iMKT using PopFly or PopHuman data

Brief intro about lots of data right now. Then, PopFly and PopHuman as great databases.

Therefore, iMKT package includes some functions which allow an easy retrieval and analysis of population genetics information stored in these genome browsers. Specifically, the functions permit the download of population genetics parameters computed for every gene annotation in several populations for both model species Drosophila and Homo sapiens.

Loading the row data

First step is to load this information into your working enviroment and how to access it in order to use it efficiently. To do so, use the loadPopFly() and loadPopHuman() functions.

Keep in mind that you are downloading the complete gene information of several populations (16 D. melanogaster and 26 Human), and this procces could take a while.

Once the functions finish, two new objects are loaded into the workspace: PopFlyData and PopHumanData. These objects can be manually examined or used only when performing the main iMKT analysis.

```
library(iMKT)
loadPopFly()
#> Loading PopFly data into your workspace.
#> This process may take some seconds to complete, please be patient.
#loadPopHuman()
#knitr::kable(head(PopFlyData,4))
head(PopFlyData, 4)
#>   Pop        Name    Start      End Chr p0 pi d0  di  m0   mi   alpha
#> 1  EA FBgn0000008 18024473 18060339  2R 28 17 36  19 647 2449 -0.1504
#> 2  EA FBgn0000014 12632936 12655771  3R  5  0 19   0 155  643      NA
#> 3  EA FBgn0000015 12752932 12797958  3R  6  1  4   0 150  630    -Inf
#> 4  EA FBgn0000017 16608966 16640982  3L 10  5 83 134 867 3263  0.6903
#>   fisher_pval     DoS   KaKs                DAF0f                DAF4f
#> 1      0.8348 -0.0323 0.5278 11;1;2;1;1;0;0;1;0;0 10;9;4;0;1;2;0;1;1;0
#> 2      1.0000  0.0000 0.0000  0;0;0;0;0;0;0;0;0;0  0;1;2;0;0;0;0;0;2;0
#> 3      1.0000 -0.1429 0.0000  0;1;0;0;0;0;0;0;0;0  0;2;1;0;2;0;0;0;1;0
#> 4      0.0530  0.2842 1.6145  0;3;1;1;0;0;0;0;0;0  0;6;1;1;0;0;0;0;2;0
#>       cM_Mb
#> 1 2.1692837
#> 2 0.7616990
#> 3 0.4352566
#> 4 0.8999361
ls() ## new object created
#>  [1] "exampleDaf"         "exampleDiverge"     "geneList"
#>  [4] "methodDGRP"         "methodFWW"          "methodiMK"
#>  [7] "PopFlyData"         "savePlotInVariable" "standard"
#> [10] "subsetPopFly"
```

Each row of the PopFlyData dataframe contains information regarding one gene annotation in one single population. In total, 16 populations and X genes are included. Metrics for each gene contain information about segrating, divergent and analyzed sites and the Derived Allele Frequency (DAF) for neutral (4fold) and putatively selected (0fold) sites; together with some neutrality tests statistics (Standard MKT, Direction of Selection, Ka/Ks).

Performing PopFly Analyses

The ***PopFlyAnalisys()*** function allows performing any MK test using a subset of PopFly data defined by custom genes and populations lists. It uses the previously loaded dataframe (PopFlyData). In addition to the genes and populations lists, the function also has the following parameters:

- recomb group genes according to recombination values (must specify number of bins). TRUE/FALSE. Recomb values (cM/Mb) from Comeron et al. 2012.
- bins number of recombination bins to compute (mandatory if recomb = TRUE)
- test which test to perform. Options include: standard (default), DGRP, FWW, asymptotic, iMK
- xlow lower limit for asymptotic alpha fit (default=0)
- xhigh higher limit for asymptotic alpha fit (default=1)

Hence, it allows deciding which test to perform, and whether to analyze genes groupped by recombination bins or not.

Example 1

In this first example, the analysis is focused in two genes and 3 populations, without considering gene's recombination context, and using DGRP methodology.

```
PopFlyAnalysis(genes=c("FBgn0000055","FBgn0003016"), pops=c("RAL","ZI","FR"), recomb=F, test="DGRP")
#> [1] "Population = FR"
#> Warning in check_input(daf, divergence, 0, 1): Input daf file contains P0 values = 0.
#> This can bias the function fitting and the estimation of alpha.
#> [1] "Population = RAL"
#> Warning in check_input(daf, divergence, 0, 1): Input daf file contains P0 values = 0.
#> This can bias the function fitting and the estimation of alpha.
#> [1] "Population = ZI"
#> $`Population =  FR`
#> $`Population =  FR`$Results
#>                alpha.symbol Fishers exact test P-value
#> Cutoff =  0      -0.3675214                  0.5274392
#> Cutoff =  0.05   -0.3675214                  0.5274392
#> Cutoff =  0.2    -0.3675214                  0.5274392
#>
#> $`Population =  FR`$`Divergence metrics`
#> $`Population =  FR`$`Divergence metrics`$`Global metrics`
#>            Ka         Ks      omega
#> 1 0.003767024 0.05807201 0.06486815
#>
#> $`Population =  FR`$`Divergence metrics`$`Estimates by cutoff`
#>                omegaA.symbol omegaD.symbol
#> Cutoff =  0      -0.02384043    0.08870859
#> Cutoff =  0.05   -0.02384043    0.08870859
#> Cutoff =  0.2    -0.02384043    0.08870859
#>
#>
#> $`Population =  FR`$`MKT tables`
#> $`Population =  FR`$`MKT tables`$`Number of segregating sites by DAF category - Cutoff =  0`
#>
#>
#> Table: cutoff
#>
#>                   DAF.below.cutoff   DAF.above.cutoff
```

```
#> ---------------  -----------------  -----------------
#> Neutral class                    0                 45
#> Selected class                   0                 16
#>
#> $`Population =  FR`$`MKT tables`$`Number of segregating sites by DAF category - Cutoff =  0.05`
#>
#>
#> Table: cutoff
#>
#>                  DAF.below.cutoff   DAF.above.cutoff
#> ---------------  -----------------  -----------------
#> Neutral class                   27                 18
#> Selected class                  10                  6
#>
#> $`Population =  FR`$`MKT tables`$`Number of segregating sites by DAF category - Cutoff =  0.2`
#>
#>
#> Table: cutoff
#>
#>                  DAF.below.cutoff   DAF.above.cutoff
#> ---------------  -----------------  -----------------
#> Neutral class                   27                 18
#> Selected class                  10                  6
#>
#> $`Population =  FR`$`MKT tables`$`MKT standard table`
#>
#>
#>                  Polymorphism   Divergence
#> ---------------  -------------  -----------
#> Neutral class              45           50
#> Selected class             16           13
#>
#>
#> $`Population =  FR`$Fractions
#>            0        0.05         0.2
#> d 0.91129141 0.909073698 0.909073698
#> f 0.08870859 0.088708587 0.088708587
#> b 0.00000000 0.002217715 0.002217715
#>
#>
#> $`Population =  RAL`
#> $`Population =  RAL`$Results
#>                alpha.symbol Fishers exact test P-value
#> Cutoff =  0     -1.19780220                 0.03712979
#> Cutoff =  0.05  -0.04395604                 1.00000000
#> Cutoff =  0.2   -0.37362637                 0.44760661
#>
#> $`Population =  RAL`$`Divergence metrics`
#> $`Population =  RAL`$`Divergence metrics`$`Global metrics`
#>            Ka         Ks      omega
#> 1 0.003767024 0.05226481 0.07207573
#>
#> $`Population =  RAL`$`Divergence metrics`$`Estimates by cutoff`
#>                omegaA.symbol omegaD.symbol
```

```
#> Cutoff =  0     -0.086332464    0.15840819
#> Cutoff =  0.05  -0.003168164    0.07524389
#> Cutoff =  0.2   -0.026929392    0.09900512
#>
#>
#> $`Population =  RAL`$`MKT tables`
#> $`Population =  RAL`$`MKT tables`$`Number of segregating sites by DAF category - Cutoff =  0`
#>
#>
#> Table: cutoff
#>
#>                  DAF.below.cutoff   DAF.above.cutoff
#> ---------------  -----------------  -----------------
#> Neutral class                    0                 63
#> Selected class                   0                 40
#>
#> $`Population =  RAL`$`MKT tables`$`Number of segregating sites by DAF category - Cutoff =  0.05`
#>
#>
#> Table: cutoff
#>
#>                  DAF.below.cutoff   DAF.above.cutoff
#> ---------------  -----------------  -----------------
#> Neutral class                   20                 43
#> Selected class                  34                  6
#>
#> $`Population =  RAL`$`MKT tables`$`Number of segregating sites by DAF category - Cutoff =  0.2`
#>
#>
#> Table: cutoff
#>
#>                  DAF.below.cutoff   DAF.above.cutoff
#> ---------------  -----------------  -----------------
#> Neutral class                   30                 33
#> Selected class                  34                  6
#>
#> $`Population =  RAL`$`MKT tables`$`MKT standard table`
#>
#>
#>                  Polymorphism   Divergence
#> ---------------  -------------  -----------
#> Neutral class                63           45
#> Selected class               40           13
#>
#>
#> $`Population =  RAL`$Fractions
#>           0       0.05        0.2
#> d 0.8415918 0.84039746 0.84178039
#> f 0.1584082 0.07524389 0.09900512
#> b 0.0000000 0.08435865 0.05921449
#>
#>
#> $`Population =  ZI`
#> $`Population =  ZI`$Results
```

```
#>                alpha.symbol Fishers exact test P-value
#> Cutoff =  0      -0.5279503                  0.2545795
#> Cutoff =  0.05   -0.1180124                  0.8623250
#> Cutoff =  0.2    -0.2670807                  0.6114433
#>
#> $`Population =  ZI`$`Divergence metrics`
#> $`Population =  ZI`$`Divergence metrics`$`Global metrics`
#>            Ka         Ks      omega
#> 1 0.003765933 0.04524362 0.083236777
#>
#> $`Population =  ZI`$`Divergence metrics`$`Estimates by cutoff`
#>                omegaA.symbol omegaD.symbol
#> Cutoff =  0     -0.043944879    0.12718165
#> Cutoff =  0.05  -0.009822973    0.09305974
#> Cutoff =  0.2   -0.022230939    0.10546771
#>
#>
#> $`Population =  ZI`$`MKT tables`
#> $`Population =  ZI`$`MKT tables`$`Number of segregating sites by DAF category - Cutoff =  0`
#>
#>
#> Table: cutoff
#>
#>                   DAF.below.cutoff   DAF.above.cutoff
#> ----------------  -----------------  -----------------
#> Neutral class                     0                161
#> Selected class                    0                 82
#>
#> $`Population =  ZI`$`MKT tables`$`Number of segregating sites by DAF category - Cutoff =  0.05`
#>
#>
#> Table: cutoff
#>
#>                   DAF.below.cutoff   DAF.above.cutoff
#> ----------------  -----------------  -----------------
#> Neutral class                   108                 53
#> Selected class                   77                  5
#>
#> $`Population =  ZI`$`MKT tables`$`Number of segregating sites by DAF category - Cutoff =  0.2`
#>
#>
#> Table: cutoff
#>
#>                   DAF.below.cutoff   DAF.above.cutoff
#> ----------------  -----------------  -----------------
#> Neutral class                   125                 36
#> Selected class                   78                  4
#>
#> $`Population =  ZI`$`MKT tables`$`MKT standard table`
#>
#>
#>                   Polymorphism   Divergence
#> ----------------  -------------  -----------
#> Neutral class              161           39
```

```
#> Selected class              82          13
#>
#>
#> $`Population =  ZI`$Fractions
#>           0       0.05        0.2
#> d 0.8728183 0.87282798 0.87229814
#> f 0.1271817 0.09305974 0.10546771
#> b 0.0000000 0.03411227 0.02223415
```

Example 2

In this second example, genes from RAL population are groupped in 2 recombination bins, using recombination values from Comeron et al (ref). The test used is iMK, with xlow and xhigh values set to 0 and 0.9, respectively.

```
geneList <- c("FBgn0053196","FBgn0086906","FBgn0261836","FBgn0031617","FBgn0260965",
              "FBgn0028899","FBgn0052580","FBgn0036181","FBgn0263077","FBgn0013733",
              "FBgn0031857","FBgn0037836")

PopFlyAnalysis(genes=geneList , pops=c("RAL"), recomb=T, bins=2, test="iMK", xlow=0, xhigh=0.9)
#> [1] "Population = RAL"
#> [1] "Recombination bin = 1"
#> [1] "Recombination bin = 2"
#> $`Population =  RAL`
#> $`Population =  RAL`$`Recombination bin =  1`
#> $`Population =  RAL`$`Recombination bin =  1`$`Asymptotic MK table`
#>         model      a       b       c alpha_asymptotic  CI_low CI_high
#> 1 exponential 0.4626 -0.8511 14.8205           0.4626 -0.5768 48.5636
#>   alpha_original
#> 1         0.2489
#>
#> $`Population =  RAL`$`Recombination bin =  1`$`Fractions of sites`
#>   Type  Fraction
#> 1    d 0.6515607
#> 2    f 0.3484393
#> 3    b 0.0000000
#>
#> $`Population =  RAL`$`Recombination bin =  1`$`Recombination bin Summary`
#>   numGenes minRecomb medianRecomb meanRecomb maxRecomb
#> 1        6 0.6230327     1.216535    1.20733  1.759126
#>
#>
#> $`Population =  RAL`$`Recombination bin =  2`
#> $`Population =  RAL`$`Recombination bin =  2`$`Asymptotic MK table`
#>         model      a       b      c alpha_asymptotic  CI_low CI_high
#> 1 exponential 0.6632 -0.5395 7.3407           0.6628 -0.2413  0.7307
#>   alpha_original
#> 1          0.426
#>
#> $`Population =  RAL`$`Recombination bin =  2`$`Fractions of sites`
#>   Type Fraction
#> 1    d 0.727223
#> 2    f 0.272777
#> 3    b 0.000000
```

```
#>
#> $`Population =  RAL`$`Recombination bin =  2`$`Recombination bin Summary`
#>   numGenes minRecomb medianRecomb meanRecomb maxRecomb
#> 1        6  2.277748     3.518252   3.398377  4.104627
```