

**name**{CPWFABC}

**packageTitle**{Changing selection in time-sampled data }

**packageDescription**{detects allele trajectories of changing selection from those of constant selection using ABC model choice, and jointly estimates the position of a change point as well as the strength of both corresponding selection coefficients (and dominance for diploid cases) using Wright-Fisher ABC methods}

**input**{

**# variable inputs**

N	population size (number of chromosomes: N individuals for haploids and N/2 individuals for diploids) (1000 by default)
sample_times	vector of exact sampling times in generations
N_sample	vector of sample sizes in number of chromosomes
min_freq	data ascertainment of a minimum frequency at one of the sampling time points (0 for no condition and 1 to condition on fixation)
N_allele	data frame of observed SNPs in row (with rownames =SNP names, column=sampled numbers))
max_sims	maximum number of simulations to do before giving up (1 by default)
no_sim	number of simulated datasets to be created (1e6 by default)
best_sim	number of best simulations to be used for estimation and model choice (1e3 by default)
set_seed	reproducible numbers (TRUE by default)
post_graph	Posterior densities of M0 and M1 (FALSE by default)
post_2D_M1	2D posteriors of M1 estimates (s1&s2, s1&CP, s2&CP) (FALSE by default)
h_fixed	h to be fixed in diploid populations (TRUE by default)
h_given	h to be used if fixed (0.5 by default)

**# fixed inputs**

ploidy	1 for haploids, 2 for diploids
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**# Assumptions**

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j          number of SNP appearing at time t0 in the
           population (given as observed initial frequency
           in N_allele * population size, except if j<1
           given as j=1)
t0         time where SNP appears in generations (same as
           data given in N_allele)
s_start    time in generation when selection starts (s=0
           before s_start) (same as t0)
}

```

### output{

```

PDFs of prior graphs for simulated parameters
Text files of summary of results (SNP_name M1_posterior_BF
    M0_estimate_s1 (M0_estimate_h) M1_estimate_s1 M1_estimate_
s2 M1_estimate_CP (M1_estimate_h))
PDFs of posterior graphs of parameters of interest (if TRUE)
PDFs of 2D posterior graphs of parameters of interest (if TRUE)
}

```

### functions{

#### WF\_2s\_simulator{

```

usage
{simulates a Wright-Fisher trajectory with changing selection or
constant selection}
arguments
{N,t,fluc_t,j,t0,s1,s2,h,s_start,ploidy,N_sample,sample_times,ma
x_sims}
}

```

#### CP\_WFABC\_diploid\_modelchoice{

```

usage
{detects allele trajectories of changing selection from those of
constant selection using ABC model choice, and jointly estimates
the position of a change point as well as the strength of both
corresponding selection coefficients and dominance for a diploid
population using Change-Point Wright-Fisher ABC methods}
arguments
{N,h_fixed,h_given,sample_times,N_sample,N_allele,min_freq,max_s
ims,no_sim,best_sim,set_seed,post_graph,post_2D_M1}
}

```

#### CP\_WFABC\_haploid\_modelchoice{

```

usage

```

```
{detects allele trajectories of changing selection from those of
constant selection using ABC model choice, and jointly estimates
the position of a change point as well as the strength of both
corresponding selection coefficients for a haploid population
using Change-Point Wright-Fisher ABC methods}
arguments
{N,sample_times,N_sample,N_allele,min_freq,max_sims,no_sim,best_
sim,set_seed,post_graph,post_2D_M1}
}
}
```

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### references{

```
Shim, H., Laurent, S., Matuszewski, S., Foll, M., Jeffrey D
Jensen (in review) Detecting and quantifying changing selection
intensities from time-sampled polymorphism data.
Foll, M.*, Shim, H.*, & Jeffrey D Jensen (2014b) WFABC: A
Wright-Fisher ABC-Based Approach for Inferring Effective
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Foll, M., Poh, Y.-P., Renzette, N., Ferrer-Admetlla, A., Bank,
C., Shim, H., Malaspinas, A.S., Ewing, G., Liu, P., Wegmann, D.,
Caffrey, D.R., Zeldovich, K.B., Bolon, D.N., Wang, J.P.,
Kowalik, T.F., Schiffer, C.A., Finberg, R.W. & Jensen, J.D.
(2014a) Influenza Virus Drug Resistance: A Time-Sampled
Population Genetics Perspective. PLoS Genetics, 10, e1004185.
}
```

**keyword**{ population genetics; fluctuating selection; change  
point analysis; time-sampled data; approximate Bayesian  
computation; Wright-Fisher model; experimental design }

**code**{<http://jensenlab.epfl.ch/page-86730-en.html>}

### examples{

```
see Example_diploid_model.R
see Example_haploid_model.R
}
```