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**van de Pol, Martijn, Brouwer, Lyanne, and Cockburn, Andrew 2020 R package
HIPHOP: parentage assignment using bi-allelic genetic markers.
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<https://CRAN.R%2Dproject.org/package=hiphop>

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What is R package hiphop for?

R package hiphop is based on the hiphop test that can be used for parentage assignment using a simple exclusion method for biallelic markers, even when comparing among close relatives. The rationale behind this parentage assignment method is described in detail in Cockburn et al. in revision *Molecular Ecology Resources* (for full reference use citation("hiphop")).

The basic idea

The basic idea behind the hiphop parentage assignment is that we can compare the genotypes of any combination of offspring-potential dam and sire (i.e. genetic mother or fathers) by comparing the exclusion scores of these individuals at bi-allelic markers. Previous methods focused on exclusion based on the Homozygous Opposite Test (HOT; Huisman 2017; <https://doi.org/10.1111/1755-0998.12665>). HOT compares the genotype of an offspring with a potential parent: a mismatch is scored when both the offspring and parent are homozygous, but for different alleles. Cockburn et al. suggested an additional exclusion criterion HIPHOP (Homozygous Identical Parents, Heterozygous Offspring are Precluded), which compares the genotype of an offspring with both potential parents (ie. a dyad of potential dam and potential sire): a mismatch is scored when the offspring is heterozygous and both parent are homozygous for the same allele. The HOT and HIPHOP scores are by default calculated as ratios: the HOT score is the number of HOT mismatches divided by the number of loci at which the offspring is homozygote, while the HIPHOP score is the number of HIPHOP mismatches divided by the number of loci the offspring is heterozygotes (this standardization is important as individuals can differ substantially in the number of loci at which they are homo- or hetero-zygote). The HOT and HIPHOP scores can be combined to provide information about the total of mismatches and is proposed as an improved exclusion criterion for parentage assignment. Finally, in species where there is contextual information (e.g. seen egg laying, lactating) that the social mother (father) is always the genetic mother (father) it is possible to condition the paternity (maternity) assignment on the dam (sire) being the social mother (father).

Installation

You can install the released version of hiphop from [CRAN](#) using `install.packages("hiphop")` and start using it with `library(hiphop)`

Vignette with worked examples

The introduction vignette associated with the package gives a worked example on the data used in Cockburn et al. paper.

Questions about the package and reporting bugs

Please ask all questions about the package and report bugs or suggestions for improvement on: <https://groups.google.com/d/forum/r-hiphop> We aim to answer these questions as quickly as possible.