Package 'fbstHWE'

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Type Package

Title FBST for Hardy-Weinberg Equilibrium Test

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Description

This package contains a straightforward method for the multiallelic Hardy-Weinberg Equilibrium (HWE) test. The core theory for the proposed method is given by the Full Bayesian Significance Test (FBST), an intuitive Bayesian approach which does not assign positive probabilities to zero measure sets when testing sharp hypotheses.

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R topics documented:

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Details

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Function: `<fbstHWE>`

Author(s)

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References

1. M.S.Lauretto, F.Nakano, S.R.Faria Jr, C.A.B.Pereira, J.M.Stern. A straightforward multiallelic significance test for the Hardy-Weinberg equilibrium law. Genetics and Molecular Biology 32(3), 619-625, 2009.

2.Pereira, C.A.B., Stern, J.M. Evidence and Credibility: Full Bayesian Significance Test for Precise Hypotheses. Entropy 1, 99-110, 1999.

3.C.A.B.Pereira, J.M.Stern, S. Wechsler. Can a significance test be genuinely Bayesian? Bayesian Analysis 3(1), 79-100, 2008.

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fbstHWE	*Full Bayesian Significance Test (FBST) for the Hardy-Weinberg Equilibrium*

Description

Performs the test for Hardy-Weinberg Equilibrium (HWE) in a locus with several alleles A1, A2,..., Ak, k>=2, and returns the hypothesis evidence Ev(H).

Usage

```
fbstHWE(X, delta = 0.005, simulate.p.value = FALSE, B = 200, verbose = FALSE)
```

Arguments

X   vector of genotype counts in a lower triangular form:

$$X = c(\qquad x11,$$
$$x21, x22,$$
$$x31, x32, x33,$$
$$...$$
$$xk1, xk2, ..., xkk$$

where k is the number of alleles

X may also contain a square matrix with genotype counts.

delta   precision parameter 0 < delta < 1, it corresponds to the maximum length for the 95% confidence interval ev(H)

simulate.p.value

boolean parameter indicating whether to compute the Empirical p-value by Monte Carlo simulation. If FALSE, only asymptotic p-value is returned.

B   number of samples to be drawn for the Empirical p-value computation

verbose   verbose method. If TRUE, prints the estimated evidences and respective preci-

sions for simulated samples during the computation of empirical p-value computation

Details

Given k alleles A1, A2, ..., Ak, k>=2, in a locus, and their genotype counts in lower triangular form X = (x_ij), 1<=j<=i<=k, this function computes the evidence for the Hardy-Weinberg Equilibrium) HWE.

The parameter of interest, denoted by theta_ij, is the population relative frequencies of genotypes AiAj (1<=j<=i<=k). Assuming a multinomial model for x and a Dirichlet(1,1,...,1) priori for theta, the posterior p.d.f is f(theta | x) = Dirichlet(x_11+1, x_12+1, ..., x_kk+1).

Parameter space: THETA = theta = (theta_ij), 1<=j<=i<=k | 0 <= thetax_ij <= 1, sum(theta)=1

Parameter space under HWE: H = theta in THETA | there exists a vector p=(p_1, p_2,..., p_k), 0 <= p <= 1, sum(p)=1, such that: theta_ij = (p_i)^2 if i=j; theta_ij = 2*p_i*p_j if i<>j

The evidence measure against the hypothesis is computed in two steps: 1) compute f_0 = max_H f(theta|x) where f(theta|x) denotes the posterior probability density function.

2) compute the integral evb = [int_H f(theta|x) dtheta] / [int_THETA f(theta|x) dtheta] where T = theta in THETA | f(theta | x) > f_0

The evidence measure suporting the hypothesis is: evid = 1 - evb

Value

`evid`	evidence of HWE hypothesis
`prec`	95% confidence interval length for evid
`p.value`	estimated asymptotic p-value
`emp.p.value`	empirical p-value (=NA if simulate.p.value=FALSE)

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References

1. M.S.Lauretto, F.Nakano, S.R.Faria Jr, C.A.B.Pereira, J.M.Stern. A straightforward multiallelic significance test for the Hardy-Weinberg equilibrium law. Genetics and Molecular Biology 32(3), 619-625, 2009.

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Examples

```
#################################################
# Example 1:
# Extracted from Louis and Dempster (1987),
# An exact test for Hardy-Weinberg and multiple alleles.
# Biometrics 43:805-811
#

X = c(
```

```
  0,
  3,  1,
  5, 18,  1,
  3,  7,  5,  2)

EvFBST1 = fbstHWE(X, simulate.p.value=TRUE, B=100, verbose=TRUE)
print(c(EvFBST1$evid, EvFBST1$delta, EvFBST1$p.value, EvFBST1$emp.p.value))
```