

Checking four basic InterMineR functions in all Mines

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Checking four basic InterMineR functions in all Mines

In order to check the correct operation of the basic InterMineR functions:

- getModel
- getTemplates
- getTemplateQuery
- runQuery

We will iterate through listMines(), apply every function and return a data.frame showing the results for each Mine:

```
library(InterMineR)

# index variables: Iterate through all available mines and return TRUE/FALSE values for
# the call of each function
ind.getmodel = c()
ind.template = c()
ind.random.template.query.name = c()
ind.template.query = c()
ind.run.random.query = c()

# iterate through available Mines
for(i in seq(length(listMines()))){

  # load Mine
  im = initInterMine(mine = listMines()[i])

  # apply getModel
  model = try(getModel(im))

  # T/F for returning a model with getModel
  ind.getmodel = c(ind.getmodel, class(model) != "try-error")

  # apply getTemplates
  template = try(getTemplates(im))

  # T/F for returning available templates with getTemplate function
  ind.template = c(ind.template, class(template) != "try-error")

  if(class(template) != "try-error"){
```

```

# Get gene-related templates
gene.templates = template[grep("gene", template$name, ignore.case=TRUE),]

# Get random gene-related query name
gt = gene.templates[sample(seq(nrow(gene.templates)),1),1]

# save random gene-related template query name
ind.random.template.query.name = c(ind.random.template.query.name, gt)

# Get random template query with getTemplateQuery function
random.query = try(getTemplateQuery(
  im,
  name = gt
))

# T/F for returning random gene-related template query
ind.template.query = c(ind.template.query, class(template) != "try-error")

# Run random gene-related query
res.random.query = try(runQuery(im, qry = random.query))

# T/F for running random gene-related query
ind.run.random.query = c(ind.run.random.query, class(res.random.query) != "try-error")

} else {

  ind.random.template.query.name = c(ind.random.template.query.name, "No_template")
  ind.template.query = c(ind.template.query, "No_template")
  ind.run.random.query = c(ind.run.random.query, "No_template")

}

}

# Get results for all four functions
functions_results = data.frame(Mines = listMines(),
                               Returned_Model = ind.getmodel,
                               Returned_Templates = ind.template,
                               Random_Template_Query = ind.random.template.query.name,
                               Returned_Random_Gene_Template_Query = ind.template.query,
                               Ran_Successfully_Random_Gene_Template_Query = ind.run.random.query)

functions_results

##                                     Mines
## FlyMine                           http://www.flymine.org/flymine
## MouseMine                         http://www.mousemine.org/mousemine
## RatMine                           http://ratmine.mcw.edu/ratmine
## WormMine                          http://www.wormbase.org/tools/wormmine
## YeastMine                         http://yeastmine.yeastgenome.org/yeastmine
## ZebraFishMine                     http://zebrafishmine.org
## TargetMine                        http://targetmine.mizuguchilab.org/targetmine
## MitoMiner                         http://mitominer.mrc-mbu.cam.ac.uk/release-3.1

```

```

## HumanMine          http://www.humanmine.org/humanmine
## indigoMine          http://www.cbrc.kaust.edu.sa/indigo
## thalemine           https://apps.araport.org/thalemine
## medicmine           http://medicmine.jcvi.org/medicmine
## PhytoMine           http://phytozome.jgi.doe.gov/phytoMine
## Returned_Model Returned_Templates
## FlyMine             TRUE             TRUE
## MouseMine           TRUE             TRUE
## RatMine             TRUE             TRUE
## WormMine            FALSE            FALSE
## YeastMine           TRUE             TRUE
## ZebraFishMine       TRUE             TRUE
## TargetMine          TRUE             TRUE
## MitoMiner           TRUE             TRUE
## HumanMine           FALSE            TRUE
## indigoMine          TRUE             TRUE
## thalemine           TRUE             TRUE
## medicmine           TRUE             TRUE
## PhytoMine           TRUE             TRUE
## Random_Template_Query
## FlyMine             DrosDel_GeneLocation
## MouseMine           GO_Interaction_Genes
## RatMine             gene_to_homologue_omim
## WormMine            No_template
## YeastMine           Gene_OMIM_Disease
## ZebraFishMine       Gene_Identifiers
## TargetMine          Gene_Disease
## MitoMiner           MTSipsortToGene
## HumanMine           Protein_GeneChromosomeLength
## indigoMine          All_Genes_in_Organism
## thalemine           Keyword_GO_genes
## medicmine           Search_Term_Genes_RNaseq_Expression
## PhytoMine           Gene_MRNA_Sequence
## Returned_Random_Gene_Template_Query
## FlyMine             TRUE
## MouseMine           TRUE
## RatMine             TRUE
## WormMine            No_template
## YeastMine           TRUE
## ZebraFishMine       TRUE
## TargetMine          TRUE
## MitoMiner           TRUE
## HumanMine           TRUE
## indigoMine          TRUE
## thalemine           TRUE
## medicmine           TRUE
## PhytoMine           TRUE
## Ran_Successfully_Random_Gene_Template_Query
## FlyMine             FALSE
## MouseMine           TRUE
## RatMine             TRUE
## WormMine            No_template
## YeastMine           TRUE
## ZebraFishMine       TRUE

```

```
## TargetMine TRUE
## MitoMiner TRUE
## HumanMine TRUE
## indigoMine FALSE
## thalemine TRUE
## medicmine TRUE
## PhytoMine TRUE
```

Warning and Error messages have been suppressed so that the text can be legible but failing to run a function for a specific Mine can be seen in the final data.frame.

SessionInfo

```
sessionInfo()
```

```
## R version 3.3.2 (2016-10-31)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 8.1 x64 (build 9600)
##
## locale:
## [1] LC_COLLATE=Greek_Greece.1253 LC_CTYPE=Greek_Greece.1253
## [3] LC_MONETARY=Greek_Greece.1253 LC_NUMERIC=C
## [5] LC_TIME=Greek_Greece.1253
##
## attached base packages:
## [1] tcltk      stats      graphics  grDevices  utils      datasets  methods
## [8] base
##
## other attached packages:
## [1] RSQLite_1.1-2      InterMineR_0.99.4
##
## loaded via a namespace (and not attached):
## [1] igraph_1.0.1      Rcpp_0.12.9       xml2_1.1.1
## [4] knitr_1.15.1      XVector_0.14.0    magrittr_1.5
## [7] BiocGenerics_0.20.0 zlibbioc_1.20.0    IRanges_2.8.1
## [10] R6_2.2.0          httr_1.2.1        stringr_1.1.0
## [13] tools_3.3.2       parallel_3.3.2    DBI_0.5-1
## [16] htmltools_0.3.5   yaml_2.1.14       rprojroot_1.2
## [19] digest_0.6.12     RJSONIO_1.3-0     S4Vectors_0.12.1
## [22] bitops_1.0-6      curl_2.3           RCurl_1.95-4.8
## [25] memoise_1.0.0     evaluate_0.10     gsubfn_0.6-6
## [28] rmarkdown_1.3     stringi_1.1.2     backports_1.0.5
## [31] Biostrings_2.42.1 stats4_3.3.2      XML_3.98-1.6
## [34] chron_2.3-49      sqldf_0.4-10      proto_1.0.0
```