

# Non-nested models?

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Suppose we have the obtained a likelihood function for the parameter  $\vartheta = (\phi, \psi)$  given the data  $x$ :

$$\mathcal{L}(\vartheta; x) = \mathbb{P}_{\vartheta}\{x\}.$$

The parameter  $\vartheta$  lies in the parameter space

$$\Theta = \{(\phi, \psi) : \phi \in \{0, 1/2, 1\}, \psi \in [0, 1]\}.$$

We want to determine whether the parameter  $\vartheta$  lies within the subspace

$$\vartheta \in \Theta_0 = \{0, 0\} \cup \{(\phi, \psi) : \phi \in \{1/2, 1\}, \psi \in [0, 1]\}$$

or

$$\vartheta \in \Theta_1 = \{(\phi, \psi) : \phi = 0, \psi \in (0, 1]\},$$

(where the former responds to the case where there is no somatic mutation, i.e., healthy cells do not differ from tumor cells in this region of the DNA, and the latter reflects the situation where a somatic mutation occurred, i.e., tumor cells differ from healthy cells). See Figure 1 for a graphical depiction. I feel that the appropriate null- and alternative hypothesis are

$$H_0 : \vartheta \in \Theta_0 \text{ (no somatic mutation)} \quad \text{vs.} \quad H_1 : \vartheta \in \Theta_1 \text{ (somatic mutation)}.$$

My question is: is this a non-nested case? Or would the classical likelihood ratio test do?

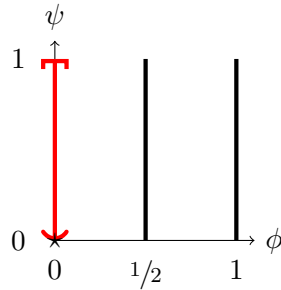


Figure 1: The parameter space  $\Theta$ . The red interval  $(0, 1]$  at  $\phi = 0$  is  $\Theta_1$  and denotes the cases where a somatic mutation occurred. The parameters related to the situation where no mutation occurred are depicted with black, including the origin  $(0, 0)$  which is for clarity shown here with a  $\star$ .