

$F_{ROH}$  medio

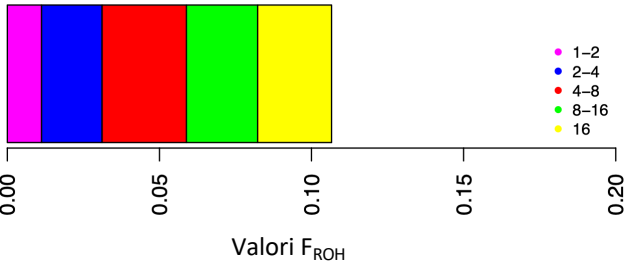
$H_e$  Attesa

$H_o$  Osservata

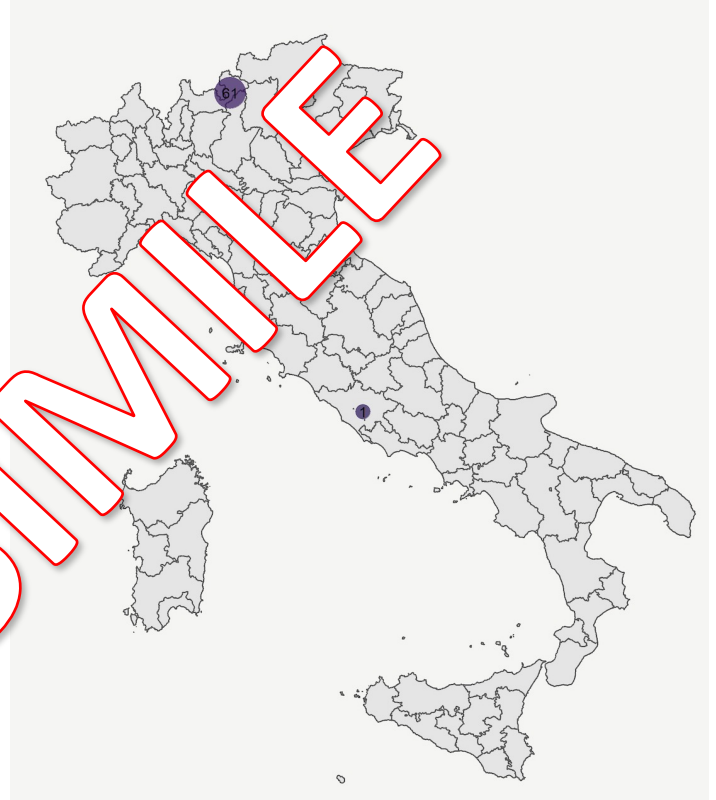
N° allevamenti

N° soggetti

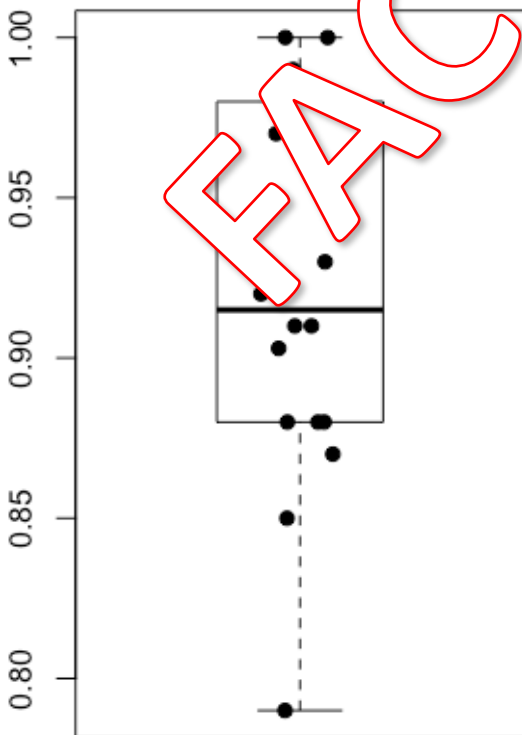
Classi  $F_{ROH}$



Distribuzione allevamenti



Distribuzione  
Componente maggiore  
del background  
genomico



Distanze genetiche

