

# AncesTrim - a tool for trimming complex pedigrees

**Julia Niskanen<sup>1, 2, 3</sup>, Elina Salmela<sup>1, 2, 3, 4</sup>, and Hannes Lohi<sup>1, 2, 3</sup>**

**1** Department of Veterinary Biosciences, University of Helsinki, Helsinki, Finland **2** Research Programs Unit, Molecular Neurology, University of Helsinki, Helsinki, Finland **3** The Folkhälsan Institute of Genetics, Helsinki, Finland **4** Department of Biosciences, University of Helsinki, Helsinki, Finland

DOI: [10.21105/joss.00179](https://doi.org/10.21105/joss.00179)

## Software

- [Review ↗](#)
- [Repository ↗](#)
- [Archive ↗](#)

## Licence

Authors of JOSS papers retain copyright and release the work under a Creative Commons Attribution 4.0 International License ([CC-BY](#)).

## Summary

AncesTrim (Niskanen, Salmela, and Lohi 2017) is a Python tool for trimming complex pedigrees. Some pedigree data can have an inherently complicated structure with a high level of inbreeding, which makes visualization of such data difficult. AncesTrim reduces the complexity of pedigrees while preserving critical relatedness structures, allowing the pedigree to be displayed in a more efficient way.

## References

Niskanen, J., E. Salmela, and H. Lohi. 2017. “AncesTrim - a Tool for Trimming Complex Pedigrees.” <https://github.com/JNisk/AncesTrim>.