ontoFAST: getting started

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Installing

To install `ontoFAST` package, you must have Rstudio and `devtools` package installed. The latter can be done by executing `install.packages("devtools")` in Rstudio. If `devtools` is intalled you can use it to install `ontoFAST` directly from GitHub:

```r
# !!! uncomment to run
#library(devtools)
#install_github("sergeitarasov/ontoFAST")
library(ontoFAST)
```

```
## Loading required package: pbapply

## Loading required package: ontologyIndex

## Loading required package: dplyr

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union

## Loading required package: shiny

## Loading required package: shinydashboard

##
## Attaching package: 'shinydashboard'

## The following object is masked from 'package:graphics':
##
##     box

## Loading required package: visNetwork

## Loading required package: stringr

## Loading required package: magrittr

## Loading required package: devtools

##
## Attaching package: 'devtools'

## The following object is masked from 'package:ontologyIndex':
##
##     check
```

Working with ontoFAST

Assembling data

Let's first read in ontology. In this example, I use Hymenoptera anatomy ontology that is available as embedded data set:

```
hao_obo<-HAO
```

Alternatively ontology can be parsed directly from `.obo` file:

```
hao_obo=get_OBO(system.file("data_onto", "HAO.obo", package = "ontoFAST"),
                extract_tags="everything", propagate_relationships = c("BFO:0000050", "is_a"))
```

Not, let's read in character statements. I prefer using a simple table format to store characters and their states. So, it can be imported in R for example using `read.csv` function. Here, I use embedded data set from Sharkey et.al. (2011):

```
char_et_states<-Sharkey_2011
```

This data sets contains 392 characters. Let's create IDs for them, which will be used to call the characters. We keep all our data in `ontologyIndex` (here `hao_obo`) object that stores the entire ontology.

```
id_characters<-paste("CHAR:",c(1:392), sep="")
hao_obo$id_characters<-id_characters
```

Now, let's add character statements to `hao_obo` and associate them with IDs.

```
name_characters<-char_et_states[,1]
names(name_characters)<-id_characters
hao_obo$name_characters<-name_characters
```

To make automatic annotation more efficient, we can use the synonyms of terms in the ontology. The synonyms are stored in `hao_obo$synonym` but they have to be preprocessed to be available for automatic annotation. To do it we use `syn_extract()` function.

```
hao_obo$parsed_synonyms<-syn_extract(hao_obo)
```

Now, we can run the automatic annotation. You can skip this step if you do not want to use synonyms.

```
hao_obo$auto_annot_characters<-annot_all_chars(hao_obo, use.synonyms=TRUE, min_set=TRUE)
```

```
## [1] "Doing automatic annotation of characters with ontology terms..."
```

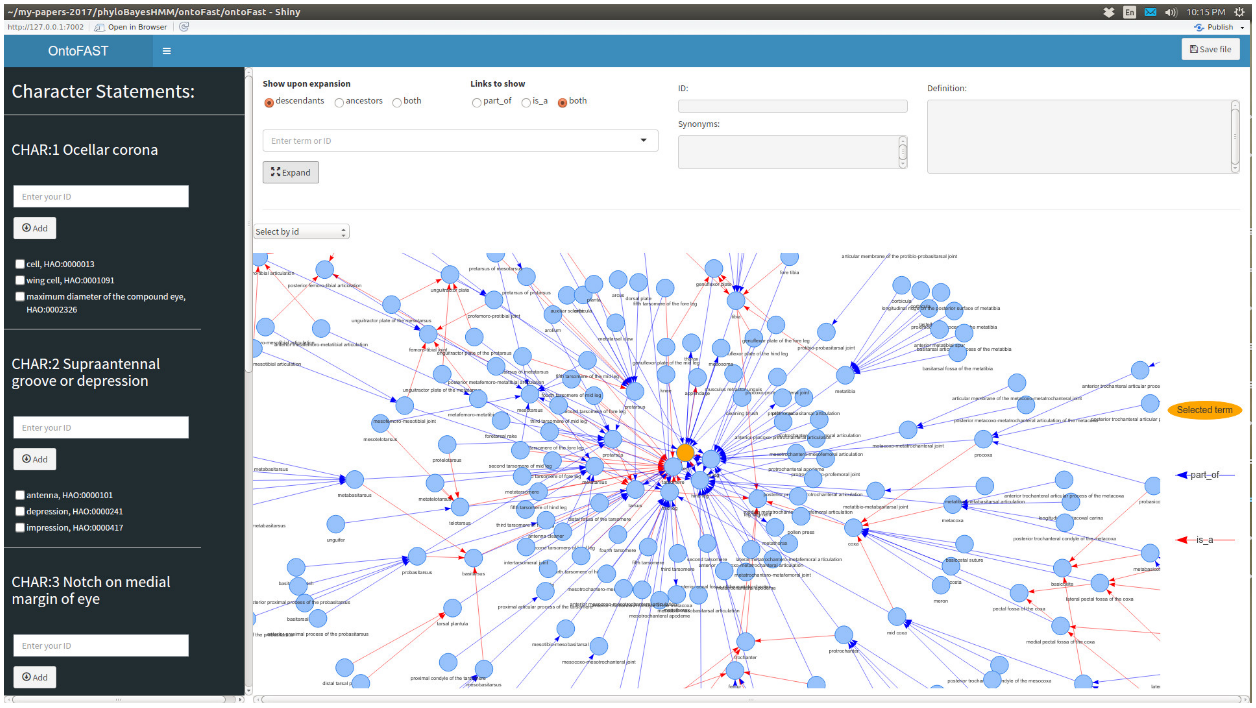
Running ontoFAST interactively

The final step before running ontoFAST in interactive mode, requires creating the global `shiny_in` object that will store all the annotations and associated data. To create the global object use the assignment operator `<<-`

```
shiny_in<<-make_shiny_in(hao_obo)
```

Now we can run ontoFAST interactively by executing the line below. It may take a few seconds until all characters are loaded.

```
# !!! uncomment to run
#runOntoFast()
```



~/my-papers-2017/phyloBayesHMM/ontoFast/ontoFast - Shiny

http://127.0.0.1:7002 | Open in Browser

OntoFAST

Character Statements:

CHAR:1 Ocellar corona

Enter your ID

Add

- cell, HAO:0000013
- wing cell, HAO:0001091
- maximum diameter of the compound eye, HAO:0002326

CHAR:2 Supraantennal groove or depression

Enter your ID

Add

- antenna, HAO:0000101
- depression, HAO:0000241
- impression, HAO:0000417

CHAR:3 Notch on medial margin of eye

Enter your ID

Add

Show upon expansion: [✓ descendants] ancestors both

Links to show: part_of is_a [✓ both]

Enter term or ID

Expand

ID:

Synonyms:

Definition:

Select by id

Save file

Figure 1: ontoFAST in interactive mode

By default ontoFAST displays all the characters in the data set. Using argument `nchar=N` you my restrict the visualization to `N` characters. You may also use ontoFAST as an ontology browser without loading characters by specifying argument `show.chars=FALSE`.