iMKT Pipeline

Brief intro about why we developed the package. The importance of detecting adaptation, and the many MKT derived methodologies. Take from paper.

Explain also that iMKT faces this variety of methodologies, and is able to compute several tests in order to detect adaptation in diverse situations.

In addition, it also provides a way to quantify negative selection, which may overlap with signals of positive selection in the target region, causing the failing of certain MK tests.

Loading the package and checking test data

First of all, install (if this is not done yet) and load the package. Notice that iMKT package includes two sample dataframes named mydafdata and mydivergencedata which are the ones used in this tutorial. This makes easier to replicate the vignettes in order to better understand all the package functionalities.

```
## Load package
# install.packages("devtools")
# devtools::install_qithub("serqihervas/iMKT")
library(iMKT)
## Sample daf data
head(mydafdata)
#>
       daf
              Pi
                    P0
#> 1 0.025 22490 17189
#> 2 0.075 3217 4780
#> 3 0.125
            1616
                  2874
#> 4 0.175
             999
                  2088
#> 5 0.225
                  1685
             754
#> 6 0.275
             679
                  1443
## Sample divergence data
mydivergencedata
#>
          mi
                Di
                       m0
                              D0
#> 1 2598805 54641 620019 52537
```

The iMKT package includes several funcions, classified as follows:

- MKT derived methodologies calculation
 - standard(): Standard MKT
 - FWW(): FWW correction
 - DGRP(): DGRP correction
 - asymptoticMK(): Asymptotic MKT
 - iMK(): integrative MKT
 - completeMKT(): perform all previous tests
- iMK using PopFly and PopHuman data

- loadPopFly(): load PopFlyData
- loadPopHuman(): load PopHumanData
- PopFlyAnalisys(): perform any test using PopFlyData
- PopHumanAnalysis(): perform any test using PopHumanData
- Miscelanious
 - multipleDatasets(): analyze all datasets in your working directory
 - checkInput(): check data before performing analyses
 - themePublication(): output plots and tables styling

Each function has an associated help page with its description, details about its parameters, usage, examples and so on. Rembember you can access it writting?? and the function name (or ??library::function) in your console (example: ??iMKT::standard).

This vignette focuses on the first category of functions: "MKT derived methodologies calculation". Specifically, it contains examples of each function using the sample data described above. However, the last section of the document provides an example on how to use the *multipleDatasets()* function. For details about functions from "iMKT using PopFly and PopHuman data" category check the corresponding vignette.

Performing MKT derived methodologies calculation

The diverse functions from this category have two common input parameters which are required to perform the corresponding test:

- daf: data frame containing DAF, Pi and P0 values (mydafdata)
- divergence: data frame containing divergent and analyzed sites for selected (i) and neutral (0) classes (mydivergencedata)

Standard MKT

Brief theoretical description about MKT

The standard() function uses daf and divergence input parameters and returns as output a list containing:

- alpha symbol: estimate of alpha using the standard MKT
- Fisher exact test P-value: p-value obtained using the Fisher exact test on a 2x2 contingency table (MKT table)
- MKT table: table containing the number of polymorphic and divergent sites for neutral and selected classes.
- Divergence metrics: table containing estimates of Ka, Ks, omega, omegaA, omegaD.

```
standard(daf=mydafdata, divergence=mydivergencedata)
#> $alpha.symbol
#> [1] 0.2364499
#>
#> *Fishers exact test P-value*
#> [1] 1.480943e-183
```

```
#>
#> $`MKT table`
#>
#>
#>
                     Polymorphism
                                   Divergence
                                          52537
#> Neutral class
                            45101
                            35816
#> Selected class
                                          54641
#>
#> $`Divergence metrics`
#>
#>
#>
           Kα
                       Ks
                                           omegaA
                                                      omeqaD
                                omega
   0.0210254
              0.0847345
                          0.2481331
                                         0.058671
                                                    0.189462
```

FWW correction

Alpha estimates can be biased by the segregation of slighlty deleterious substitutions. One method to partially controlled its effects is to remove low frequency polymorphisms from the analysis, as proposed by Fay et al. (2001).

The **FWW()** function uses daf and divergence input parameters, along with a default list of cutoffs (0, 0.05, 0.1) and returns as output a list containing:

- Results: alpha estimates (and their associated Fisher exact test P-value) for each cutoff.
- Divergence metrics: global metrics (Ka, Ks, omega) and estimates by cutoff (omegaA, omegaD)
- MKT tables: tables containing the number of polymorphic and divergent sites for neutral and selected classes for each cutoff.

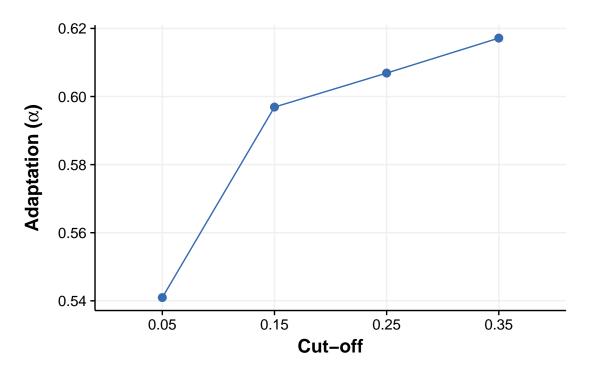
```
FWW(daf=mydafdata, divergence=mydivergencedata)
#> $Results
#>
                  alpha.symbol Fishers exact test P-value
                     0.2364499
\# Cutoff = 0
                                          1.480943e-183
\# Cutoff = 0.05
                     0.5409548
                                            0.000000e+00
#> Cutoff = 0.1
                     0.5798139
                                             0.000000e+00
#> $`Divergence metrics`
#> $`Divergence metrics`$`Global metrics`
#>
            Ka
                Ks
                             omega
#> 1 0.02102543 0.0847345 0.2481331
#>
#> $`Divergence metrics`$`Estimates by cutoff`
                 omegaA.symbol omegaD.symbol
\# Cutoff = 0
                    0.05867104
                                   0.1894620
\# Cutoff = 0.05
                    0.13422877
                                    0.1139043
                    0.14387102
\# Cutoff = 0.1
                                   0.1042621
#>
#>
#> $`MKT tables`
#> $`MKT tables`$`Cutoff = 0`
```

```
#>
#>
#> Table: cutoff
#>
                   Polymorphism
                                 Divergence
#> -----
                   -----
#> Neutral class
                          45101
                                       52537
#> Selected class
                          35816
                                       54641
#>
#> $`MKT tables`$`Cutoff = 0.05`
#>
#>
#> Table: cutoff
#>
#>
                   Polymorphism
                                 Divergence
                          27912
                                       52537
#> Neutral class
#> Selected class
                          13326
                                       54641
#>
#> $`MKT tables`$`Cutoff = 0.1`
#>
#>
#> Table: cutoff
#>
#>
                   Polymorphism Divergence
                  -----
#> Neutral class
                          23132
                                       52537
#> Selected class
                          10109
                                       54641
```

By default the argument **list_cutoff** uses a list of cutoffs with the following values: 0, 0.05, 0.1. Moreover, the function has an optional argument, **plot**, which is set to **FALSE** by default. This parameters can be customized, like in the following example, where we use a list of 4 cutoffs (0.05, 0.15, 0.25, 0.35) and set the plot argument to **TRUE**.

The output in this case contains a **Graph** which shows the adaptation value (alpha) obtained using each cutoff.

```
FWW(daf=mydafdata, divergence=mydivergencedata, list_cutoff=c(0.05, 0.15,0.25,0.35), plot=TRUE)
#> $Results
#>
                  alpha.symbol Fishers exact test P-value
                     0.5409548
\# Cutoff = 0.05
#> Cutoff = 0.15
                     0.5969015
                                                        0
#> Cutoff = 0.25
                     0.6068868
                                                        0
#> Cutoff = 0.35
                                                        0
                     0.6171609
#>
#> $Graph
```



```
#>
#> $`Divergence metrics`
#> $`Divergence metrics`$`Global metrics`
            Ka
                Ks omega
#> 1 0.02102543 0.0847345 0.2481331
#>
#> $`Divergence metrics`$`Estimates by cutoff`
#>
                 omegaA.symbol omegaD.symbol
                 0.1342288
#> Cutoff = 0.05
                               0.11390431
#> Cutoff = 0.15
                     0.1481110
                               0.10002208
#> Cutoff = 0.25
                               0.09754438
                     0.1505887
#> Cutoff = 0.35
                     0.1531380
                               0.09499504
#>
#>
#> $`MKT tables`
#> $`MKT tables`$`Cutoff = 0.05`
#>
#>
#> Table: cutoff
#>
#>
                    Polymorphism Divergence
#> Neutral class
                           27912
                                       52537
#> Selected class
                          13326
                                       54641
#>
#> $`MKT tables`$`Cutoff = 0.15`
#>
#>
#> Table: cutoff
#>
#>
                   Polymorphism Divergence
```

```
#> Neutral class
                             20258
                                           52537
#> Selected class
                              8493
                                           54641
#>
#> $`MKT tables`$`Cutoff =
#>
#>
#> Table: cutoff
#>
#>
                      Polymorphism
                                     Divergence
#>
#> Neutral class
                             16485
                                           52537
                              6740
                                           54641
#>
  Selected class
#>
#> $`MKT tables`$`Cutoff = 0.35`
#>
#>
#> Table: cutoff
#>
#>
                     Polymorphism
                                     Divergence
#>
                                     _____
#> Neutral class
                             13778
                                           52537
#> Selected class
                              5486
                                           54641
```

DGRP correction

To take adaptive and slightly deleterious mutation mutually into account, Pn, the count of segregating sites in the non-synonymous class, should be separated into the number of neutral variants and the number of weakly deleterious variants, Pn = Pn(neutral) + Pn(weakly del.). If both numbers are estimated, adaptive and weakly deleterious selection can be evaluated independently.

Consider a pair of 2×2 contingency tables. The first one corresponds to the standard MKT table with the theoretical counts of segregating sites and divergent sites for each cell.

The second table contains the count of Pn and Ps for two-frequency categories: below and over a threshold cutoff.

Add brief explanation about 2nd table!

To estimate alpha from the standard MKT table correcting by the segregation of weakly deleterious variants, we have to substitute the Pn by the expected number of neutral segregating sites, Pn(neutral). The correct estimate of alpha is then alpha = 1 - (Pn (neutral)/Ps)(Ds/Dn).

The **DGRP()** function behaves similar to the **FWW()** function. It takes the same input argument and returns the same output but containing also estimates on the **fractions of negative selection** (d: strongly deleterious, f: neutral and b: weakly deleterious).

```
DGRP(daf=mydafdata, divergence=mydivergencedata)
#> $Results
#>
                  alpha.symbol Fishers exact test P-value
#> Cutoff =
                     0.2364499
                                             1.480943e-183
             0
                     0.4249071
\# Cutoff = 0.05
                                              0.000000e+00
                                              0.000000e+00
\# Cutoff = 0.2
                     0.3842950
#>
#> $`Divergence metrics`
```

```
#> $`Divergence metrics`$`Global metrics`
#> Ka Ks omega
#> 1 0.02102543 0.0847345 0.2481331
#> $`Divergence metrics`$`Estimates by cutoff`
#> omegaA.symbol omegaD.symbol
#> Cutoff = 0 0.05867104 0.1894620
#> Cutoff = 0.05  0.10543351  0.1426996
#> Cutoff = 0.2  0.09535630  0.1527768
#>
#>
#> $`MKT tables`
#> $`MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0`
#>
#>
#> Table: cutoff
#>
#>
                 DAF.below.cutoff DAF.above.cutoff
#> -----
                               0
#> Neutral class
                                             45101
#> Selected class
                               0
                                             35816
#> $`MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0.05`
#>
#>
#> Table: cutoff
                 DAF.below.cutoff DAF.above.cutoff
                          17189
                                           27912
#> Neutral class
#> Selected class
                           22490
                                            13326
#>
#> $`MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0.2`
#>
#> Table: cutoff
#>
          {\it DAF.below.cutoff} {\it DAF.above.cutoff}
#> ------ ------
                                            18170
#> Neutral class
                           26931
#> Selected class
                           28322
                                             7494
#> $`MKT tables`$`MKT standard table`
#>
#>
           Polymorphism Divergence
#> ----- -----
#> Neutral class 45101 52537
#> Selected class 35816 54641
                                   54641
#>
#>
#> $Fractions
#> 0 0.05 0.2
#> d 0.810538 0.81053943 0.81053627
```

```
#> f 0.189462 0.14269958 0.15277678
#> b 0.000000 0.04676099 0.03668695
```

Again, by default the argument **list_cutoff** uses a list of cutoffs with the following values: 0, 0.05, 0.1, and the argument **plot** is set to **FALSE**. This parameters can be customized, like in the following example, where we use a list of 4 cutoffs (0.05, 0.15, 0.25, 0.35) and set the plot argument to **TRUE**.

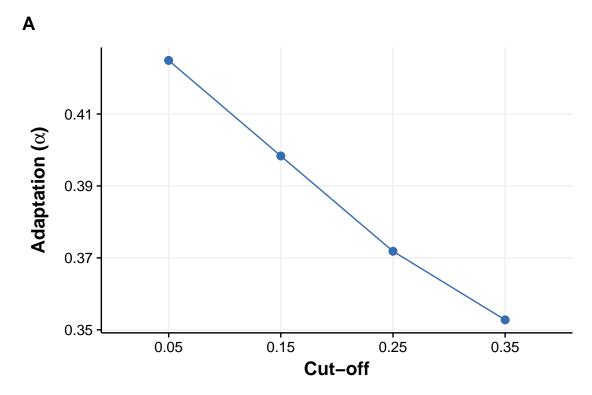
The output in this case contains two **Graphs** which show the adaptation value (alpha) and the negative selection fractions obtained using each cutoff.

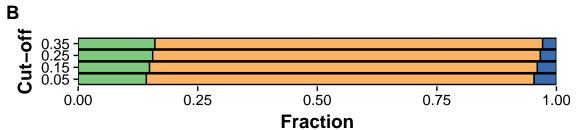
DGRP(<u>daf=mydafdata</u>, <u>divergence=mydivergencedata</u>, <u>list_cutoff=</u>c(0.05, 0.15,0.25,0.35), <u>plot=</u>TRUE)

#> \$Results

#> alpha.symbol Fishers exact test P-value

#> \$Graph





Fraction dffb

```
#>
#> $`Divergence metrics`
#> $`Divergence metrics`$`Global metrics`
             Ka
                       Кs
                              omega
#> 1 0.02102543 0.0847345 0.2481331
#> $`Divergence metrics`$`Estimates by cutoff`
                  omegaA.symbol omegaD.symbol
                                    0.1426996
#> Cutoff = 0.05
                     0.10543351
#> Cutoff = 0.15
                     0.09884233
                                    0.1492908
\# Cutoff = 0.25
                     0.09226702
                                    0.1558661
#> Cutoff = 0.35
                     0.08753258
                                    0.1606005
#>
#>
#> $`MKT tables`
#> $`MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0.05`
#>
#> Table: cutoff
```

```
#>
               DAF.below.cutoff DAF.above.cutoff
#> -----
#> Neutral class
                         17189
                                        27912
#> Selected class
                         22490
                                        13326
#>
#> $`MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0.15`
#>
#>
#> Table: cutoff
                DAF.below.cutoff DAF.above.cutoff
#> -----
#> Neutral class
                        24843
                                       20258
#> Selected class
                         27323
                                        8493
#> $`MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0.25`
#>
#> Table: cutoff
#>
                DAF.below.cutoff DAF.above.cutoff
#> ------
#> Neutral class
                         28616
                                        16485
#> Selected class
                        29076
                                        6740
#> $`MKT tables`$`Number of segregating sites by DAF category - Cutoff = 0.35`
#>
#>
#> Table: cutoff
#>
               DAF.below.cutoff DAF.above.cutoff
#> ------
                         31323
#> Neutral class
                                       13778
#> Selected class
                         30330
                                        5486
#> $`MKT tables`$`MKT standard table`
#>
#>
               Polymorphism Divergence
#> -----
                    45101
#> Neutral class
                               52537
                 35816
#> Selected class
                               54641
#>
#>
#> $Fractions
        0.05 0.15 0.25 0.35
#>
#> d 0.81053943 0.81053552 0.8105368 0.81054057
#> f 0.14269958 0.14929076 0.1558661 0.16060050
#> b 0.04676099 0.04017372 0.0335971 0.02885892
```

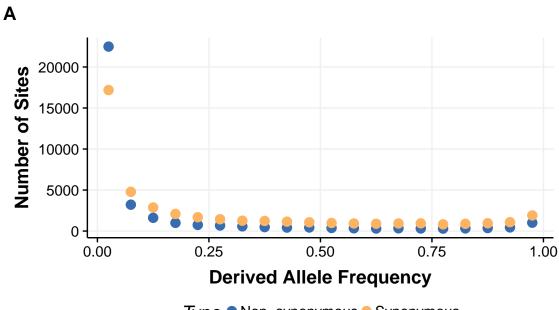
Asymptotic MKT

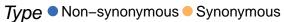
Petrov reference + explanation

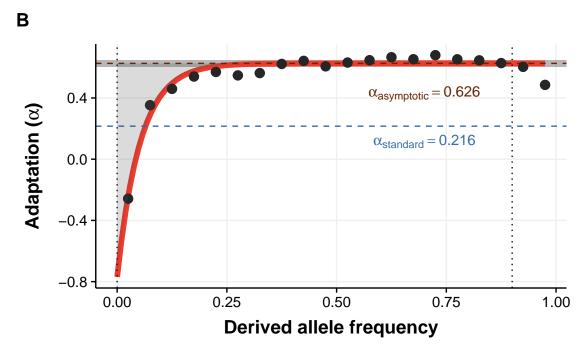
iMK

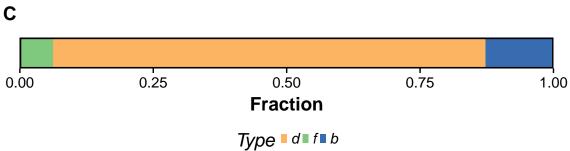
 $A symptotic \ explanation + Sergi \ slightly \ deleterious \ approach$

```
iMK(<u>daf=mydafdata</u>, divergence=mydivergencedata, <u>xlow=</u>0, xhigh=0.9, plot=TRUE)
#> $`Asymptotic MK table`
#>
                                      c alpha_asymptotic CI_low CI_high
          model
                              b
                                         0.6259 0.6045 0.6474
#> 1 exponential 0.6259 -1.3951 18.9619
#> alpha_original
#> 1
            0.2157
#>
#> $`Fractions of sites`
    Type Fraction
       d 0.81053796
#> 1
#> 2
       f 0.06232362
#> 3
       b 0.12713842
#> $Graphs
```









Miscelanious

The **multipleDatasets()** function allows performing any MK test using all files (or a subset of them) in a given directory. Files in directory must be named: file1.**daf**, file1.**divergence**, file2.**daf**, file2.**divergence**, ..., where file corresponds to the samples of interest.