \mathcal{M}_m$ , there exists some sequence  $(t_k)_{k \geq 1}$  of elements of  $\mathcal{M}'_m$  such that for every  $x \in A'$ ,  $\ln(t_k(x))$  tends to  $\ln(t(x))$  as  $k$  tends to infinity.



**Theorem 2.** Let  $X_1, \dots, X_n$  be iid random variables with unknown density  $s$  with respect to some positive measure  $\mu$ . Let  $\{\mathcal{M}_m\}_{m \in \mathbb{M}}$  be some at most countable collection of models, each fulfilling (M). We consider a corresponding collection of  $\rho$ -MLEs  $(\hat{s}_m)_{m \in \mathbb{M}}$ . Let  $\{x_m\}_{m \in \mathbb{M}}$  be some family of nonnegative numbers such that

$$\sum_{m \in \mathbb{M}} e^{-x_m} = \Sigma < \infty,$$

and for every  $m \in \mathbb{M}$  considering  $\phi_m$  with property (i) define  $\sigma_m$  as the unique positive solution of the equation

$$\phi_m(\sigma) = \sqrt{n}\sigma^2. \quad (14)$$

Let  $\mathbf{pen}_n : \mathbb{M} \rightarrow \mathbb{R}_+$  and consider the penalized log-likelihood criterion

$$\mathbf{crit}(m) = \gamma_n(\hat{s}_m) + \mathbf{pen}_n(m).$$

Then, there exists some absolute constants  $\kappa$  and  $C$  such that whenever

$$\mathbf{pen}_n(m) \geq \kappa \left( \sigma_m^2 + \frac{x_m}{n} \right) \text{ for every } m \in \mathbb{M},$$

some random variable  $\hat{m}$  minimizing  $\mathbf{crit}$  over  $\mathbb{M}$  exists and moreover, whatever the density  $s$

$$\mathbb{E}_s [\mathbf{h}^2(s, \hat{s}_{\hat{m}})] \leq C \left( \inf_{m \in \mathbb{M}} (\mathbf{KL}(s, \mathcal{M}_m) + \mathbf{pen}_n(m)) + \rho + \frac{\Sigma}{n} \right).$$

In Theorem 2,  $\sigma_m^2$  has the role of a variance term of  $\hat{s}_m$ , while the weights  $x_m$  take into account the number of models  $m$  having the same dimension.

### 3.3. Proof of Theorem 1

In order to apply Theorem 2, we need to compute metric entropy with bracketing of each model  $\mathcal{M}_{(K,S)}$ . This is done in the following result, which is proved in Appendix A.

**Proposition 1** (Bracketing entropy of a model). Let  $\eta : \mathbb{R}_+ \rightarrow \mathbb{R}_+$  be the increasing convex function defined by

$$\eta(\varepsilon) = (1 + \varepsilon) (1 + \sqrt{2}\varepsilon(2 + \varepsilon))^L - 1. \quad (15)$$

For any choice of  $K$  and  $S$ ,  $\mathcal{M}_{(K,S)}$  fulfills (M). For any  $\varepsilon \in (0, 1)$ ,

$$H_{[\cdot]}(\eta(\varepsilon), \mathcal{M}_{(K,S)}, \mathbf{h}) \leq D_{(K,S)} \ln \left( \frac{1}{\varepsilon} \right) + C_{(K,S)},$$

where

$$\begin{aligned} C_{(K,S)} = & \frac{1}{2} \left( \ln(2\pi e) D_{(K,S)} + \ln(4\pi e) (1 + L + (K - 1)|S|) \right. \\ & \left. + \ln(K + 1) + \sum_{l=1}^L \ln(A_l + 1) + (K - 1) \sum_{l \in S} \ln(A_l + 1) \right) \end{aligned} \quad (16)$$

$C_{(K,S)}$  is a technical quantity measuring the complexity of a model  $\mathcal{M}_{(K,S)}$ .

In the next step we establish an expression for  $\phi_m$ . All following results are proved in [Appendix B](#).

**Proposition 2.** *For any choice of  $m = (K, S)$ , the function  $\phi_m$  defined on  $(0, \eta(1)]$  by*

$$\phi_m(\sigma) = \left( 2\sqrt{\ln 2} \sqrt{D_{(K,S)}} + \sqrt{C_{(K,S)} - D_{(K,S)} \ln \eta^{-1}(\sigma)} \right) \sigma$$

fulfills [\(I\)](#).

We do not define  $\phi_m$  for  $\sigma$  bigger than  $\eta(1) = 2(1 + 3\sqrt{2})^L - 1$ , to avoid more complicated expressions. This is why a condition on  $\xi$  appears in the following lemma:

**Lemma 1.** *Let  $M = \sup_{1 \leq l \leq L} A_l$ , and  $\xi = \frac{4\sqrt{M}\sqrt{L}}{2(1 + 3\sqrt{2})^L - 1}$ . Then, for all  $n \geq 1$  if  $\xi < 1$ , and for  $n > \xi^2 K$  otherwise, the solution  $\sigma_m$  of [\(14\)](#) verifies  $\sigma_m < \eta(1)$ .*

From [Proposition 2](#) we can deduce an upper bound for  $\sigma_m$ , with a similar reasoning to [\[8\]](#). First,  $\sigma_m \leq \eta(1)$  entails  $\eta^{-1}(\sigma_m) \leq 1$ , and we obtain the lower bound  $\sigma_m \geq \tilde{\sigma}_m$ , where

$$\tilde{\sigma}_m = \frac{1}{\sqrt{n}} \left( 2\sqrt{\ln 2} \sqrt{D_m} + \sqrt{C_m} \right). \quad (17)$$

This can be used to get an upper bound

$$\sigma_m \leq \frac{1}{\sqrt{n}} \left( 2\sqrt{\ln 2} \sqrt{D_m} + \sqrt{C_m - D_m \ln \eta^{-1}(\tilde{\sigma}_m)} \right). \quad (18)$$

Let us now choose the weights  $x_m$ . If we take something bigger than  $n\sigma_m^2$ , this will change the shape of the penalty in [Theorem 2](#). We define

$$x_m = (\ln 2) D_m.$$

The following Lemma shows that this choice is suitable.

**Lemma 2.** *For any model  $\mathcal{M}_m$ , with  $m \in \mathbb{M}$  as above, let us set  $x_m = (\ln 2) D_m$ . Then*

$$\sum_{m \in \mathbb{M}} e^{-x_m} \leq (3/4)^L.$$

To express the penalty function we have to lower bound  $\eta^{-1}(\tilde{\sigma}_m)$ . This is done in following Lemma.

**Lemma 3.** *Using the preceding notations,*

$$\sigma_m^2 + \frac{x_m}{n} \leq \frac{D_{(K,S)}}{n} \left( 5 + \sqrt{\max \left( \frac{1}{2} \ln n + \frac{1}{2} \ln L, \frac{\ln 2}{2} + \ln L \right)} \right)^2.$$

This ends the proof of [Theorem 1](#). Let us now introduce a complementary argument.

## 4. In practice

In real datasets the numbers  $A_l$  of possible alleles at each locus  $l$  are not necessarily known. The numbers  $\hat{A}_l$  of observed alleles can be used instead. In fact, the MLE estimator select a density with null weight on non-observed alleles. Then, in each model  $\mathcal{M}_{(K,S)}$ , an approximated MLE estimator can be computed thanks to the Expectation-Maximization (EM) algorithm (see [13]).

The other two points that have to be done before reaching the final estimator  $\hat{P}_{(\hat{K}_n, \hat{S}_n)}$  are the choice of the penalty function, and the sub-collection of models on which the EM algorithm will be used. These two points are discussed in Subsections 4.1 and 4.2. Then simulations are presented in Subsection 4.3.

### 4.1. Slope heuristics and Dimension jump

Theorem 1 suggests to take a penalty function of the shape (13), defined modulo a multiplicative constant  $\lambda$  which has to be calibrated. Slope heuristics, as presented in [6, 7], provide a practical method to find an optimal penalty  $\mathbf{pen}_{\text{opt}}(m) = \lambda_{\text{opt}} D_m/n$ . These heuristics are based on the conjecture that there exists a minimal penalty  $\mathbf{pen}_{\text{min}}(m) = \lambda_{\text{min}} D_m/n$  required for the model selection procedure to work: when the penalty is smaller that  $\mathbf{pen}_{\text{min}}$ , the selected model is one of the most complex models, and the risk of the selected estimator is large. On the contrary, when the penalty is larger than  $\mathbf{pen}_{\text{min}}$ , the complexity of the selected model is much smaller. Then the optimal penalty is close to twice the minimal penalty:

$$\mathbf{pen}_{\text{opt}}(m) \approx 2\lambda_{\text{min}} D_m/n.$$

The name ‘‘slope heuristics’’ comes from  $\lambda_{\text{min}}$  being the slope of the linear regression  $\gamma_n(\hat{P}_m) \sim D_m/n$  for a certain sub-collection of the most competing models  $m$ . For example, on the left panel of Figure 1 below, a slope is visible for the models containing the true model  $\mathcal{M}_{(K_0, S_0)}$ .

Instead of estimating  $\lambda_{\text{min}}$  by linear regression, another method is jump detection. Suppose we have at hand a reasonable grid  $\lambda_1 < \dots < \lambda_r$  of candidate estimates of  $\lambda_{\text{min}}$ , and a sub-collection  $\mathbb{M}_{\text{ex}}$  of most competitive models. Each  $\lambda_i$  leads to a selected model  $\hat{m}_i$  with dimension  $D_{\hat{m}_i}$ . If you plot  $D_{\hat{m}_i}$  as a function of  $\lambda_i$ ,  $\lambda_{\text{min}}$  is expected to lie at the locus of the biggest jump. However, the right panel of Figure 1 illustrates an important point: in that example the biggest jump is at  $\lambda \approx 5.1$ , but the optimal value of  $\lambda_{\text{min}}$  is around 0.9, which corresponds to several successive jumps. We propose an improved version of the dimension jump method of [7], based on a sliding window: we consider at a time all jumps in an window of  $h \geq 1$  following intervals in the grid. Algorithm 1 below describes the procedure.

### 4.2. Sub-collection of models for calibration

For a given maximum value  $K_{\text{max}}$  of the number of clusters, the number of models under competition is equal to  $1 + (K_{\text{max}} - 1) * (2^L - 1)$ . Since this number is huge in most situations, it is very painful to consider all competing models for calibration of the constant  $\lambda$ . On the other hand, we need enough models to ensure that there is a clear jump in the sequence of selected dimension. We consider the modified backward-stepwise algorithm proposed in [4], which

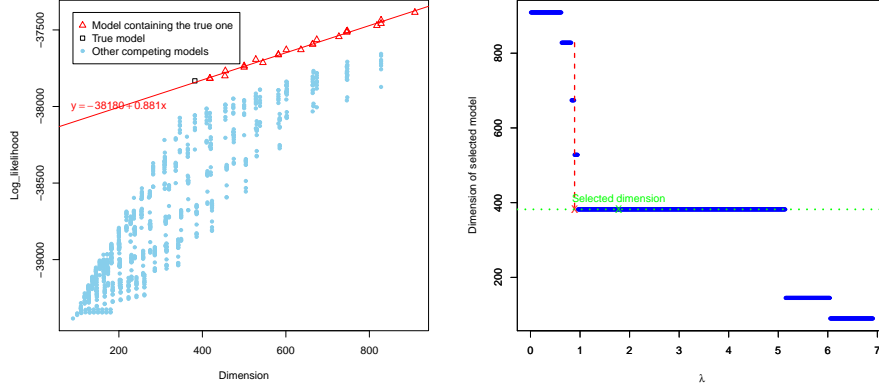


Figure 1: Two ways to compute the slope, on a simulated sample of 1000 individuals, with 8 clustering loci among 10, and 5 populations. Models have been explored via the modified backward-stepwise described in subsection 4.2, the number  $K$  of clusters varying from 1 to 10. The size of the sliding window is 0.15.

---

**Algorithm 1** Calibration of Penalty  $(\mathbb{M}_{ex}, (\lambda_i)_{i=1, \dots, r}, h)$

---

**for**  $i = 1$  to  $n_\lambda$  **do**  
 $\hat{m}_i \leftarrow \arg \min_{m \in \mathbb{M}_{ex}} \left\{ \mathbb{P}_n \left( -\ln \hat{P}_m \right) + \lambda_i D_m \right\}$   
**end for**  
 $i_{jump} \leftarrow \min_{i \in \{h+1, \dots, r\}} \arg \max \left\{ D_{\hat{m}_{i-h}} - D_{\hat{m}_i} \right\}$   
 $i_{init} \leftarrow \max \left\{ j \in [i_{jump} - h, i_{jump} - 1], D_{\hat{m}_j} - D_{\hat{m}_{i_{jump}}} = D_{\hat{m}_{i_{jump}-h}} - D_{\hat{m}_{i_{jump}}} \right\}$   
 $\hat{\lambda}_{min} \leftarrow \frac{\alpha_{i_{init}} + \alpha_{i_{jump}}}{2}$   
**return**  $\hat{\lambda}_{min}$

---

enables to gather the most competitive models among all possible  $S$  for a given number  $K$  of clusters and a given penalty function  $\mathbf{pen}_n$ . It gives also the choice to add a complementary exploration step based on a similarly modified forward strategy. We will refer to this algorithm as *explorer*  $(K, \mathbf{pen}_n)$ .

Since we do not know the final penalty during the exploration step, we consider a reasonable grid  $\frac{1}{2n} = \lambda_1 < \dots < \lambda_r = \frac{\ln n}{n}$  containing both penalty functions associated to **AIC** and **BIC**. To each value  $\lambda_i$  of the grid is associated a penalty function  $\mathbf{pen}_{\lambda_i}$ . We launch *explorer*  $(K, \mathbf{pen}_{\lambda_i})$  for all values of  $K$  in  $\{1, \dots, K_{max}\}$  and for all values of  $\lambda_i$  of the above grid, and we gather the explored models in  $\mathbb{M}_{ex}$ . This sub-collection seemly contains the most competitive models and it is then used to calibrate  $\lambda$ .

### 4.3. Numerical experiments

Our proposed procedure with a data-driven calibration of the penalty function has been implemented in the software `MixMoGenD` (Mixture Model using Genotypic Data), which already proposed a selection procedure based on asymptotic criteria **BIC** and **AIC** (see [4]). Here, we conduct numerical experiments on simulated datasets for performances assessment of the new non asymptotic criterion with respect to **BIC** and **AIC**. The penalty functions of these last criteria are respectively defined by

$$\begin{aligned}\text{pen}_{\text{BIC}}(m) &= \frac{\ln n}{2n} \cdot D_m; \\ \text{pen}_{\text{AIC}}(m) &= \frac{1}{n} \cdot D_m.\end{aligned}$$

We present two experiments. The first one considers the consistency of the selected model: we study how the procedure retrieves the main features of the true model as the number of individuals in the datasets increases. In the second one, we are rather interested in the density estimation: we compare the risk of the selected estimator to the oracle risk.

#### 4.3.1. Consistency performances

In this experiment we consider a setting with  $L = 10$  loci of 10 alleles each. We chose a parameter with  $K_0 = 5$  populations of equal probability. The allelic frequencies have been chosen such that the genetic differentiation between the populations is decreasing with the locus number. In the first 6 loci, the populations are more separated. In the following 2 loci, the populations are poorly differentiated. In the last 2 loci, the alleles follow the same uniform distribution in all populations. The whole parameter is available at <http://www.math.u-psud.fr/~toussile/>.

We considered different values  $n$  of the sample size in  $[50, 900]$  and for each of them, 10 datasets have been simulated. The results are summarized in Figure 2. The left panel gives the proportion of selecting the subset  $\hat{S}_n$  of clustering variables containing the first 6 variables, which are the most genetically differentiated variables. The right panel gives the proportion of selected models with  $\hat{K}_n = K_0$ .

In this experiment, the **AIC** seems to be the best criterion for variable selection; however the different between **AIC** and the new criterion is not significant. It also appears that **AIC** estimates the number of clusters better than the other criteria for small sample sizes (around  $n = 100$  and  $n = 200$ ), but it overestimates this number from  $n = 500$ . On the contrary, the new criterion perfectly estimates the number of clusters for sample sizes  $\geq 300$ . **BIC** performs poorly for both variables selection and classification on datasets with small sizes. As expected, the data-driven calibration of the penalty function improves globally the performances of the selection procedure, and it gives thus an answer to the question “Which penalty for which sample size?”.

It may happen that the results obtained on small sample sizes change a little from one run to another. In fact, the EM algorithm can miss the global maximum on such sample sizes, in particular in models of higher dimension. In our experiments, it is probably the case with some datasets of size  $n \leq 300$ , when the number of free parameters in the simulated model is  $\geq 310$ .

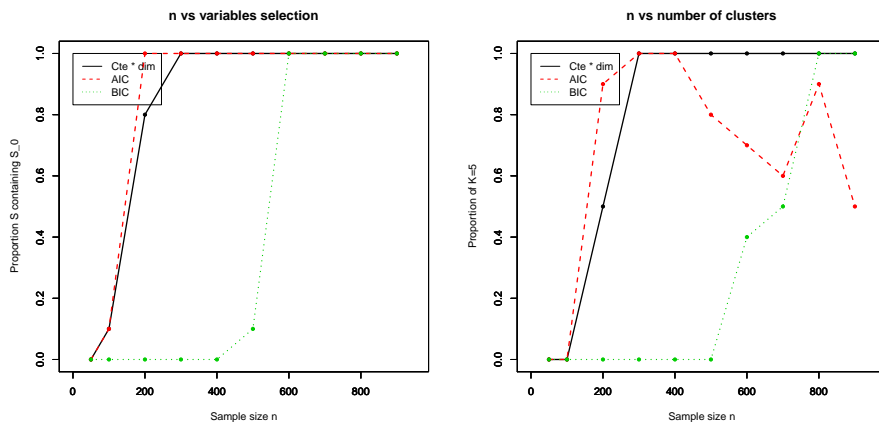


Figure 2: The figure in the left panel gives the proportion of selected models with  $\widehat{S}_n \supseteq \{1, \dots, 6\}$ , and the one in the right gives the proportion of selected models with  $\widehat{K}_n = K_0$ , versus the sample size.

#### 4.3.2. Oracle performances of the estimator

Since the new criterion is designed for density estimation, it is interesting to compare the associated estimator to the oracle for Hellinger risk. Recall that the oracle is the estimator associated to the model indexed by the minimizer  $(K^*, S^*)$  of the risk  $\mathbb{E} \left[ \mathbf{h}^2 \left( P_0, \widehat{P}_{(K, S)} \right) \right]$  over the collection of models  $\mathbb{M}$ .

In this experiment, we consider simulated datasets with reduced variability in order to reduce the computation time. The parameter underlying the data admits  $L = 6$  loci, 3 alleles for each locus, and  $K_0 = 3$  populations with equal probability. The allelic frequencies have been chosen in such a way that the genetic differentiation between the population is significant on the first 3 loci, very small on the 4<sup>th</sup> and 5<sup>th</sup> loci, while the alleles of the 6<sup>th</sup> locus follow the uniform distribution in all populations. Thus the true model is defined by  $K_0 = 3$  and  $S_0 = \{1, 2, 3, 4, 5\}$ . The whole parameter is available at <http://www.math.u-psud.fr/~toussile/>.

We estimated the oracle using a Monte Carlo procedure on 100 simulated datasets of size 500 each, and got  $\widehat{K}^* = 3$  and  $\widehat{S}^* = \{1, 2, 3, 4\}$ . The results we obtained are summarized in Figure 3 and Table 1.

	AIC	BIC
<b>BIC</b>	$< 4.4e - 08$	-
<b>Cte*Dim</b>	$< 1.1e - 05$	$< 2e - 16$

Table 1: Pairwise student tests comparing the means of the  $\mathbf{h}^2 \left( P_0, \widehat{P}_{(\widehat{K}_n, \widehat{S}_n)} \right)$ .

The worst behavior comes from **BIC** and it is not a surprise for two main reasons. First **BIC** is designed to find the true model which is different to the oracle in our experiments. Second, it is based on asymptotic approximation and then may requires large samples. In contrary, compared to **AIC** and **BIC**, the

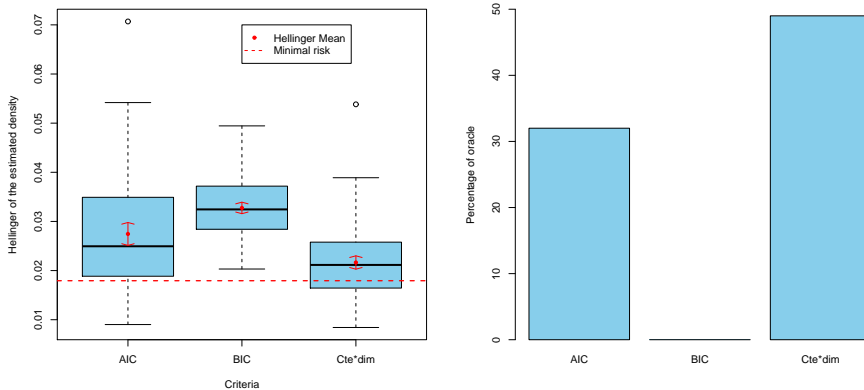


Figure 3: The left panel gives the boxplots, means and their 95% confident intervals, for  $\mathbf{h}^2(P_0, \hat{P}_{(\hat{K}_n, \hat{S}_n)})$ ; the right panel gives the percentages of selection of the estimated oracle  $(\hat{K}^*, \hat{S}^*)$ ; three criteria have been used: **AIC**, **BIC**, and **Cte\*Dim** which denotes the new criterion with data-driven calibration of the penalty function.

new criterion with data-driven calibration of the penalty function is significantly the best in the sense of Hellinger risk and the capacity of selecting the oracle. Recall that both **AIC** and the new criterion are designed to find the oracle (see Table 1). But like **BIC**, **AIC** is based on asymptotic approximations. So the advantage of the new criterion over **AIC** is probably that it is designed in a non asymptotic perspective.

## 5. Conclusion

In this paper, we have considered a model selection via penalization, which performs simultaneously a variables selection and a detection of the number of populations, in the specific framework of multilocus genotypic data. Our main result provides an oracle inequality, under the condition of some lower bound on the penalty function. The weakness of such a result is that the associated penalized criterion is not directly usable. Nevertheless, it suggests a shape of the penalty function which is of the form  $\mathbf{pen}_n(m) = \lambda D_m/n$ , where  $\lambda = \lambda(n, \mathbb{M})$  is a parameter which depends on the data and the collection of the competing models. In practice  $\lambda$  is calibrated via the slope heuristics.

In the simulated experiments we conducted, the new criterion with penalty calibration shows good behaviors for density estimation as well as for the selection of the true model. It also performs well both when the number of individuals is large and when it is small. This gives an answer to the question “Which criterion for with sample size?”

In the modeling we considered, the model dimension grows rapidly. In real experiments the number of individuals can be small, so other modeling with reduced dimension may be needed. We currently work on models which cluster the populations differently at each locus, as well as models which allocate the same probability to several alleles.

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## References

- [1] J. K. Pritchard, M. Stephens, P. Donnelly, Inference of population structure using multilocus genotype data., *Genetics* 155 (2) (2000) 945–59.
- [2] C. Chen, F. Forbes, O. Francois, fastruct: model-based clustering made faster, *Molecular Ecology Notes* 6 (4) (2006) 980–983.
- [3] J. Corander, P. Marttinen, J. Sirén, J. Tang, Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations, *BMC Bioinformatics* 9 (2008) 539.
- [4] W. Toussile, E. Gassiat, Variable selection in model-based clustering using multilocus genotype data, *Advances in Data Analysis and Classification* 3 (2) (2009) 109–134.
- [5] P. Massart, Concentration inequalities and model selection, Vol. 1896 of *Lecture Notes in Mathematics*, Springer-Verlag, Berlin, 2007.
- [6] L. Birgé, P. Massart, Minimal penalties for Gaussian model selection, *Probability Theory and Related Fields* 138 (1-2) (2007) 33–73.
- [7] S. Arlot, P. Massart, Data-driven calibration of penalties for least-squares regression, *Journal of Machine Learning Research* 10 (2009) 245–279.
- [8] C. Maugis, B. Michel, A non asymptotic penalized criterion for Gaussian mixture model selection, *ESAIM: P&S* Accepted for publication.
- [9] É. Lebarbier, Quelques approches pour la détection de rupture à horizon fini, Ph.D. thesis, Univ. Paris-Sud 11, F-91405 Orsay (Jul. 2002).
- [10] N. Verzelen, Adaptive estimation to regular Gaussian Markov random fields, Ph.D. thesis, Univ. Paris-Sud 11 (Dec. 2009).
- [11] F. Villers, Tests et selection de modèles pour l’analyse de données protéomiques et transcriptomiques, Ph.D. thesis, Univ. Paris-Sud 11 (2007).
- [12] E. K. Latch, G. Dharmarajan, J. C. Glaubitz, O. E. Rhodes Jr., Relative performance of Bayesian clustering software for inferring population substructure and individual assignment at low levels of population differentiation, *Conservation Genetics* 7 (2) (2006) 295.
- [13] A. P. Dempster, N. M. Lairdsand, D. B. Rubin, Maximum likelihood from incomplete data via the EM algorithm, *Journal of the Royal Statistical Society, Series B* 39 (1977) 1–38.
- [14] C. R. Genoveve, L. Wasserman, Rates of convergence for the Gaussian mixture sieve, *Ann. Statist.* 28 (4) (2000) 1105–1127.



## Appendix A. Metric entropy with bracketing

Let us state several results about entropy with bracketing, which will be used as tools to prove Proposition 1. They are mainly adapted from [14].

We consider a measurable space  $(A, \mathcal{A})$ , and  $\mu$  a  $\sigma$ -finite positive measure on  $A$ . We consider a model  $\mathcal{M}$ , which is a set of probability density functions with respect to  $\mu$ . All functions considered in the following will be positive functions in  $\mathbb{L}^1(\mu)$ .

**Lemma 4.** *Let  $\varepsilon > 0$ . Let  $[l, u]$  be a bracket in  $\mathbb{L}^1(\mu)$ , with  $\mathbf{h}$ -diameter less than  $\varepsilon$ , and containing  $s$ , a probability density function with respect to  $\mu$ . Then*

$$\int l d\mu \leq 1 \leq \int u d\mu \leq (1 + \varepsilon)^2.$$

*Proof.* First two inequalities are immediate, from  $l \leq s \leq u$ . For the last one, we use triangle inequality in  $\mathbb{L}^2(\mu)$ , and the definition of  $\mathbf{h}$ :

$$\begin{aligned} \int u d\mu &= \int \left( \sqrt{l} + \left( \sqrt{u} - \sqrt{l} \right) \right)^2 d\mu \\ &\leq \left( \sqrt{\int l d\mu} + \mathbf{h}(u, l) \right)^2 \\ &\leq (1 + \varepsilon)^2. \end{aligned}$$

□

**Lemma 5** (Bracketing entropy of product densities). *Let  $n \geq 2$ , and consider a collection  $(A_i, \mathcal{A}_i, \mu_i)_{1 \leq i \leq n}$  of measured space. For any  $1 \leq i \leq n$ , let  $\mathcal{M}_i$  be a collection of probability density functions on  $A_i$  fulfilling (M). Consider the product model*

$$\mathcal{M} = \{s = \otimes_{i=1}^n s_i; \forall 1 \leq i \leq n, s_i \in \mathcal{M}_i\}.$$

$\mathcal{M}$  contains density functions on  $A = \prod_{i=1}^n A_i$  with respect to  $\mu = \otimes_{i=1}^n \mu_i$ .

$\mathcal{M}$  fulfills (M) and, for any  $\delta > 0$ , if  $\varepsilon \geq (1 + \delta)^n - 1$  then

$$H_{[\cdot]}(\varepsilon, \mathcal{M}, \mathbf{h}) \leq \sum_{i=1}^n H_{[\cdot]}(\delta, \mathcal{M}_i, \mathbf{h}).$$

*Proof.* Let us consider some  $s = \otimes_{i=1}^n s_i$  in  $\mathcal{M}$ . For  $1 \leq i \leq n$ , let  $\mathcal{M}'_i, A'_i$  and a sequence  $(t_{i,k})_{k \geq 1}$  be such as needed for  $\mathcal{M}_i$  to verify (M). Then, with the choice  $t_k = \otimes_{i=1}^n t_{i,k}$  and  $A' = \prod_{i=1}^n A'_i$ , (M) is true for  $\mathcal{M}$  too.

Let  $\delta > 0$ . For any  $1 \leq i \leq n$ , let  $[l_i, u_i]$  a bracket containing  $s_i$ , with  $\mathbf{h}$ -diameter less than  $\delta$ . Let us set  $l = \otimes_{i=1}^n l_i$ , and  $u = \otimes_{i=1}^n u_i$ . Then  $s$  belongs to bracket  $[l, u]$ . We can compute its  $\mathbf{h}$ -diameter:

$$\begin{aligned} \mathbf{h}(l, u) &= \sqrt{\int_A \left( \sum_{j=1}^n \left( \prod_{i=1}^{j-1} \sqrt{l_i} \prod_{i=j}^n \sqrt{u_i} - \prod_{i=1}^j \sqrt{l_i} \prod_{i=j+1}^n \sqrt{u_i} \right) \right)^2 d\mu} \\ &\leq \sum_{j=1}^n \prod_{i=1}^{j-1} \sqrt{\int_{A_i} l_i d\mu_i} \prod_{i=j+1}^n \sqrt{\int_{A_i} u_i d\mu_i} \mathbf{h}(l_j, u_j) \\ &\leq \sum_{j=1}^n \delta (1 + \delta)^{n-j} = (1 + \delta)^n - 1 \end{aligned}$$

thanks to triangle inequality and Lemma 4 (empty products equal 1).

Let  $\varepsilon \geq (1 + \delta)^n - 1$ . For any  $1 \leq i \leq n$  consider a minimal covering of  $\mathcal{M}_i$  with brackets of  $\mathbf{h}$ -diameter less than  $\delta$ . With the previous process we can build a covering of  $\mathcal{M}$  with brackets of  $\mathbf{h}$ -diameter less than  $\varepsilon$ . So the minimal cardinality of such a covering verifies

$$N_{[\cdot]}(\varepsilon, \mathcal{M}, \mathbf{h}) \leq \prod_{i=1}^n N_{[\cdot]}(\delta, \mathcal{M}_i, \mathbf{h}).$$

□

**Lemma 6** (Bracketing entropy of mixture densities). *Let  $n \geq 2$ , and for any  $1 \leq i \leq n$ , let  $\mathcal{M}_i$  be a set of probability density functions, all on the same measured space  $(A, \mathcal{A}, \mu)$  and fulfilling (M). Let us consider the set of all mixture densities*

$$\mathcal{M} = \left\{ \sum_{i=1}^n \pi_i s_i : \pi = (\pi_i)_{1 \leq i \leq n} \in \mathbb{S}_{n-1}; \forall 1 \leq i \leq n, s_i \in \mathcal{M}_i \right\}.$$

Then  $\mathcal{M}$  fulfills (M), and for any  $\delta > 0$ ,  $\eta > 0$ , and  $\varepsilon \geq \delta + \eta + \delta\eta$ ,

$$H_{[\cdot]}(\varepsilon, \mathcal{M}, \mathbf{h}) \leq H_{[\cdot]}(\delta, \mathbb{S}_{n-1}, \mathbf{h}) + \sum_{i=1}^n H_{[\cdot]}(\eta, \mathcal{M}_i, \mathbf{h}).$$

*Proof.* First, let us note that  $\mathbb{S}_{n-1}$  is separable for its usual topology. Then, checking that  $\mathcal{M}$  fulfills (M) is easy, and we do not explicit it.

We do not develop either the proof of last relation, because it is exactly the same as in [14, proof of Theorem 2]. Let us just say that at the end we get, using our Lemma 4 instead of [14, Lemma 3],

$$\begin{aligned} \mathbf{h}^2(l, u) &\leq \eta^2 (1 + \delta)^2 + \delta^2 + 2\eta\delta(1 + \delta) \\ &\leq \varepsilon^2. \end{aligned}$$

□

Next result is just Lemma 2 from [14]:

**Lemma 7** (Bracketing entropy of the simplex). *Let  $n \geq 2$  be an integer. Let  $\mu$  be the counting measure on  $\{1, \dots, n\}$ . We identify any probability on  $\{1, \dots, n\}$  with its density  $s \in \mathbb{S}_{n-1}$  with respect to  $\mu$ . Then, if  $0 < \delta \leq 1$ ,*

$$H_{[\cdot]}(\delta, \mathbb{S}_{n-1}, \mathbf{h}) \leq (n-1) \ln \left( \frac{1}{\delta} \right) + \frac{\ln 2 + \ln(n+1) + n \ln(2\pi e)}{2}.$$

Preceding lemmas can be seen as a toolbox to calculate metric entropy with bracketing of complex models from the metric entropy of simpler elements. In our framework such an element is the collection of all Hardy-Weinberg genotype distributions at a given locus.

**Lemma 8** (Bracketing entropy of Hardy-Weinberg genotype distributions). *Suppose that, at some locus  $l$ , there exist  $A_l \geq 2$  different alleles. Let  $\Omega_l$  be the collection of all genotype distributions following Hardy-Weinberg model (2). Then  $\Omega_l$  fulfills (M), and for any  $\delta > 0$  and  $\varepsilon \geq \sqrt{2}\delta(2 + \delta)$ ,*

$$H_{[\cdot]}(\varepsilon, \Omega_l, \mathbf{h}) \leq H_{[\cdot]}(\delta, \mathbb{S}_{A_l-1}, \mathbf{h}).$$

*Proof.* (2) permits to associate a parameter  $\alpha = (\alpha_1, \dots, \alpha_{A_l}) \in \mathbb{S}_{A_l-1}$  to any density in  $\Omega_l$ . More generally, for any  $\alpha \in [0, 1]^{A_l}$ , we define a function

$$d_\alpha(x) = (2 - \mathbb{1}_{x_1=x_2}) \alpha_{x_1} \alpha_{x_2}$$

on the set of all genotypes  $x = \{x^1, x^2\}$  on  $A_l$  alleles. Consider some  $\delta > 0$  and  $d_\alpha \in \Omega_l$ . Let  $[l, u]$  be some bracket containing  $\alpha$ , with  $\mathbf{h}$ -diameter less than  $\delta$ . Then  $d_\alpha$  belongs to the bracket  $[d_l, d_u]$ . Let us calculate its diameter.

$$\begin{aligned} \mathbf{h}^2(d_l, d_u) &= \sum_{a=1}^{A_l} (u_a - l_a)^2 + \sum_{1 \leq a < b \leq A_l} \left( \sqrt{2u_a u_b} - \sqrt{2l_a l_b} \right)^2 \\ &\leq 2 \sum_{a=1}^{A_l} \sum_{b=1}^{A_l} \left( \sqrt{u_a u_b} - \sqrt{u_a l_b} + \sqrt{u_a l_b} - \sqrt{l_a l_b} \right)^2 \\ &\leq 2 \left( \sqrt{\sum_{a=1}^{A_l} u_a \sum_{b=1}^{A_l} (\sqrt{u_b} - \sqrt{l_b})^2} + \sqrt{\sum_{a=1}^{A_l} (\sqrt{u_a} - \sqrt{l_a})^2 \sum_{b=1}^{A_l} l_b} \right)^2 \\ &\leq 2((1 + \delta)\delta + \delta)^2 \end{aligned}$$

using Lemma 4. So  $\mathbf{h}(d_l, d_u) \leq \sqrt{2}\delta(2 + \delta)$ .

Let  $(\alpha^{(k)})_{k \geq 1}$  a sequence of elements of  $\mathbb{S}_{A_l-1} \cap \mathbb{Q}^{A_l}$ , which tends to  $\alpha$  for the usual topology as  $k$  tends to infinity. Then, for any genotype  $x = \{x^1, x^2\}$ ,  $\ln d_{\alpha^{(k)}}(x)$  tends to  $\ln d_\alpha(x)$ . Therefore  $\Omega_l$  fulfills (M).  $\square$

*Proof of Proposition 1.* Using (4) we see that a probability  $P_{(K,S)}(\cdot | \theta)$  is the product of a mixture density corresponding to the loci in  $S$ , and a product density in  $\bigotimes_{l \notin S} \Omega_l$  for the other loci. Let us call  $\mathcal{M}$  the collection of all mixtures of  $K$  densities in  $\bigotimes_{l \in S} \Omega_l$ .

We first deal with the non clustering loci. Using Lemma 5 and Lemma 8,  $\bigotimes_{l \notin S} \Omega_l$  fulfills (M). For any  $\varepsilon \in (0, 1)$ ,

$$\begin{aligned} H_{[\cdot]} \left( (1 + 2\sqrt{2}\varepsilon + \sqrt{2}\varepsilon^2)^{L-|S|} - 1, \bigotimes_{l \notin S} \Omega_l, \mathbf{h} \right) &\leq \sum_{l \notin S} H_{[\cdot]} \left( 2\sqrt{2}\varepsilon + \sqrt{2}\varepsilon^2, \Omega_l, \mathbf{h} \right) \\ &\leq \sum_{l \notin S} H_{[\cdot]} (\varepsilon, \mathbb{S}_{A_l-1}, \mathbf{h}). \end{aligned}$$

On the same way

$$H_{[\cdot]} \left( (1 + 2\sqrt{2}\varepsilon + \sqrt{2}\varepsilon^2)^{|S|} - 1, \bigotimes_{l \in S} \Omega_l, \mathbf{h} \right) \leq \sum_{l \in S} H_{[\cdot]} (\varepsilon, \mathbb{S}_{A_l-1}, \mathbf{h}).$$

We can apply Lemma 6, and get that  $\mathcal{M}$  fulfills (M) and

$$\begin{aligned} H_{[\cdot]} \left( (1 + 2\sqrt{2}\varepsilon + \sqrt{2}\varepsilon^2)^{|S|} (1 + \varepsilon) - 1, \mathcal{M}, \mathbf{h} \right) \\ \leq H_{[\cdot]} (\varepsilon, \mathbb{S}_{K-1}, \mathbf{h}) + K \sum_{l \in S} H_{[\cdot]} (\varepsilon, \mathbb{S}_{A_l-1}, \mathbf{h}). \end{aligned}$$

Lemma 5 again, applied to  $\mathcal{M}$  and  $\bigotimes_{l \notin S} \Omega_l$ , gives that  $\mathcal{M}_{(K,S)}$  fulfills (M), and for any  $\varepsilon \in (0, 1)$ ,

$$\begin{aligned} H_{[\cdot]}(\eta(\varepsilon), \mathcal{M}_{(K,S)}, \mathbf{h}) \\ \leq H_{[\cdot]}(\varepsilon, \mathbb{S}_{K-1}, \mathbf{h}) + K \sum_{l \in S} H_{[\cdot]}(\varepsilon, \mathbb{S}_{A_l-1}, \mathbf{h}) + \sum_{l \notin S} H_{[\cdot]}(\varepsilon, \mathbb{S}_{A_l-1}, \mathbf{h}). \end{aligned}$$

At this point, we use Lemma 7:

$$\begin{aligned} H_{[\cdot]}(\eta(\varepsilon), \mathcal{M}_{(K,S)}, \mathbf{h}) &\leq \left( \ln\left(\frac{1}{\varepsilon}\right) + \frac{\ln(2\pi e)}{2} \right) D_{(K,S)} \\ &\quad + \frac{\ln(n+1) + \ln(4\pi e)}{2} (1 + K|S| + L - |S|). \end{aligned}$$

□

## Appendix B. Establishing the penalty

First, we need to establish some properties of function  $\eta$ .

**Lemma 9** (Properties of function  $\eta$ ). *We consider the function  $\eta$  defined in Proposition 1, from  $\mathbb{R}_+$  into  $\mathbb{R}_+$ .  $\eta$  is nonnegative, increasing and convex.  $\eta(0) = 0$  and  $\eta'(0) = 2\sqrt{2}L + 1$ .*

*Proof.* Setting  $u(x) = 1 + 2\sqrt{2}x + \sqrt{2}x^2$ , we can write  $\eta(x) = (1+x)u(x)^L - 1$ . Then, calculus gives

$$\eta'(x) = (2L+1)u(x)^L + 2L(\sqrt{2}-1)u(x)^{L-1}.$$

Since  $u$  is positive on  $(0, +\infty)$ ,  $\eta$  is increasing. But  $\eta(0) = 0$ , so  $\eta$  is nonnegative on  $\mathbb{R}_+$ . We also have  $\eta'(0) = 2\sqrt{2}L + 1$ . Next,

$$\eta''(x) = 2\sqrt{2}(1+x) \left( (2L^2 + L)u(x)^{L-1} + 2L(L-1)(\sqrt{2}-1)u(x)^{L-2} \right)$$

which is positive on  $\mathbb{R}_+$ . □

*Proof of Proposition 2.* Let  $0 < \sigma \leq \eta(1)$ , and  $\delta = \eta^{-1}(\sigma)$ . Then, for any  $u \in \mathcal{M}_m$ ,

$$\begin{aligned} &\int_0^\sigma \sqrt{H_{[\cdot]}(x, \mathcal{M}_m(u, \sigma), \mathbf{h})} dx \\ &\leq \sum_{j=1}^{\infty} \int_{\eta(2^{-j}\delta)}^{\eta(2^{-j+1}\delta)} \sqrt{H_{[\cdot]}(x, \mathcal{M}_m, \mathbf{h})} dx \\ &\leq \sum_{j=1}^{\infty} (\eta(2^{-j+1}\delta) - \eta(2^{-j}\delta)) \sqrt{C_m - D_m \ln \delta + D_m j \ln 2} \\ &\leq \eta(\delta) \sqrt{C_m - D_m \ln \delta} \\ &\quad + \sqrt{D_m \ln 2} \sum_{j=1}^{\infty} \sqrt{j} (\eta(2^{-j+1}\delta) - \eta(2^{-j}\delta)). \end{aligned}$$

We deal with the last term of this sum in the following way:

$$\begin{aligned} \sum_{j=1}^{\infty} \sqrt{j} (\eta(2^{-j+1}\delta) - \eta(2^{-j}\delta)) &\leq \sum_{j=1}^{\infty} j (\eta(2^{-j+1}\delta) - \eta(2^{-j}\delta)) \\ &= \sum_{k=1}^{\infty} \eta(2^{-k+1}\delta) \\ &\leq \sum_{k=1}^{\infty} 2^{-k+1}\eta(\delta) = 2\sigma. \end{aligned}$$

So

$$\int_0^{\sigma} \sqrt{H_{[\cdot]}(x, \mathcal{M}_m(u, \sigma), \mathbf{h})} dx \leq \phi_m(\sigma).$$

Since  $\eta$  is increasing,  $\phi_m(x)/x$  is decreasing. To check that  $\phi_m$  is nondecreasing, it is enough to prove that function  $f(x) = x\sqrt{b - \ln \eta^{-1}(x)}$  is nondecreasing on  $(0, \eta(1)]$ , where  $b = \frac{C_m}{D_m}$ . From (16), we get  $C_m > \frac{\ln(2\pi e)}{2} D_m > D_m$ , so  $b > 1$ . Calculus gives

$$f'(x) = \sqrt{b - \ln \eta^{-1}(x)} - \frac{x}{2\eta^{-1}(x) \eta'(\eta^{-1}(x)) \sqrt{b - \ln \eta^{-1}(x)}}.$$

$\eta$  is convex on  $(0, 1]$ , and that entails  $\frac{\eta(x)}{x\eta'(x)} \leq 1$ . So, for any  $y \in (0, 1]$ ,

$$\sqrt{b - \ln y} f'(\eta(y)) \geq b - \ln y - 1 > 0.$$

□

*Proof of Lemma 1.* (I) entails that, for any  $\sigma > 0$  such that  $\sqrt{n}\sigma^2 > \phi_m(\sigma)$ ,  $\sigma > \sigma_m$ . So, we look when  $\sqrt{n} > \frac{\phi_m(\eta(1))}{\eta^2(1)}$ .

For all  $1 \leq l \leq L$ ,  $A_l \geq 2$ . Since  $\frac{1}{2}(\ln 2 + \ln(1+x)) \leq x-1$  for  $x \geq 2$ , we get the following bounds

$$\frac{1 + \ln(2\pi)}{2} D_m \leq C_m \leq \left(2 + \ln(2\pi) + \frac{\ln 2}{2}\right) D_m. \quad (\text{B.1})$$

Therefore

$$\frac{\phi_m(\eta(1))}{\eta^2(1)} < \frac{4\sqrt{D_m}}{2(1 + 3\sqrt{2})^L - 1}$$

On another hand, we have

$$D_m \leq K L M.$$

So, since  $\phi_m(x)/x^2$  is decreasing,  $\sigma_m < \eta(1)$  as soon as  $n > \xi^2 K$ . This is true when  $\xi < 1$ , since  $K \leq n$ : the number of clusters is not bigger than the number of individuals. □

*Proof of Lemma 2.* We define  $\delta = 1/2$ , from which  $e^{-x_m} = \delta^{D_m}$ . If we consider the collection  $\mathbb{M}$ , we can discern two cases:  $K = 1$  and  $S = \emptyset$ , or  $K \geq 2$  and

$S \neq \emptyset$ . So, using (9),

$$\begin{aligned}
\sum_{m \in \mathbb{M}} e^{-x_m} &= \delta^{\sum_{l=1}^L (A_l - 1)} \left( 1 + \sum_{S \neq \emptyset} \sum_{K \geq 2} \left( \delta^{1 + \sum_{l \in S} (A_l - 1)} \right)^{K-1} \right) \\
&= \delta^{\sum_{l=1}^L (A_l - 1)} \left( 1 + \sum_{S \neq \emptyset} \frac{\delta^{1 + \sum_{l \in S} (A_l - 1)}}{1 - \delta^{1 + \sum_{l \in S} (A_l - 1)}} \right) \\
&\leq \delta^L \left( 1 + \frac{\delta}{1 - \delta} \sum_{S \neq \emptyset} \delta^{|S|} \right) \\
&= \delta^L (1 + \delta)^L.
\end{aligned}$$

□

*Proof of Lemma 3.* Since  $\eta$  is a convex function and  $\eta'(0) = 2\sqrt{2}L + 1$ , we have

$$\eta^{-1}(2) \leq \frac{2}{2\sqrt{2}L + 1} \leq \frac{1}{\sqrt{2}L}.$$

Then

$$\eta\left(\frac{1}{\sqrt{2}L}\right) \leq 2 \left( 1 + \frac{2 + 1/\sqrt{2}}{L} \right)^L \leq 2 \exp\left( 2 + \frac{1}{\sqrt{2}} \right)$$

and, using again the convexity of  $\eta$ , for any  $0 \leq x \leq 2$ ,

$$\begin{aligned}
\eta^{-1}(2) &\geq \frac{2}{\sqrt{2}L} \left( \eta\left(\frac{1}{\sqrt{2}L}\right) \right)^{-1} \geq \frac{1}{\sqrt{2}L} \exp\left\{ -\left( 2 + \frac{1}{\sqrt{2}} \right) \right\} \\
\eta^{-1}(x) &\geq \frac{x}{2} \eta^{-1}(2) \geq \frac{x}{2\sqrt{2}L} \exp\left\{ -\left( 2 + \frac{1}{\sqrt{2}} \right) \right\}.
\end{aligned}$$

So for any  $0 \leq x \leq \eta(1)$ ,

$$-\ln \eta^{-1}(x) \leq 2 + \frac{1}{\sqrt{2}} + \frac{3 \ln 2}{2} + \ln L - \ln \min(x, 2).$$

On another hand, (17) and (B.1) entail

$$\tilde{\sigma}_m \geq C_1 \sqrt{\frac{D_m}{n}} \tag{B.2}$$

where  $C_1 = 2\sqrt{\ln 2} + \sqrt{\frac{1 + \ln(2\pi)}{2}} > 2\sqrt{2}$ . Since  $D_m \geq L$ ,

$$-\ln \eta^{-1}(\tilde{\sigma}_m) \leq 2 + \frac{1}{\sqrt{2}} + \max\left( \frac{1}{2} \ln n + \frac{1}{2} \ln L, \frac{\ln 2}{2} + \ln L \right).$$

Therefore, using (18),

$$\begin{aligned}
\sigma_m^2 + \frac{x_m}{n} &\leq \frac{D_m}{n} \left( \frac{1}{2} + \left( 2\sqrt{\ln 2} + \sqrt{2 + \ln(2\pi) + \frac{\ln 2}{2} - \ln \eta^{-1}(\tilde{\sigma}_m)} \right)^2 \right) \\
&\leq \frac{D_m}{n} \left( \frac{1}{\sqrt{2}} + 2\sqrt{\ln 2} + \sqrt{4 + \ln(2\pi) + \frac{\sqrt{2} + \ln 2}{2}} \right. \\
&\quad \left. + \sqrt{\max\left(\frac{\ln n + \ln L}{2}, \frac{\ln 2}{2} + \ln L\right)} \right)^2 \\
&\leq \frac{D_m}{n} \left( 5 + \sqrt{\max\left(\frac{\ln n + \ln L}{2}, \frac{\ln 2}{2} + \ln L\right)} \right)^2.
\end{aligned}$$

□