

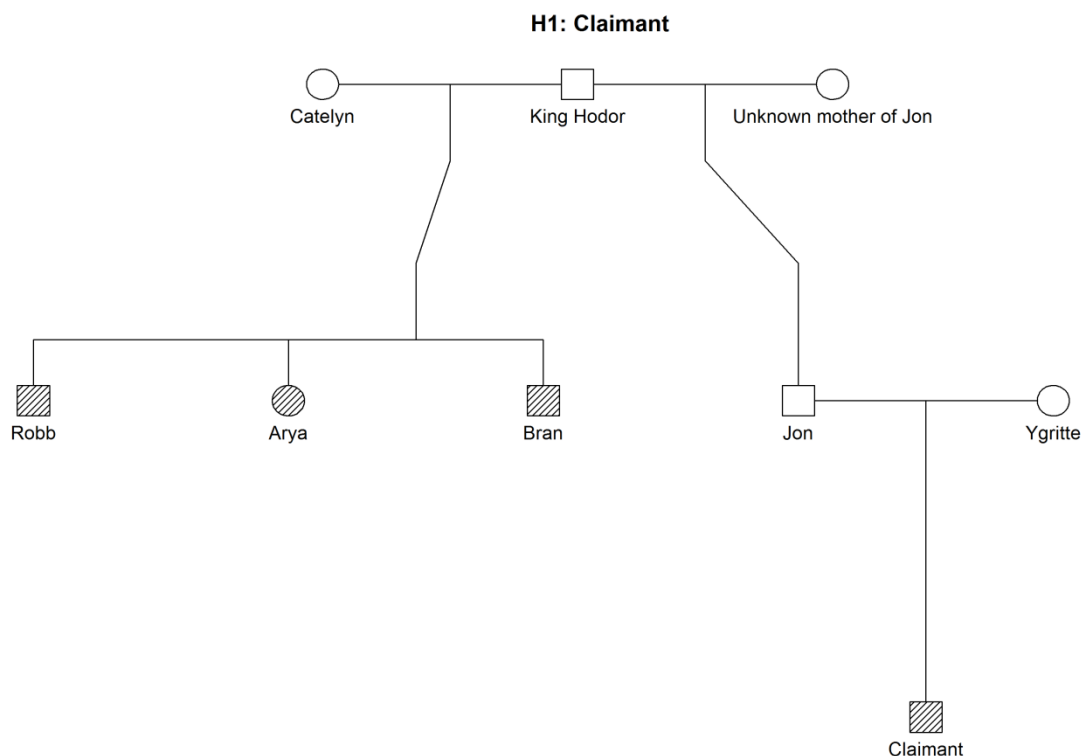
## ESWG PAPER CHALLENGE 2018

### *Part 1 : Case – A claim to the throne*

This year's paper challenge involves an ancient tale from a realm known as Westeros. The history has it that a claimant to the throne presents himself. He proposes that he is the grandchild of the deceased king. At the time, the allegations could not be ascertained and the claimant was regarded as a false pretender.

Using modern DNA techniques we are able to obtain samples and results from three known descendants of the King as well as from the Claimant.

Conduct a kinship analysis to uncover whether the Claimant is related to the three descendants of the king the way he claims. The pedigree corresponding to the claimant's allegations is depicted below. In the alternative hypothesis, the Claimant is unrelated to the descendants who are themselves still full siblings.





### *Part 2 : Simulations (Optional)*

Following the results, your lab decides to perform a simulation study to evaluate whether including further relatives could improve the results. We may assume we have already analyzed all available genetic markers. Evaluate the following scenarios,

- a) Exhumation of the mother of the descendants (Catelyn).
- b) Exhumation of the mother of the Claimant (Ygritte).
- c) Exhumation of the King (Hodor).
- d) Exhumation of all the above mentioned individuals.

Report the median of your simulations as well as the probability that the LR will exceed 1000 for each given scenario. Perform at least 1000 simulations.

What is your conclusion regarding the four possible scenarios? For instance, can we reach a more certain conclusion by only exhuming one extra individual (a-c) or do we need to exhume all three of them (d).

### *Details*

In Part 1 you should submit a likelihood ratio (LR) for each autosomal marker and the total LR combining the individual markers. Also, submit a LR for the results from the Y chromosomal haplotype. Present a conclusion based on the joint results from the autosomal and Y chromosomal markers.

The autosomal [typing results](#) and frequency data ([Plain frequencies](#) and [Familias database](#)) are available in the given links. The Y-results are available as an [YHRD compatible file](#). All individuals can be assumed to be of Western European ancestry. The typing results are also collected into a single file available at [http://familias.name/ESWG/ESWG\\_Collected\\_Data\\_2018.xlsx](http://familias.name/ESWG/ESWG_Collected_Data_2018.xlsx).

Please use the supplied Excel questionnaire to fill in your answers.