TRANSLATOR Coreference Resolution

KBC

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This code includes:

- 1. A representation of annotations in the BioNLP-ST format
- 2. Semantic rules for coreference resolution
- 3. Syntactic rules for coreference resolution

BioNLP-ST data: Representing in R

Question: Why use the BioNLP-ST format?

Answer: Because despite putting a bunch of time into the XML and JSON formats, neither of them really worked out very well. Plus, when I looked through what information is in which kind of annotation project, this format gets me to everything that I need, particularly with respect to mapping named entity and coreference annotations to character offsets and mapping between those and the sentence boundaries. Those sentence boundaries are really important for coreference resolution...

Let's try a generalized class for representing a BioNLP-ST "annotation" in R. The goal is for this to work across any type of label, and if all annotations are in the same format, it will.

The format seems to be: one file per article/paper/whatever. Let's say "document." A line seems to have the following things in it:

- 1. An identifier, numbered sequentially and with a tag that might or might not have some morphology.
- 2. A tag.
- 3. A start index.
- 4. An end index.
- 5. The covered text (although maybe there isn't any for some types of annotation?)

These five things are in three tab-separated columns:

- 1. Identifier
- 2. Space-separated tag, start index, and end index
- 3. The covered text

Example:

T1 NN 0 7 Complex T2 sentence 0 96 Complex trait analysis of the mouse striatum: independent QTLs modulate volume and neuron number T3 NN 8 13 trait T4 NN 14 22 analysis T5 IN 23 25 of T6 DT 26 29 the T7 NN 30 35 mouse T8 NN 36 44 striatum T9 : 44 45 :

Why does the word *Complex* come before the sentence that contains it, while the rest of the words come after it? I have no idea.

What can we get out of the CRAFT annotations?

We have seen the rationale for using the BioNLP-ST format in general. What can we get from it for the specific purposes of coreference resolution in the CRAFT corpus?

NB that we won't necessarily have the same thing for any other data, but maybe we can tag other data automatically... I guess that if we *can't* build taggers off of the CRAFT annotations, then the project was a loss, so let's operate on the assumption that we *can*, which seems like a reasonable bet.

- 1. Sentence index is available in the CONLLU format, but I don't see it anywhere else. The sentence index is continuous throughout a paper, i.e. it does not pay attention to paragraph boundaries. (In fact, I don't think it even pays attention to the distinction between a title, a section heading, and a paragraph of text.)
- 2. I don't see a paragraph index anywhere. Not necessarily a problem, since the sentence indices are continuous.

3.

- CONLLU: paragraph index, sentence index. No spans.
- CONLLX: no paragraph index, no sentence index, no spans.
- Treebank: no paragraph index, no sentence index, no spans.
- Sections and typography: no paragraph index, no sentence index. Spans for formatting.
- Coreference: no paragraph index, no sentence index. Spans for text of markables.
- Named entities: no paragraph index, no sentence index. Spans for text of markables.

So, it seems like there are some minor hacks for comparing strings and for comparing semantic classes, and that's almost it, within the realm of decency. If we want any of the sentence position stuff, we will have to do some truly filthy hacking to map the coref/named entity annotations, which have character offsets but no sentence indices, to the CONLLU data, which has sentence indices, but no character offsets...

- 1. We can get noun group and text information out of the coreference annotations. With that, we have boundaries, and we can check for exact string matches and for case-toggled string matches. Maybe for a first step, we count how many within-document sets of each there are?
- 2. We can map spans in the coreference annotations to spans in the named entity annotations. That way we can see if we have semantic class matches. Maybe for a second step, we count those?

Class BioNLP-ST defined

- 1. Constructor
- 2. Method: convert between a list and a dataframe NO
- 3. Method: convert between a dataframe and a list NO
- 4. Test driver

TODO: need a way to handle discontinuous spans.

Question: What's the best way to handle semantic class labels? I get leaf nodes from any normalization system, which is wonderful if it matches, but if that matches, it's probably redundant to string match, more often than not... I certainly don't want to toss that level of granular information out, though.

The highest possible node-let's say the equivalent of just knowing what kind of named entity you got labelled with-is much more likely to be widely useful, I suspect. If we want that, we need to trim it off of the concept ID, as far as I know. We should certainly use it...

So, we're resolved that we will keep/use both the named entity class, and the concept ID. The next question: how do we represent them? The choices: as factors, or as strings. Factors seem conceptually cleaner. Strings are simpler from the point of programming logic, though, I suspect... Maybe start with strings, and then refactor (haha) to factors at some later point if it seems clear that it would be helpful?

```
# Concise discussion of object-oriented programming with S4 in R:
# https://www.datamentor.io/r-programming/s4-class/
# example of defining the class with setClass(), from https://www.datamentor.io/r-progra
mming/s4-class/:
#setClass("student", slots=list(name="character", age="numeric", GPA="numeric"))
setClass("BioNLPST",
         slots = list(
           filename = "character",
           id = "character",
           label = "factor", # should be a factor, but I need to define that somehow, so
for now make it a character, and convert that with as.factor()
           start = "numeric",
           end = "numeric",
           #discontinuous = "boolean",
           covered.text = "character",
           label.and.indices = "character",
           original.line = "character"))
#bionlp.test.01 <- new(Class = "BioNLPST",</pre>
     filename = "myfilename",
     id = "T1",
#
#
     label = "GENE",
#
     start = 100,
     end = 150,
#
    covered.text = "this length should equal that of start to end offsets",
#
     label.and.indices = "GENE 100 150",
     original.line = "boopity boop")
# print() and show() are both pretty space-intensive, so let's write something that woul
d effectively overwrite print() -- and if I figure out how to do that, this can be the imp
lementation!
# args: bionlpst is an object of class BioNLPST
bioprint <- function(bionlpst) {</pre>
  # TODO: test that you've been passed the right class
 # TODO: test that mandatory slots are filled (why? not the responsibility
  # of this function...)
  print(paste("Filename:", bionlpst@filename))
 print(paste("ID:", bionlpst@id))
 print(paste("Label:", bionlpst@label))
 print(paste("Covered text:", bionlpst@covered.text))
 print(paste("Start position:", bionlpst@start))
  print(paste("End position:", bionlpst@end))
} # close function definition bioprint()
#bioprint(bionlp.test.01) # was using the old df-based type.
# TODO: rewrite test with the new class BioNLPST
# bng = base noun group, which actually at this point is an object
# of class BioNLPST...
```

```
getBioNlpStId <- function(bng) {
  return(bng@id)
} # close function definition getBioNlpStId()</pre>
```

Class IdentPair defined

This class represents a pair of anaphor and antecedent *or* candidate antecedent. At some point we should have a representation of a coref chain, but let's start simple for now. We should probably also be able to represent singletons in some similar way.

For a tidy representation, maybe we do this...

- 1. ID for the pair
- 2. IDs of its two elements
- 3. The sieve that got it

This would let you group by pair ID. If pair IDs are sortable, well... you could sort by them. So, these should probably be numeric.

It would also let you group by each anaphor and (potential) antecedent. So, for example, if you group by anaphor, you could have a list of its potential antecedents and their scores. Crucially: you could have more than one potential antecedent. I guess you could also group by (potential) antecedent and see which ones are connected to (potentially) more than one anaphor. I'm not sure how you would use that algorithmically, but from an analytical perspective, it would help you to characterize the complexity/difficulty of the problem for a given dataset.

It would also let you group by sieves, which seems pretty valuable for evaluation.

Assumptions:

- 1. Not representing singletons (bad)
- 2. Not representing appositives (bad)

```
library(tidyverse)
setClass("IdentPair",
         slots = list(
           filename = "character",
           pair.id = "numeric",
           anaphor = "BioNLPST",
           candidate = "BioNLPST",
           sieve = "character", # maybe I need a *score*, plus an *array* of sieves...
           anaphor.id = "character", # see note about antecedent ID
           antecedent.id = "character", # check for consistency with class
                                        # BioNLPST
           #covered.texts = paste(getString(anaphor), "::", getString(candidate)) # unfo
rtunately, can't do this here, so ...
           #covered.texts = paste(anaphor@covered.text, "::", candidate@covered.text)
           # SHIT--there doesn't seem to be any way to get the covered texts from within
this constructor,
           # so I quess I'll have to have a setter for that...
           # ...but, I still do need to define that
           covered.texts = "character"
           ))
# is there a way to "just" override print()?
# This function prints an IdentPair more prettily than calling structure()
# or something like that.
identPrint <- function(ident.pair) {</pre>
 # TODO: validate that you did, indeed, get passed an IdentPair
 print(paste("IdentPair", getPairID(ident.pair)))
 print(paste("Sieve:" , getSieve(ident.pair)))
 print(paste("Anaphor:", getBioNlpStId(anaphor)))
 print(paste("Antecedent:", getBioNlpStId(candidate)))
 print(paste())
 print(paste())
} # close function definition identPrint()
print("NO TESTS IMPLEMENTED FOR IdentPair class")
```

```
## [1] "NO TESTS IMPLEMENTED FOR IdentPair class"
```

Operations on IdentPairs

```
library(tidyverse)

printIdentPair <- function(filename, pair.id, sieve, anaphor.id, antecedent.id) {
    print(paste(pair.id, sieve, anaphor.id, antecedent.id))
    print(paste())
} # close function definition printIdentPair()

getPairID <- function(ident.pair) {
    return(ident.pair@pair.id)
}
print("NO TESTS IMPLEMENTED FOR getPairID()")</pre>
```

```
## [1] "NO TESTS IMPLEMENTED FOR getPairID()"
```

```
getSieve <- function(ident.pair) {
    return(ident.pair@sieve)
}

# args: an IdentPair and two bngs (BioNLPST objects)
setCoveredTexts <- function(ident.pair, anaphor, candidate) {
    ident.pair@covered.texts <- paste(getString(anaphor), "::", getString(candidate))
} # close function definition setCoveredTexts()

# args: an IdentPair
# returns: string
getCoveredTexts <- function(ident.pair) {
    return(ident.pair@covered.texts)
}

print("NO TESTS IMPLEMENTED FOR getSieve()")</pre>
```

```
## [1] "NO TESTS IMPLEMENTED FOR getSieve()"
```

Convert a line of BioNLP-ST data to a BioNLPST object

This will replace the function to turn a line of BioNLP-ST data to a BioNLPST object.

```
DEBUG <- FALSE
# Given a line from a file in BioNLP-ST format, parse it, make a new
# BioNLPST object, and return that
# args: a line from a file in BioNLP-ST format (see above)
lineToBioNLPST <- function(input.line) {</pre>
  input.line.contents <- unlist(strsplit(input.line, "\u0009"))
# \u0009 is hex for tab. Might not be necessary.
  if (DEBUG) { print(paste("Input line splits to a vector of length", length(input.line.
contents))) }
  if (DEBUG) { print(paste("Input line contents split to:", input.line.contents))}
  if (DEBUG) {
    print(paste("Element 1:", input.line.contents[1]))
    print(paste("Element 2:", input.line.contents[2]))
    print(paste("Element 3:", input.line.contents[3]))
  }
  id <- input.line.contents[1]</pre>
  label.and.indices <- input.line.contents[2]</pre>
  covered.text <- input.line.contents[3]</pre>
  # separate the label and indices into the label, the start index,
  # and the end index ("index" means character offset, sorry)
  label.and.indices.split <- unlist(strsplit(label.and.indices, "\\s"))</pre>
  label <- label.and.indices.split[1]</pre>
   start <- label.and.indices.split[2]</pre>
   end <- label.and.indices.split[3]</pre>
   label <- as.factor(label)</pre>
   start <- as.numeric(start) # has to be numeric for later processing
   end <- as.numeric(end) # has to be numeric for later processing
bionlp.new <- new(Class = "BioNLPST",
    filename = "myfilename",
    id = id,
    label = label,
    start = start,
    end = end,
    covered.text = covered.text,
    label.and.indices = label.and.indices,
    original.line = input.line)
    return(bionlp.new)
} # close function definition lineToBioNLPST()
```

Line of BioNLP-ST data in, dataframe out

This will be deprecated after replacement with code to read in a line of BioNLP-ST data and output a BioNLPST object.

This function does the basic parsing of a line of data in the BioNLP-ST format into its components.

The fact that this makes a dataframe is an artifact of an earlier conception of the approach. A separate function allows you to turn it into a list() (see above).

Note that this code chunk contains some useful examples of how to utilize the stuff returned from various string-manipulating functions.

```
library(tidyverse)
# nice post on futzing with columns: https://www.marsja.se/how-to-remove-a-column-in-r-u
sing-dplyr-by-name-and-index/
# args: a line from a .bionlp file
# returns: a tibble with the following columns:
# id: the identifier in the .bionlp file
# tag: could be POS, "sentence," whatever
# start: beginning character offset
# end: ending character offset
# covered.text: the original text covered by the span start -> end
parse.bionlp.st <- function(input.line) {</pre>
 FUNCTION.DEBUG <- FALSE
 if (FUNCTION.DEBUG) { print("In function as.bionlp.st().")}
 if (FUNCTION.DEBUG) { print(input.line) }
 # see here: https://stackoverflow.com/questions/46518228/return-value-of-strsplit
 input.line.contents <- unlist(strsplit(input.line, "\u0009"))</pre>
  #input.line.contents <- str split(string = input.line, pattern = "\u0009") # \u0009 is
hex for tab. Might not be necessary -- I think my bug might be related to not understandin
g what str_split() returns... Is it a list??
  if (FUNCTION.DEBUG) { print(paste("Input line splits to a vector of length", length(in
put.line.contents))) }
 if (FUNCTION.DEBUG) { print(paste("Input line contents split to:", input.line.content
s))}
  if (FUNCTION.DEBUG) {
   print(paste("Element 1:", input.line.contents[1]))
   print(paste("Element 2:", input.line.contents[2]))
   print(paste("Element 3:", input.line.contents[3]))
 #if (TRUE) { print("Type of return from str split:", typeof(input.line.contents))}
  input.line.df <- data.frame(id = input.line.contents[1],</pre>
                              tag.and.offsets = input.line.contents[2],
                              covered.text = input.line.contents[3],
                              input.line = input.line)
 #colnames(input.line.df) <- c("input.line")</pre>
 if (TRUE) { head(input.line.df) }
  # convert the data frame into a tibble:
 input.line.df <- as tibble(input.line.df)</pre>
  # now you should have a 3-column tibble.
  # next you need to split the column containing the tag and character offsets into thre
e separate columns.
  #input.line.df <- tidyr::separate(data = input.line.df,</pre>
                                     col = tag.and.offsets,
  #
                                     into = c("tag", "start", "end"),
 if (TRUE) { print(head(input.line.df)) }
  # break up the tag and offsets into separate columns:
  input.line.df <- tidyr::separate(data = input.line.df,
                col = tag.and.offsets,
                into = c("tag", "start", "end"),
                sep = " ",
```

```
remove = FALSE)
 if (TRUE) { print("After splitting tag.and.offsets into separate columns:") }
 if (TRUE) { head(input.line.df) }
 # now you can remove the columns that contain (1) the complete input line from
 # the file, and (2) the combination of tag and offsets that you just split
 # into separate columns.
 #input.line.df <- select(input.line.df, -c(input.line, taq.and.offsets))</pre>
 #input.line.df <- select(input.line.df, -c(tag.and.offsets)) but, maybe this gets blow
n away by the call to separate that I do above?
  # THOUGHT: I actually wouldn't mind keeping it, if for no other reason than for valida
ting tags and offsets in later processing steps...
 if (TRUE) { print("Variable input.line.df:") }
 if (TRUE) { head(input.line.df) }
 return(input.line.df)
} # close function definition as.bionlp.st()
if (TRUE) {
  lines <- readLines("/Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/</pre>
testData/11319941.bionlp")
 print(paste("Number of lines read in:", length(lines)))
 print("First 5 lines:")
 print(lines[1:5])
 #print("Last 5 lines:")
 # clunky, but: should print the last 5 lines
 #...but, I think it prints the whole fucking array ;-)
 #print(lines[length(lines)-4:length(lines)])
 #print("") # I just want a little space in the output
 #before the next stuff starts happening...
  # set this as you like. use it to cut down on how much output you get if you're debugg
ing and don't want/need to see hundreds of lines. For the contents of an entire file, se
t the variable to the number of lines in the file (length(lines)). To limit the amount o
f output that you have to wade through, set it to a smaller number than that!
 #number.of.lines.to.print <- length(lines)</pre>
 number.of.lines.to.print <- 2</pre>
 if (TRUE) { print("START ITERATING OVER LINES") }
 for (i in 1:number.of.lines.to.print) {
   line <- lines[i]</pre>
   print(paste("Read in line", i, ":", line))
    line.bionlp.st <- parse.bionlp.st(line)</pre>
   print("RETURNED FROM parse.bionlp.st():")
   print(line.bionlp.st)
  } # close for-loop through file
}
```

Getting sentence offsets from the BioNLP-ST data

To figure out sentence positions (same sentence, preceding sentence, preceding sentence left edge/right edge), we want character offsets. We will get those from the CRAFT files in BioNLP-ST format, which contain lines that give character offsets for sentences, like this:

T1 NN 0 7 Complex T2 sentence 0 96 Complex trait analysis of the mouse striatum: independent QTLs modulate volume and neuron number T3 NN 8 13 trait T4 NN 14 22 analysis T5 IN 23 25 of

```
library(tidyverse) # TODO: Can I suppress the warnings about build versions?
DEBUG <- FALSE
# for now, we'll just do one file at a time. See here for a loop to open everything in a
directory: https://rpubs.com/LMunyan/363306
#sentences.directory <- "/Users/kevincohen/Dropbox/a-m/Corpora/craft-sentences-bionlp/*.
bionlp"
#sentences.df <- read.table(sentences.directory, sep = "\t", header = FALSE)
sentences.df <- read.table("/Users/kevincohen/Dropbox/a-m/Corpora/craft-sentences-bionl
p/11319941.bionlp", sep = "\t", header = FALSE)
if (DEBUG) { head(sentences.df) }
colnames(sentences.df) <- c("token.id", "tag.and.offsets", "text")</pre>
if (DEBUG) { head(sentences.df) }
sentences.tibble <- as_tibble(sentences.df)</pre>
sentences.df <- "" # just free up the memory...
# drop the columns you don't want -- we can always change our minds about this later.
# nice post on futzing with columns: https://www.marsja.se/how-to-remove-a-column-in-r-u
sing-dplyr-by-name-and-index/
sentences.tibble <- select(sentences.tibble, -c(token.id, text))</pre>
if (DEBUG) { head(sentences.tibble) }
sentences.tibble <- sentences.tibble %>% filter(str detect(tag.and.offsets, "sentence"))
if (DEBUG) { head(sentences.tibble) }
#str split()
sentences.tibble <- tidyr::separate(data = sentences.tibble,</pre>
                col = tag.and.offsets,
                into = c("tag", "start", "end"),
                sep = "")
# we can just drop the "sentence" tag column...
if (DEBUG) { head(sentences.tibble) }
sentences.tibble <- select(sentences.tibble, -c(tag))</pre>
if (TRUE) { head(sentences.tibble) }
```

```
## # A tibble: 6 × 2
     start end
##
##
   <chr> <chr>
           96
## 1 0
## 2 98
           106
## 3 108
           118
## 4 120
           213
## 5 214
           399
## 6 401
           408
```

Overlapping annotations

Sometimes you need to know whether or not two separate annotations cover the same text. Sometimes you need to know whether or not the text covered by one annotation is within the range of text covered by another. These functions provide that functionality.

```
# I've got a coreference annotation covering character offsets XX to YY. Is there a name
d entity annotation exactly matching/within/containing that range?
# document ID
# span start
# span end
# range() returns a vector containing the minimum and maximum of all of the given argume
nts. Not quite what we want... It just gives you the minimum and the maximum, which if y
ou gave it a span start and span end, would be the span start and the span end. No value
added. I think what we want is, a function that given the start and the end, will give y
ou a vector of all of the integers between them. Then you can ask whether or not two OTH
ER span positions (start/end) are in that vector.
generateFullRange <- function(start, end) {</pre>
  fullRange <- c(start:end)
 return(fullRange)
testFullRange <- generateFullRange(start = 345, end = 500)
#print("345 to 500:")
#print(testFullRange)
if (400 %in% testFullRange) { print(".") }
## [1] "."
if (1000 %in% testFullRange) { print("FAIL") } else { print(".") }
```

Span match/within/containing logic

This builds on the generateFullRange() function that is defined in the previous code chunk. Cases:

1. No overlap at all between the two.

OK, that works alright.

[1] "."

- 2. Markable span matches named entity span.
- 3. Markable span within named entity span.
- 4. Markable span contains named entity span.
- 5. Spans overlap, markable to left of named entity.
- 6. Spans overlap, markable to right of named entity.

There might not be a meaningful difference between (5) and (6), in which case I guess we just call it (partial) overlap or something.

question we're trying to answer: given a markable, do we know its semantic class, and
if so: what is it?

if there is an exact span match between the markable and some named entity, then yes,
we do know its semantic class, and its semantic class is the semantic class of the named
entity.

if the overlap is not complete (see 3-6 above), then it's a bit more complicated, but we can use a heuristic. Let's say maybe like this: if there is overlap between the markable and one and only one named entity, then we assign the named entity's semantic class to the markable. If there is overlap between the markable and more than one named entity, then we assign the semantic class of the named entity that covers the largest span. Or the smallest!;-)

Implementation of some semantic rules

If the semantic classes of the two NGs match, then they're more likely to be coreferential than if they don't.

Limitations of this implementation:

- 1. Both NGs have to be labelled with a semantic class.
- 2. I don't have an easy *and effective* way to take shared ancestors (or lack thereof) between the leaf nodes and the root node into account.

TODO: This will need to be rewritten to take a list as input, rather than a dataframe. Otherwise the elements of the base noun group will get returned as arrays, rather than as singletons.

```
# bng is a base noun group
# ...technically, an object of class BioNLPST
# bng is a base noun group represented as a BioNLPST object
# returns: a string, or a factor? A factor, now.
getSemanticClassLabel <- function(bng) {</pre>
  FUNCTION.DEBUG <- FALSE
  if (FUNCTION.DEBUG) {
    print("In function getSemanticClassLabel().")
  } # close if-debug
  semanticClassLabel <- bng@label</pre>
 return(semanticClassLabel)
} # close function definition getSemanticClassLabel()
# returns: TRUE/FALSE
hasSemanticClassLabel <- function(bng) {</pre>
  # this is essentially a hack to attempt to force R to make a copy of the object
  # TODO: see if I can take out this hack, now that I have fixed the previous problem wi
th bngs being a list versus a vector
    bng@filename <- filename</pre>
  if (is.na(getSemanticClassLabel(bng))) {
    return (FALSE)
  } else { return (TRUE) }
} # close function definition hasSemanticClassLabel()
# anaphor and candidate are base noun groups
# returns: TRUE/FALSE
semanticClassesMatch <- function(anaphor, candidate) {</pre>
  anaphorSemanticClass <- getSemanticClassLabel(anaphor)</pre>
  print(paste("anaphor semantic class:", anaphorSemanticClass))
  candidateSemanticClass <- getSemanticClassLabel(candidate)</pre>
  print(paste("candidate semantic class:", candidateSemanticClass))
  if (anaphorSemanticClass == candidateSemanticClass) {
    return (TRUE)
  } else {
    return (FALSE)
} # close function definition semanticClassesMatch()
testSemanticMethods <- function() {</pre>
  print("NO SEMANTIC METHOD TESTS RUNNING YET.")
} # close function definition testSemanticMethods()
testSemanticMethods()
```

```
## [1] "NO SEMANTIC METHOD TESTS RUNNING YET."
```

Non-semantic functions on base noun groups

- 1. Getters for strings and for paragraph and sentence indices
- 2. Comparators for strings and for paragraph and sentence indices

TODO: as above, these functions need to be rewritten to take a list as the input argument, rather than a dataframe...

```
DEBUG <- FALSE
# TODO: change name of this function from the not-very-informative getString()
# to the more informative getCoveredText(), or something similar
# bng is a base noun group
# returns: char
getString <- function(bng) {</pre>
 return(bng@covered.text)
} # close function definition
# args: bng is a base noun group/BioNLPST object
# return: integer (TODO: be sure to make these be integers!)
getSentenceIndex <- function(bng) {</pre>
 return(bng@sentence.index) # not sure this actually exists!
} # close function definition getSentenceIndex()
# args: bng is a base noun group
# return: integer (TODO: be sure to make these be integers!)
#getSentenceIndex <- function(bng) {</pre>
# return(bng$sentenceIndex)
#} # close function definition getSentenceIndex()
getParagraphIndex <- function(bng) {</pre>
  return(bng@paragraph.index) # not sure this actually exists!
} # close function definition getParagraphIndex()
stringsMatch <- function(anaphor, candidate) {</pre>
 DEBUG.FUNCTION <- FALSE
  # TODO validate: both of these should be BioNLPST objects
 anaphor.covered.text <- anaphor@covered.text
 candidate.covered.text <- candidate@covered.text</pre>
 if (DEBUG.FUNCTION) {print(paste("In function stringsMatch(). Anaphor:", anaphor.cover
ed.text, "Candidate:", candidate.covered.text))}
 # is this the right comparator for strings??
 if (anaphor.covered.text == candidate.covered.text) {
   print("Match in function stringsMatch()!")
   return(TRUE)
 } else {
    if (DEBUG.FUNCTION) { print("No match in function stringsMatch()...") }
   return(FALSE)
} # close function definition stringsMatch()
print("NO TESTS IMPLEMENETED FOR stringsMatch() FUNCTION.")
```

[1] "NO TESTS IMPLEMENETED FOR stringsMatch() FUNCTION."

```
# note that you should only be calling this if you have already found that they *don't*
match *without* toggling the case.
# args: two base noun groups
# returns: T/F
stringsMatchIfCaseToggled <- function(anaphor, candidate) {</pre>
 DEBUG.FUNCTION <- FALSE
 # TODO validate: both of these should be BioNLPST objects
 if (DEBUG.FUNCTION) {
    print("In function stringsMatchIfCaseToggled()")
   print("Anaphor:")
   class(anaphor)
   mode(anaphor)
   str(anaphor)
   print("Candidate:")
   class(candidate)
   mode(candidate)
    str(candidate)
 }
 anaphor.lowercase <- tolower(anaphor@covered.text)</pre>
 candidate.lowercase <- tolower(candidate@covered.text)</pre>
 # is this the right comparator for strings??
 if (anaphor.lowercase == candidate.lowercase) {
   return (TRUE)
 } else {
   return(FALSE)
} # close function definition stringsMatchIfCaseToggled()
# TODO: convert from list to BioNLPST object
# anaphor and candidate are base noun groups
# returns: TRUE/FALSE
# OOH, BIG BUG (that I have fixed): I have assumed that you ALREADY checked that the PAR
AGRAPH indices match!!! So, I was just checking the sentence indices. So, the function w
ould return TRUE even if the sentences were in different paragraphs. For example, the fi
rst sentence of paragraph 1 and the first sentence of paragraph 2 would return TRUE. Iss
ue here is that what I *really* want to know is not whether or not they have the same se
ntence index number, but whether or not they are in THE SAME SENTENCE... So, I have now
added a check of the paragraph indices into the sentence-indices-checking function. All
is now well.
sentenceIndicesMatch <- function(anaphor, candidate) {</pre>
 # if they're not in the same paragraph, then they're not in the same sentence...
 if ( ! (paragraphIndicesMatch(anaphor, candidate)) ){
   return(FALSE)
  }
  # now that we've verified that they're in the same paragraph, we can go on to check wh
ether or not they're in the same sentence within that paragraph.
 if (anaphor$sentenceIndex == candidate$sentenceIndex) {
   return (TRUE)
 } else {
    return (FALSE)
```

```
} # close function definition sentenceIndicesMatch()

# anaphor and candidate are base noun groups
# returns: TRUE/FALSE
paragraphIndicesMatch <- function(anaphor, candidate) {
    if (anaphor$paragraphIndex == candidate$paragraphIndex) {
        return(TRUE)
    } else {
        return(FALSE)
    }

} # close function definition paragraphIndicesMatch()

testNonSemanticRules <- function() {
    print("NON-SEMANTIC RULES NOT IMPLEMENTED.")
    print("BE SURE TO TEST FOR MISMATCH BETWEEN ZERO-BASED AND 1-BASED INDICES.")
} # close function definition testNonSemanticRules()

testNonSemanticRules()</pre>
```

```
## [1] "NON-SEMANTIC RULES NOT IMPLEMENTED."
## [1] "BE SURE TO TEST FOR MISMATCH BETWEEN ZERO-BASED AND 1-BASED INDICES."
```

How to compare relative sentence positions?

What do you need to do for a Hobbs-like approach to coreference resolution? You need to know things like whether or not the candidate is at the beginning of the preceding sentence, end of the preceding sentence, further away than the preceding sentence... What would you have to do to represent that?

Let's suppose you wanted a function that returned true if the candidate is in the preceding sentence, and false otherwise... (We'll leave aside the "beginning" versus "end" issue for the moment.)

- 1. First and second sentences of the same paragraph should return TRUE.
- 2. Last sentence of one paragraph and first sentence of the next paragraph should return TRUE.

What would the sentence index and paragraph index relationships be in those two cases?

- 1. Paragraph indices are identical. Sentence index of anaphor is > sentence index of candidate.
- Paragraph index of anaphor is 1 larger than paragraph index of candidate; sentence index of anaphor is 1
 (or zero in a language other than R); sentence index of candidate equals the maximum value of sentence
 index for its paragraph.

```
# NB: not great from a programming point of view--there are two exit points...
# @args: two base noun groups
# returns: boolean
inSameSentence <- function(anaphor, candidate) {</pre>
  if (paragraphIndicesMatch(anaphor = anaphor, candidate = candidate)) {
    if (sentenceIndicesMatch(anaphor = anaphor, candidate = candidate)) { return(TRUE) }
else { return(FALSE) }
 } else {
   return(FALSE)
} # close function definition inSameSentence()
#inAdjacentSentences <- function(anaphor, candidate) {</pre>
  if (paragraphIndicesMatch(anaphor = anaphor, candidate = candidate)) {
     if (anaphor$sentenceIndex == (candidate$sentenceIndex + 1)) {
       return(TRUE) # leaves out possibility of cataphoric reference
# } elsif (anaphor$sentenceIndex == min(#oh, this is bad--I need the max sentence index
for a paragraph...)) {}
#} # close function definition inAdjacentSentences()
```

```
# given two sentences: is this one the immediate precedent of that one?
# TODO: convert from list to BioNLPST object
# given one sentence: is a given entity/markable at the left edge, at the right edge, or
neither?
# args: sentence beginning/end, entity beginning/end
# returns: boolean TRUE if at beginning of sentence, FALSE if not
atLeftEdge <- function(sentence.offsets, entity.offsets) {</pre>
  sentence.start <- sentence.offsets[1]</pre>
  sentence.end <- sentence.offsets[2]</pre>
 entity.start <- entity.offsets[1]</pre>
  entity.end <- entity.offsets[2]</pre>
  if (sentence.start == entity.start) {
    return (TRUE)
  } else {
    return(FALSE)
} # close function definition atLeftEdge()
# test
if (atLeftEdge(c(1, 100), c(1, 10))) { print(".")} # should return TRUE
```

```
## [1] "."
```

```
if ( ! atLeftEdge(c(1, 100), c(90, 100))) { print(".") } # should return FALSE
```

```
## [1] "."
```

```
# TODO: convert from list to BioNLPST object
# args:
# returns: boolean TRUE if entity at end of sentence, FALSE otherwise
atRightEdge <- function(sentence.offsets, entity.offsets) {
   sentence.start <- sentence.offsets[1]
   sentence.end <- sentence.offsets[2]
   entity.start <- entity.offsets[1]
   entity.end <- entity.offsets[2]
   if (sentence.end == entity.end) {
      return(TRUE)
   } else {
      return(FALSE)
   }
} # close function definition atRightEdge()
# test
if (! atRightEdge(c(1, 100), c(1, 10))) { print(".")} # should return FALSE</pre>
```

```
## [1] "."
```

```
if (atRightEdge(c(1, 100), c(90, 100))) { print(".") } # should return TRUE
```

```
## [1] "."
```

```
# TODO: convert from list to BioNLPST object
# ASSUMPTION: TWO-CHARACTER DIFFERENCE BETWEEN SENTENCES!
# args: start/end offsets for two separate sentences.
# assumption: the one on the left really is on the left
# returns: boolean TRUE if the one on the left immediately precedes the one on the right
# assumption/limitation: cataphoric reference is not covered
sentencesAdjacent <- function(left.sentence.offsets, right.sentence.offsets) {</pre>
  left.sentence.start <- left.sentence.offsets[1]</pre>
 left.sentence.end <- left.sentence.offsets[2]</pre>
 right.sentence.start <- right.sentence.offsets[1]</pre>
 right.sentence.end <- right.sentence.offsets[2]
 if (left.sentence.end + 2 == right.sentence.start) {
    return (TRUE)
  } else {
    return(FALSE)
} # close function definition sentencesAdjacent()
if (sentencesAdjacent(c(1, 100), c(102, 202))) { print(".") }
```

```
## [1] "."
```

```
if ( ! sentencesAdjacent(c(1, 100), c(200, 300))) { print(".") }
```

[1] "."

What would happen if I looped through the sentence offsets for an entire file? Every p air should return TRUE--if not, I'll have found some special cases that need to be taken care of...

Process a file

This part of the code reads in the contents of a file and stores all potential anaphora/candidates in a vector of base noun groups (loosely defined). Subsequent parts of the code will then operate on that vector.

Assumption: there will not be enough stuff in that vector to exceed available memory.

```
#DEBUG <- TRUE
DEBUG <- FALSE
# store the full set of annotations in this object ...
bngs <- c() # bng = base noun group. We will make the (incorrect) assumption
# that every annotation is of a base noun group. Later we can filter for character overl
aps...
# can I make absolutely sure that bngs is and remains forever a vector, # versus a list?
#covered.texts.anis <- c()</pre>
filename <- "/Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/testData/
11319941.bionlp"
#lines <- readLines("/Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/t
estData/11319941.bionlp")
lines <- readLines(filename)</pre>
number.of.lines <- length(lines)</pre>
if (DEBUG) { print(paste("Number of lines read in:", number.of.lines)) }
if (DEBUG) { print("First 5 lines:") }
if (DEBUG) { print(lines[1:5]) }
if (DEBUG) { print(paste("")) }
#print("Last 5 lines:")
# clunky, but: should print the last 5 lines
#...but, I think it prints the whole fucking array ;-)
#print(lines[length(lines)-4:length(lines)])
#print("") # I just want a little space in the output
#before the next stuff starts happening...
# set this as you like. use it to cut down on how much output you get if you're debuggin
q and don't want/need to see hundreds of lines. For the contents of an entire file, set
the variable to the number of lines in the file (length(lines)). To limit the amount of
output that you have to wade through, set it to a smaller number than that!
#number.of.lines.to.print <- 3</pre>
number.of.lines.to.print <- number.of.lines</pre>
if (DEBUG) { print("START ITERATING OVER LINES") }
 for (i in 1:number.of.lines.to.print) {
    line <- lines[i]</pre>
    if (DEBUG) { print(paste("Read in line", i, ":", line)) }
    new.bionlpst <- lineToBioNLPST(line)</pre>
    if (DEBUG) { print("RETURNED FROM lineToBioNLPST():") }
    if (DEBUG) { bioprint(new.bionlpst) }
    if (DEBUG) { print(paste("Type of object returned by new:", typeof(new.bionlpst))) }
    if (DEBUG) { print(paste("...which is a", is(new.bionlpst))) }
    #print(new.bionlpst[[slots]])
    if (DEBUG) { print(str(new.bionlpst)) } # this is printing NULL--why?? # especially
    # puzzling in light of the fact that the next line does print out
    # the covered text...
    if (DEBUG) { print(paste("Covered text:", new.bionlpst@covered.text)) }
```

```
bngs <- c(bngs, new.bionlpst)
if (DEBUG) { print("Just added this object to the list bngs:") }
if (DEBUG) { print(new.bionlpst) }
if (DEBUG) { print("Call some method with it:") }
if (DEBUG) { hasSemanticClassLabel(new.bionlpst) }
if (DEBUG) { print("Great, it didn't crash! Pass it and a copy of it to some method:") }
if (DEBUG) { getSemanticClassLabel(new.bionlpst) }
if (DEBUG) { print("Great, it didn't crash when I called hasSemanticClassLabel()!") }
if (DEBUG) { copy.new.bionlpst <- new.bionlpst }
if (DEBUG) { stringsMatchIfCaseToggled(new.bionlpst, copy.new.bionlpst) }
if (DEBUG) { print("Great, it still hasn't crashed!") }
if (DEBUG) { stringsMatch(new.bionlpst, copy.new.bionlpst) }
}
}
# close for-loop through file</pre>
```

```
## Warning in lineToBioNLPST(line): NAs introduced by coercion
```

```
if (DEBUG) { print("FINISHED ITERATING THROUGH FILE.")}
if (DEBUG) { print("")}

# now let's see what's in the vector bngs, since that's what's giving
# me trouble later...
if (DEBUG) {
  print(paste("Length of vector bngs:", length(bngs)))
  print(paste("First three elements of bngs:"))
  print(bngs[1:3])
} # close if-debug
```

Try the string match functions

```
DEBUG.CHUNK = FALSE
library(tidyverse)
# store IdentPairs here. Must be a tibble to take full advantage of it...
# ident.pairs <- as_tibble(filenames = c(),</pre>
                           pair.ids = c(),
#
                           anaphor.ids = c(),
#
                            antecedent.ids = c(),
                            sieves = c()) # wait, no--fuck... my representation of IdentP
airs is as a class!!! OK, let's rethink this...
current.pair.id = 0 # an incrementable counter for IdentPairs. Can I increment this with
in a ctor?
ident.pairs.in.list <- c()</pre>
# At this point in the game, you have all of the annotations in the file (which contains
one per line) stored in bngs.
# The problem is, you mean for bngs to be a vector, but for some reason, it's a fucking
list:
# So: you must go through it as a list.
# override the value of this variable if you don't want to see the entire
# file contents
number.of.lines <- 3
number.of.lines <- length(bngs)</pre>
print(paste("LOOP THROUGH THE list, first", number.of.lines))
```

```
## [1] "LOOP THROUGH THE list, first 542"
```

```
for (i in 1:number.of.lines) {
 # what happens if you try this with the first one??
 # at that point, you don't have a preceding one to check against...
 if (1 == i) { next; }
 # variable bngs is supposed to be a vector of BioNLPST objects,
 # but I'm getting a complaint about type when I call the string-
 # matching function, so let's check:
 if (DEBUG.CHUNK) { print(paste("Type of current bngs element:", is(bngs[[i]]))) }
 # Can't build the SeuratObject library--tripping over some C++ stuff, and
 # I don't want to go down that rabbit hole...
 #SeuratObject::ListToS4()
 anaphor <- bngs[[i]]</pre>
 candidate <- bngs[[i-1]]</pre>
 if (stringsMatch(anaphor = anaphor, candidate = candidate)) {
   print(paste("STRINGS MATCH!", getString(anaphor), getString(candidate)))
    if (DEBUG.CHUNK) {
      print("Anaphor:")
      bioprint(anaphor)
      print("Candidate:")
      bioprint(candidate)
    # add pair to *something* here
    current.pair.id <- current.pair.id + 1 # need to increment the numeric</pre>
                                            # ID for pairs every time that you
                                            # match any sieve
                                            # ...so I should have a function for
                                            # adding new pairs to wherever it
                                            # is that I'm storing them...
   current.pair <- new (Class = "IdentPair",</pre>
                         filename = filename,
                         pair.id = current.pair.id,
                         anaphor.id = getBioNlpStId(anaphor),
                         antecedent.id = getBioNlpStId(candidate),
                         sieve = "STRING.MATCH.EXACT")
    identPrint(current.pair)
    ident.pairs.in.list <- c(ident.pairs.in.list, current.pair)</pre>
  } # close if-exact-string-match
 #if (stringsMatchIfCaseToggled(bngs[[i]], bngs[[i - 1]])) {
 if (stringsMatchIfCaseToggled(anaphor = anaphor, candidate = candidate)) {
    #print(paste("Strings match if case-toggled:", bngs[[i]]@covered.text), bngs[[i-1]]@
covered.text)
   print(paste("STRINGS MATCHED! (case-toggled)", getString(anaphor), getString(candida
te)))
   current.pair <- new (Class = "IdentPair",</pre>
                         filename = filename,
                         pair.id = current.pair.id,
                         anaphor.id = getBioNlpStId(anaphor),
                         antecedent.id = getBioNlpStId(candidate),
```

```
sieve = "STRING.MATCH.CASE.TOGGLED")
ident.pairs.in.list <- c(ident.pairs.in.list, current.pair)

if (DEBUG.CHUNK) {
    print("Anaphor:")
    bioprint(anaphor)
    print("Candidate:")
    bioprint(candidate)
}

# close if-case-toggled-string-match
} # close for-loop through file</pre>
```

```
## [1] "STRINGS MATCHED! (case-toggled) brain Brain"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! neuron neuron"
## [1] "IdentPair 1"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T28"
## [1] "Antecedent: T27"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) neuron neuron"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! neuron neuron"
## [1] "IdentPair 2"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T29"
## [1] "Antecedent: T28"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) neuron neuron"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! striatal striatal"
## [1] "IdentPair 3"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T33"
## [1] "Antecedent: T32"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) striatal striatal"
## [1] "STRINGS MATCHED! (case-toggled) Brain brain"
## [1] "STRINGS MATCHED! (case-toggled) brain Brain"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! mice mice"
## [1] "IdentPair 4"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T123"
## [1] "Antecedent: T122"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) mice mice"
## [1] "STRINGS MATCHED! (case-toggled) striatal Striatal"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! brain brain"
## [1] "IdentPair 5"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T128"
## [1] "Antecedent: T127"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) brain brain"
## [1] "STRINGS MATCHED! (case-toggled) Neuron neuron"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! neurons neurons"
```

```
## [1] "IdentPair 6"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T145"
## [1] "Antecedent: T144"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) neurons neurons"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! neurons neurons"
## [1] "IdentPair 7"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T146"
## [1] "Antecedent: T145"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) neurons neurons"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! neurons neurons"
## [1] "IdentPair 8"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T147"
## [1] "Antecedent: T146"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) neurons neurons"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! animals animals"
## [1] "IdentPair 9"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T159"
## [1] "Antecedent: T158"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) animals animals"
## [1] "STRINGS MATCHED! (case-toggled) Striatal striatal"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! striatal striatal"
## [1] "IdentPair 10"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T173"
## [1] "Antecedent: T172"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) striatal striatal"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! striatal striatal"
## [1] "IdentPair 11"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T190"
## [1] "Antecedent: T189"
## character(0)
## character(0)
```

```
## [1] "STRINGS MATCHED! (case-toggled) striatal striatal"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! allele allele"
## [1] "IdentPair 12"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T214"
## [1] "Antecedent: T213"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) allele allele"
## [1] "STRINGS MATCHED! (case-toggled) Striatal striatal"
## [1] "STRINGS MATCHED! (case-toggled) striatal Striatal"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! brain brain"
## [1] "IdentPair 13"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T220"
## [1] "Antecedent: T219"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) brain brain"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! striatal striatal"
## [1] "IdentPair 14"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T229"
## [1] "Antecedent: T228"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) striatal striatal"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! neurons neurons"
## [1] "IdentPair 15"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T240"
## [1] "Antecedent: T239"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) neurons neurons"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! neuron neuron"
## [1] "IdentPair 16"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T252"
## [1] "Antecedent: T251"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) neuron neuron"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! mice mice"
## [1] "IdentPair 17"
## [1] "Sieve: STRING.MATCH.EXACT"
```

```
## [1] "Anaphor: T291"
## [1] "Antecedent: T290"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) mice mice"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! neuron neuron"
## [1] "IdentPair 18"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T305"
## [1] "Antecedent: T304"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) neuron neuron"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! Vax1 Vax1"
## [1] "IdentPair 19"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T403"
## [1] "Antecedent: T402"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) Vax1 Vax1"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! brain brain"
## [1] "IdentPair 20"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T430"
## [1] "Antecedent: T429"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) brain brain"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! neuron neuron"
## [1] "IdentPair 21"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T437"
## [1] "Antecedent: T436"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) neuron neuron"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! brain brain"
## [1] "IdentPair 22"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T455"
## [1] "Antecedent: T454"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) brain brain"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! brain brain"
```

```
## [1] "IdentPair 23"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T462"
## [1] "Antecedent: T461"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) brain brain"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! brain brain"
## [1] "IdentPair 24"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T465"
## [1] "Antecedent: T464"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) brain brain"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! mice mice"
## [1] "IdentPair 25"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T474"
## [1] "Antecedent: T473"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) mice mice"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! mice mice"
## [1] "IdentPair 26"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T475"
## [1] "Antecedent: T474"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) mice mice"
## [1] "STRINGS MATCHED! (case-toggled) Brains brains"
## [1] "STRINGS MATCHED! (case-toggled) brain Brain"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! brain brain"
## [1] "IdentPair 27"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T497"
## [1] "Antecedent: T496"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) brain brain"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! brain brain"
## [1] "IdentPair 28"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T498"
## [1] "Antecedent: T497"
## character(0)
```

```
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) brain brain"
## [1] "STRINGS MATCHED! (case-toggled) Brain brain"
## [1] "Match in function stringsMatch()!"
## [1] "STRINGS MATCH! brain brain"
## [1] "IdentPair 29"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T540"
## [1] "Antecedent: T539"
## character(0)
## character(0)
## [1] "STRINGS MATCHED! (case-toggled) brain brain"
```

```
# whoops, I meant to do string-matching!
print("FINISHED LOOPING THROUGH INPUT FILE.")
```

```
## [1] "FINISHED LOOPING THROUGH INPUT FILE."
```

Try the semantic functions

TODO: Add a function that just checks whether or not the annotations come from the same ontology. I could do this by looking at the beginning strings of the two bngs, but the cleaner way would probably be to make this an additional element of the class definition, and figure it out when I call new()...

TODO: When you find a match, output the full details of each of the two bngs with bioprint().

TODO: When you find a match, store it away by the two annotation IDs.

```
# TODO: convert from list to BioNLPST object

# why am I doing this off of bngs, rather than passing in two objects? Oh, I guess I am

passing in two objects--but, doing so via bngs only makes sense if I'm doing a whole fil

e at a time. Actually, that sorta makes sense *if* I add to each individual annotation/o

bject a list of the other objects that have a matched semantic class. Wouldn't it make m

ore sense conceptually to do that via a discourse model, though?

# here's a sort of test across an entire file...

print("")
```

```
## [1] ""
```

```
print("RUNNING semanticClassesMatch() on entire file...")
```

```
## [1] "RUNNING semanticClassesMatch() on entire file..."
```

```
print("")
```

```
## [1] ""
```

```
# set to length(bngs) to process entire file,
# or to smaller number for devtesting
number.of.lines <- length(bngs)</pre>
#number.of.lines <- 3
if (DEBUG) {
  # start at 2 because you can't do this for the first one alone
  for (i in 2:number.of.lines) {
    print(paste("Index to bngs:", i))
    anaphor <- bngs[[i]]</pre>
    candidate <- bngs[[i-1]]</pre>
    if (DEBUG) {
      print("Anaphor:")
      bioprint(anaphor)
      print("Candidate:")
      bioprint(candidate)
    }
    if (semanticClassesMatch(anaphor, candidate)) {
      print(paste("Semantic match!", getSemanticClassLabel(anaphor), getSemanticClassLab
el(candidate)))
      if (TRUE) {
        print("Anaphor:")
        bioprint(anaphor)
        print("Candidate:")
        bioprint(candidate)
      current.pair <- new (Class = "IdentPair",</pre>
                      filename = filename,
                       pair.id = current.pair.id,
                       anaphor.id = getBioNlpStId(anaphor),
                       antecedent.id = getBioNlpStId(candidate),
                       sieve = "SEMANTIC.LEAF.NODE.MATCH")
      ident.pairs.in.list <- c(ident.pairs.in.list, current.pair)</pre>
  } # close for-loop through all annotations
  print("")
  print("FINISHED RUNNING SEMANTIC CHECKS ON FULL FILE")
 print("")
  # TODO: add a filter for noncontinuous annotations until such a time as I can handle t
} # close run across entire file
```

```
## [1] "Index to bngs: 2"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T2"
## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatum"
## [1] "Start position: 36"
## [1] "End position: 44"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T1"
## [1] "Label: NCBITaxon:10088"
## [1] "Covered text: mouse"
## [1] "Start position: 30"
## [1] "End position: 35"
## [1] "anaphor semantic class: UBERON:0002435"
## [1] "candidate semantic class: NCBITaxon:10088"
## [1] "Index to bngs: 3"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T3"
## [1] "Label: SO:0000771"
## [1] "Covered text: QTLs"
## [1] "Start position: 58"
## [1] "End position: 62"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T2"
## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatum"
## [1] "Start position: 36"
## [1] "End position: 44"
## [1] "anaphor semantic class: SO:0000771"
## [1] "candidate semantic class: UBERON:0002435"
## [1] "Index to bngs: 4"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T4"
## [1] "Label: GO:0065007"
## [1] "Covered text: modulate"
## [1] "Start position: 63"
## [1] "End position: 71"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T3"
## [1] "Label: SO:0000771"
## [1] "Covered text: QTLs"
## [1] "Start position: 58"
## [1] "End position: 62"
## [1] "anaphor semantic class: GO:0065007"
## [1] "candidate semantic class: SO:0000771"
## [1] "Index to bngs: 5"
```

[1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T5" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 83" ## [1] "End position: 89" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T4" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulate" ## [1] "Start position: 63" ## [1] "End position: 71" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: GO:0065007" ## [1] "Index to bngs: 6" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T6" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 124" ## [1] "End position: 132" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T5" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 83" ## [1] "End position: 89" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 7" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T7" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulating" ## [1] "Start position: 157" ## [1] "End position: 167" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T6" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 124" ## [1] "End position: 132" ## [1] "anaphor semantic class: GO:0065007" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 8" ## [1] "Anaphor:"

[1] "Filename: myfilename" ## [1] "ID: T8" ## [1] "Label: GO:0050890" ## [1] "Covered text: cognitive" ## [1] "Start position: 194" ## [1] "End position: 203" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T7" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulating" ## [1] "Start position: 157" ## [1] "End position: 167" ## [1] "anaphor semantic class: GO:0050890" ## [1] "candidate semantic class: GO:0065007" ## [1] "Index to bngs: 9" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T9" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 239" ## [1] "End position: 247" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T8" ## [1] "Label: GO:0050890" ## [1] "Covered text: cognitive" ## [1] "Start position: 194" ## [1] "End position: 203" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: GO:0050890" ## [1] "Index to bngs: 10" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T10" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neuron" ## [1] "Start position: 239" ## [1] "End position: NA" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T9" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 239" ## [1] "End position: 247" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 11" ## [1] "Anaphor:" ## [1] "Filename: myfilename"

[1] "ID: T11" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 276" ## [1] "End position: 280" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T10" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neuron" ## [1] "Start position: 239" ## [1] "End position: NA" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 12" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T12" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 344" ## [1] "End position: 349" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T11" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 276" ## [1] "End position: 280" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 13" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T13" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulate" ## [1] "Start position: 355" ## [1] "End position: 363" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T12" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 344" ## [1] "End position: 349" ## [1] "anaphor semantic class: GO:0065007" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 14" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T14"

[1] "Label: UBERON:0010011" ## [1] "Covered text: basal ganglia" ## [1] "Start position: 385" ## [1] "End position: 398" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T13" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulate" ## [1] "Start position: 355" ## [1] "End position: 363" ## [1] "anaphor semantic class: UBERON:0010011" ## [1] "candidate semantic class: GO:0065007" ## [1] "Index to bngs: 15" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T15" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 410" ## [1] "End position: 415" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T14" ## [1] "Label: UBERON:0010011" ## [1] "Covered text: basal ganglia" ## [1] "Start position: 385" ## [1] "End position: 398" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0010011" ## [1] "Index to bngs: 16" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T16" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 424" ## [1] "End position: 429" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T15" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 410" ## [1] "End position: 415" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Semantic match! UBERON:0000955 UBERON:0000955" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T16" ## [1] "Label: UBERON:0000955"

[1] "Covered text: brain" ## [1] "Start position: 424" ## [1] "End position: 429" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T15" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 410" ## [1] "End position: 415" ## [1] "Index to bngs: 17" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T17" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 434" ## [1] "End position: 442" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T16" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 424" ## [1] "End position: 429" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 18" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T18" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neuron" ## [1] "Start position: 434" ## [1] "End position: NA" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T17" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 434" ## [1] "End position: 442" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 19" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T19" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: Striatal" ## [1] "Start position: 661" ## [1] "End position: 669"

- ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T18" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neuron" ## [1] "Start position: 434" ## [1] "End position: NA" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 20" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T20" ## [1] "Label: CL:0000540" ## [1] "Covered text: Neuron" ## [1] "Start position: 703" ## [1] "End position: 709" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T19" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: Striatal" ## [1] "Start position: 661" ## [1] "End position: 669" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 21" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T21" ## [1] "Label: CL:0000540" ## [1] "Covered text: neurons" ## [1] "Start position: 770" ## [1] "End position: 777" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T20" ## [1] "Label: CL:0000540" ## [1] "Covered text: Neuron" ## [1] "Start position: 703" ## [1] "End position: 709" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: CL:0000540" ## [1] "Semantic match! CL:0000540 CL:0000540" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T21" ## [1] "Label: CL:0000540" ## [1] "Covered text: neurons" ## [1] "Start position: 770" ## [1] "End position: 777" ## [1] "Candidate:"

[1] "Filename: myfilename" ## [1] "ID: T20" ## [1] "Label: CL:0000540" ## [1] "Covered text: Neuron" ## [1] "Start position: 703" ## [1] "End position: 709" ## [1] "Index to bngs: 22" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T22" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 791" ## [1] "End position: 799" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T21" ## [1] "Label: CL:0000540" ## [1] "Covered text: neurons" ## [1] "Start position: 770" ## [1] "End position: 777" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 23" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T23" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neuron" ## [1] "Start position: 791" ## [1] "End position: 806" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T22" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 791" ## [1] "End position: 799" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 24" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T24" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 857" ## [1] "End position: 864" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T23" ## [1] "Label: CL:0002613"

[1] "Covered text: striatal neuron" ## [1] "Start position: 791" ## [1] "End position: 806" ## [1] "anaphor semantic class: NCBITaxon:33208" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 25" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T25" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brains" ## [1] "Start position: 877" ## [1] "End position: 883" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T24" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 857" ## [1] "End position: 864" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: NCBITaxon:33208" ## [1] "Index to bngs: 26" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T26" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striata" ## [1] "Start position: 895" ## [1] "End position: 902" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T25" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brains" ## [1] "Start position: 877" ## [1] "End position: 883" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 27" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T27" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 913" ## [1] "End position: 919" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T26" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striata"

[1] "Start position: 895" ## [1] "End position: 902" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 28" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T28" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 975" ## [1] "End position: 981" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T27" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 913" ## [1] "End position: 919" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: CL:0000540" ## [1] "Semantic match! CL:0000540 CL:0000540" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T28" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 975" ## [1] "End position: 981" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T27" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 913" ## [1] "End position: 919" ## [1] "Index to bngs: 29" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T29" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 1067" ## [1] "End position: 1073" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T28" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 975" ## [1] "End position: 981" ## [1] "anaphor semantic class: CL:0000540"

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[1] "Covered text: neurons" ## [1] "Start position: 1859" ## [1] "End position: 1866" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 49" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T49" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 1907" ## [1] "End position: 1911" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T48" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 1874" ## [1] "End position: 1882" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 50" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T50" ## [1] "Label: NCBITaxon:9606" ## [1] "Covered text: humans" ## [1] "Start position: 1941" ## [1] "End position: 1947" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T49" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 1907" ## [1] "End position: 1911" ## [1] "anaphor semantic class: NCBITaxon:9606" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 51" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T51" ## [1] "Label: GO:0042995" ## [1] "Covered text: projection" ## [1] "Start position: 1997" ## [1] "End position: 2007" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T50" ## [1] "Label: NCBITaxon:9606" ## [1] "Covered text: humans"

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## [1] "Label: CL:0000099"
## [1] "Covered text: interneurons"
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## [1] "End position: 2354"
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## [1] "ID: T60"
## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatal"
## [1] "Start position: 2333"
## [1] "End position: 2341"
## [1] "anaphor semantic class: CL:0000099"
## [1] "candidate semantic class: UBERON:0002435"
## [1] "Index to bngs: 62"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T62"
## [1] "Label: GO:0050890"
## [1] "Covered text: cognition"
## [1] "Start position: 2426"
## [1] "End position: 2435"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T61"
## [1] "Label: CL:0000099"
## [1] "Covered text: interneurons"
## [1] "Start position: 2342"
## [1] "End position: 2354"
## [1] "anaphor semantic class: GO:0050890"
## [1] "candidate semantic class: CL:0000099"
## [1] "Index to bngs: 63"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T63"
## [1] "Label: http://purl.obolibrary.org/obo/MONDO 0007739"
## [1] "Covered text: Huntington disease"
## [1] "Start position: 2452"
## [1] "End position: 2470"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T62"
## [1] "Label: GO:0050890"
## [1] "Covered text: cognition"
## [1] "Start position: 2426"
## [1] "End position: 2435"
## [1] "anaphor semantic class: http://purl.obolibrary.org/obo/MONDO 0007739"
## [1] "candidate semantic class: GO:0050890"
```

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## [1] "Index to bngs: 64"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T64"
## [1] "Label: CL:1001474"
## [1] "Covered text: medium spiny neurons"
## [1] "Start position: 2518"
## [1] "End position: 2538"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T63"
## [1] "Label: http://purl.obolibrary.org/obo/MONDO 0007739"
## [1] "Covered text: Huntington disease"
## [1] "Start position: 2452"
## [1] "End position: 2470"
## [1] "anaphor semantic class: CL:1001474"
## [1] "candidate semantic class: http://purl.obolibrary.org/obo/MONDO_0007739"
## [1] "Index to bngs: 65"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T65"
## [1] "Label: http://purl.obolibrary.org/obo/MONDO 0005395"
## [1] "Covered text: movement disorder"
## [1] "Start position: 2557"
## [1] "End position: 2574"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T64"
## [1] "Label: CL:1001474"
## [1] "Covered text: medium spiny neurons"
## [1] "Start position: 2518"
## [1] "End position: 2538"
## [1] "anaphor semantic class: http://purl.obolibrary.org/obo/MONDO 0005395"
## [1] "candidate semantic class: CL:1001474"
## [1] "Index to bngs: 66"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T66"
## [1] "Label: NCBITaxon:9606"
## [1] "Covered text: humans"
## [1] "Start position: 2583"
## [1] "End position: 2589"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T65"
## [1] "Label: http://purl.obolibrary.org/obo/MONDO 0005395"
## [1] "Covered text: movement disorder"
## [1] "Start position: 2557"
## [1] "End position: 2574"
## [1] "anaphor semantic class: NCBITaxon:9606"
## [1] "candidate semantic class: http://purl.obolibrary.org/obo/MONDO 0005395"
## [1] "Index to bngs: 67"
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- ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T67" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 2605" ## [1] "End position: 2610" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T66" ## [1] "Label: NCBITaxon:9606" ## [1] "Covered text: humans" ## [1] "Start position: 2583" ## [1] "End position: 2589" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: NCBITaxon:9606" ## [1] "Index to bngs: 68" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T68" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 2641" ## [1] "End position: 2646" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T67" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 2605" ## [1] "End position: 2610" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 69" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T69" ## [1] "Label: GO:0065007" ## [1] "Covered text: control" ## [1] "Start position: 2661" ## [1] "End position: 2668" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T68" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 2641" ## [1] "End position: 2646" ## [1] "anaphor semantic class: GO:0065007" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 70" ## [1] "Anaphor:"
- file:///Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/TRANSLATOR-Coreference-Resolution.html

[1] "Filename: myfilename" ## [1] "ID: T70" ## [1] "Label: GO:0008283" ## [1] "Covered text: proliferation" ## [1] "Start position: 2673" ## [1] "End position: 2686" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T69" ## [1] "Label: GO:0065007" ## [1] "Covered text: control" ## [1] "Start position: 2661" ## [1] "End position: 2668" ## [1] "anaphor semantic class: GO:0008283" ## [1] "candidate semantic class: GO:0065007" ## [1] "Index to bngs: 71" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T71" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 2721" ## [1] "End position: 2729" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T70" ## [1] "Label: GO:0008283" ## [1] "Covered text: proliferation" ## [1] "Start position: 2673" ## [1] "End position: 2686" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: GO:0008283" ## [1] "Index to bngs: 72" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T72" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neurons" ## [1] "Start position: 2721" ## [1] "End position: 2737" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T71" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 2721" ## [1] "End position: 2729" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 73" ## [1] "Anaphor:" ## [1] "Filename: myfilename"

- ## [1] "ID: T73" ## [1] "Label: GO:0051867" ## [1] "Covered text: adaptive behavior" ## [1] "Start position: 2799" ## [1] "End position: 2816" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T72" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neurons" ## [1] "Start position: 2721" ## [1] "End position: 2737" ## [1] "anaphor semantic class: GO:0051867" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 74" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T74" ## [1] "Label: SO:0000704" ## [1] "Covered text: genetic" ## [1] "Start position: 2862" ## [1] "End position: 2869" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T73" ## [1] "Label: GO:0051867" ## [1] "Covered text: adaptive behavior" ## [1] "Start position: 2799" ## [1] "End position: 2816" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: GO:0051867" ## [1] "Index to bngs: 75" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T75" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 2967" ## [1] "End position: 2972" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T74" ## [1] "Label: SO:0000704" ## [1] "Covered text: genetic" ## [1] "Start position: 2862" ## [1] "End position: 2869" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: SO:0000704" ## [1] "Semantic match! SO:0000704 SO:0000704" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T75"

[1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 2967" ## [1] "End position: 2972" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T74" ## [1] "Label: SO:0000704" ## [1] "Covered text: genetic" ## [1] "Start position: 2862" ## [1] "End position: 2869" ## [1] "Index to bngs: 76" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T76" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulate" ## [1] "Start position: 2991" ## [1] "End position: 2999" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T75" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 2967" ## [1] "End position: 2972" ## [1] "anaphor semantic class: GO:0065007" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 77" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T77" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 3031" ## [1] "End position: 3039" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T76" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulate" ## [1] "Start position: 2991" ## [1] "End position: 2999" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: GO:0065007" ## [1] "Index to bngs: 78" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T78" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neurons" ## [1] "Start position: 3031"

[1] "End position: 3047" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T77" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 3031" ## [1] "End position: 3039" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 79" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T79" ## [1] "Label: GO:0050767" ## [1] "Covered text: neurogenetic control" ## [1] "Start position: 3069" ## [1] "End position: 3089" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T78" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neurons" ## [1] "Start position: 3031" ## [1] "End position: 3047" ## [1] "anaphor semantic class: GO:0050767" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 80" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T80" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 3093" ## [1] "End position: 3101" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T79" ## [1] "Label: GO:0050767" ## [1] "Covered text: neurogenetic control" ## [1] "Start position: 3069" ## [1] "End position: 3089" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: GO:0050767" ## [1] "Index to bngs: 81" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T81" ## [1] "Label: SO:0000704" ## [1] "Covered text: genetic" ## [1] "Start position: 3258" ## [1] "End position: 3265"

[1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T80" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 3093" ## [1] "End position: 3101" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 82" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T82" ## [1] "Label: SO:0000704" ## [1] "Covered text: genic" ## [1] "Start position: 3337" ## [1] "End position: 3342" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T81" ## [1] "Label: SO:0000704" ## [1] "Covered text: genetic" ## [1] "Start position: 3258" ## [1] "End position: 3265" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: SO:0000704" ## [1] "Semantic match! SO:0000704 SO:0000704" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T82" ## [1] "Label: SO:0000704" ## [1] "Covered text: genic" ## [1] "Start position: 3337" ## [1] "End position: 3342" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T81" ## [1] "Label: SO:0000704" ## [1] "Covered text: genetic" ## [1] "Start position: 3258" ## [1] "End position: 3265" ## [1] "Index to bngs: 83" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T83" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 3564" ## [1] "End position: 3569" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T82"

[1] "Label: SO:0000704" ## [1] "Covered text: genic" ## [1] "Start position: 3337" ## [1] "End position: 3342" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 84" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T84" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 3570" ## [1] "End position: 3578" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T83" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 3564" ## [1] "End position: 3569" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 85" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T85" ## [1] "Label: NCBITaxon:40674" ## [1] "Covered text: mammalian" ## [1] "Start position: 3669" ## [1] "End position: 3678" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T84" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 3570" ## [1] "End position: 3578" ## [1] "anaphor semantic class: NCBITaxon:40674" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 86" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T86" ## [1] "Label: UBERON:0001017" ## [1] "Covered text: CNS" ## [1] "Start position: 3679" ## [1] "End position: 3682" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T85" ## [1] "Label: NCBITaxon:40674"

[1] "Covered text: mammalian" ## [1] "Start position: 3669" ## [1] "End position: 3678" ## [1] "anaphor semantic class: UBERON:0001017" ## [1] "candidate semantic class: NCBITaxon:40674" ## [1] "Index to bngs: 87" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T87" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 3795" ## [1] "End position: 3800" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T86" ## [1] "Label: UBERON:0001017" ## [1] "Covered text: CNS" ## [1] "Start position: 3679" ## [1] "End position: 3682" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: UBERON:0001017" ## [1] "Index to bngs: 88" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T88" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 3801" ## [1] "End position: 3806" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T87" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 3795" ## [1] "End position: 3800" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 89" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T89" ## [1] "Label: UBERON:0005382" ## [1] "Covered text: dorsal striatum" ## [1] "Start position: 3820" ## [1] "End position: 3835" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T88" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain"

[1] "Start position: 3801" ## [1] "End position: 3806" ## [1] "anaphor semantic class: UBERON:0005382" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 90" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T90" ## [1] "Label: SO:0000771" ## [1] "Covered text: quantitative trait loci" ## [1] "Start position: 3924" ## [1] "End position: 3947" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T89" ## [1] "Label: UBERON:0005382" ## [1] "Covered text: dorsal striatum" ## [1] "Start position: 3820" ## [1] "End position: 3835" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: UBERON:0005382" ## [1] "Index to bngs: 91" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T91" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTLs" ## [1] "Start position: 3949" ## [1] "End position: 3953" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T90" ## [1] "Label: SO:0000771" ## [1] "Covered text: quantitative trait loci" ## [1] "Start position: 3924" ## [1] "End position: 3947" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: SO:0000771" ## [1] "Semantic match! SO:0000771 SO:0000771" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T91" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTLs" ## [1] "Start position: 3949" ## [1] "End position: 3953" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T90" ## [1] "Label: SO:0000771" ## [1] "Covered text: quantitative trait loci" ## [1] "Start position: 3924"

[1] "End position: 3947" ## [1] "Index to bngs: 92" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T92" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 3967" ## [1] "End position: 3975" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T91" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTLs" ## [1] "Start position: 3949" ## [1] "End position: 3953" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 93" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T93" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neuron" ## [1] "Start position: 3967" ## [1] "End position: 3982" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T92" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 3967" ## [1] "End position: 3975" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 94" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T94" ## [1] "Label: GO:0065007" ## [1] "Covered text: control" ## [1] "Start position: 4036" ## [1] "End position: 4043" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T93" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neuron" ## [1] "Start position: 3967" ## [1] "End position: 3982" ## [1] "anaphor semantic class: GO:0065007" ## [1] "candidate semantic class: CL:0002613"

[1] "Index to bngs: 95" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T95" ## [1] "Label: UBERON:0001893" ## [1] "Covered text: telencephalic" ## [1] "Start position: 4047" ## [1] "End position: 4060" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T94" ## [1] "Label: GO:0065007" ## [1] "Covered text: control" ## [1] "Start position: 4036" ## [1] "End position: 4043" ## [1] "anaphor semantic class: UBERON:0001893" ## [1] "candidate semantic class: GO:0065007" ## [1] "Index to bngs: 96" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T96" ## [1] "Label: GO:0021537" ## [1] "Covered text: telencephalic development" ## [1] "Start position: 4047" ## [1] "End position: 4072" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T95" ## [1] "Label: UBERON:0001893" ## [1] "Covered text: telencephalic" ## [1] "Start position: 4047" ## [1] "End position: 4060" ## [1] "anaphor semantic class: GO:0021537" ## [1] "candidate semantic class: UBERON:0001893" ## [1] "Index to bngs: 97" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T97" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 4102" ## [1] "End position: 4107" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T96" ## [1] "Label: GO:0021537" ## [1] "Covered text: telencephalic development" ## [1] "Start position: 4047" ## [1] "End position: 4072" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: GO:0021537" ## [1] "Index to bngs: 98"

[1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T98" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 4123" ## [1] "End position: 4129" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T97" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 4102" ## [1] "End position: 4107" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 99" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T99" ## [1] "Label: GO:0008283" ## [1] "Covered text: proliferation" ## [1] "Start position: 4130" ## [1] "End position: 4143" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T98" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 4123" ## [1] "End position: 4129" ## [1] "anaphor semantic class: GO:0008283" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 100" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T100" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 4171" ## [1] "End position: 4179" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T99" ## [1] "Label: GO:0008283" ## [1] "Covered text: proliferation" ## [1] "Start position: 4130" ## [1] "End position: 4143" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: GO:0008283" ## [1] "Index to bngs: 101" ## [1] "Anaphor:"

[1] "Filename: myfilename" ## [1] "ID: T101" ## [1] "Label: UBERON:0001890" ## [1] "Covered text: forebrain" ## [1] "Start position: 4202" ## [1] "End position: 4211" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T100" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 4171" ## [1] "End position: 4179" ## [1] "anaphor semantic class: UBERON:0001890" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 102" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T102" ## [1] "Label: SO:0000704" ## [1] "Covered text: genetic" ## [1] "Start position: 4275" ## [1] "End position: 4282" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T101" ## [1] "Label: UBERON:0001890" ## [1] "Covered text: forebrain" ## [1] "Start position: 4202" ## [1] "End position: 4211" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: UBERON:0001890" ## [1] "Index to bngs: 103" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T103" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 4326" ## [1] "End position: 4334" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T102" ## [1] "Label: SO:0000704" ## [1] "Covered text: genetic" ## [1] "Start position: 4275" ## [1] "End position: 4282" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 104" ## [1] "Anaphor:" ## [1] "Filename: myfilename"

[1] "ID: T104" ## [1] "Label: CL:0000540" ## [1] "Covered text: neurons" ## [1] "Start position: 4353" ## [1] "End position: 4360" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T103" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 4326" ## [1] "End position: 4334" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 105" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T105" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulated" ## [1] "Start position: 4385" ## [1] "End position: 4394" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T104" ## [1] "Label: CL:0000540" ## [1] "Covered text: neurons" ## [1] "Start position: 4353" ## [1] "End position: 4360" ## [1] "anaphor semantic class: GO:0065007" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 106" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T106" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuronal" ## [1] "Start position: 4520" ## [1] "End position: 4528" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T105" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulated" ## [1] "Start position: 4385" ## [1] "End position: 4394" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: GO:0065007" ## [1] "Index to bngs: 107" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T107"

[1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 4544" ## [1] "End position: 4549" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T106" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuronal" ## [1] "Start position: 4520" ## [1] "End position: 4528" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 108" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T108" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 4550" ## [1] "End position: 4558" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T107" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 4544" ## [1] "End position: 4549" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 109" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T109" ## [1] "Label: SO:0000704" ## [1] "Covered text: genetic" ## [1] "Start position: 4597" ## [1] "End position: 4604" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T108" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 4550" ## [1] "End position: 4558" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 110" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T110" ## [1] "Label: SO:0000771"

[1] "Covered text: QTL" ## [1] "Start position: 4620" ## [1] "End position: 4623" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T109" ## [1] "Label: SO:0000704" ## [1] "Covered text: genetic" ## [1] "Start position: 4597" ## [1] "End position: 4604" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 111" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T111" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuronal" ## [1] "Start position: 4662" ## [1] "End position: 4670" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T110" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 4620" ## [1] "End position: 4623" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 112" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T112" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 4689" ## [1] "End position: 4694" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T111" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuronal" ## [1] "Start position: 4662" ## [1] "End position: 4670" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 113" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T113" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum"

[1] "Start position: 4695" ## [1] "End position: 4703" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T112" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 4689" ## [1] "End position: 4694" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 114" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T114" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 4738" ## [1] "End position: 4743" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T113" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 4695" ## [1] "End position: 4703" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 115" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T115" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: Striatal" ## [1] "Start position: 4755" ## [1] "End position: 4763" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T114" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 4738" ## [1] "End position: 4743" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 116" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T116" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 4829"

[1] "End position: 4834" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T115" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: Striatal" ## [1] "Start position: 4755" ## [1] "End position: 4763" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 117" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T117" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 4853" ## [1] "End position: 4858" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T116" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 4829" ## [1] "End position: 4834" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Semantic match! UBERON:0000955 UBERON:0000955" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T117" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 4853" ## [1] "End position: 4858" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T116" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 4829" ## [1] "End position: 4834" ## [1] "Index to bngs: 118" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T118" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 5029" ## [1] "End position: 5034" ## [1] "Candidate:" ## [1] "Filename: myfilename"

[1] "ID: T117" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 4853" ## [1] "End position: 4858" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Semantic match! UBERON:0000955 UBERON:0000955" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T118" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 5029" ## [1] "End position: 5034" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T117" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 4853" ## [1] "End position: 4858" ## [1] "Index to bngs: 119" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T119" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 5192" ## [1] "End position: 5200" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T118" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 5029" ## [1] "End position: 5034" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 120" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T120" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 5244" ## [1] "End position: 5249" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T119" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal"

[1] "Start position: 5192" ## [1] "End position: 5200" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 121" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T121" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striata" ## [1] "Start position: 5273" ## [1] "End position: 5280" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T120" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 5244" ## [1] "End position: 5249" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 122" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T122" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 5335" ## [1] "End position: 5339" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T121" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striata" ## [1] "Start position: 5273" ## [1] "End position: 5280" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 123" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T123" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 5545" ## [1] "End position: 5549" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T122" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 5335"

[1] "End position: 5339" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Semantic match! NCBITaxon:10088 NCBITaxon:10088" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T123" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 5545" ## [1] "End position: 5549" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T122" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 5335" ## [1] "End position: 5339" ## [1] "Index to bngs: 124" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T124" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 5555" ## [1] "End position: 5560" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T123" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 5545" ## [1] "End position: 5549" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 125" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T125" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: Striatal" ## [1] "Start position: 5724" ## [1] "End position: 5732" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T124" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 5555" ## [1] "End position: 5560" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0000955"

[1] "Index to bngs: 126" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T126" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 5778" ## [1] "End position: 5786" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T125" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: Striatal" ## [1] "Start position: 5724" ## [1] "End position: 5732" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Semantic match! UBERON:0002435 UBERON:0002435" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T126" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 5778" ## [1] "End position: 5786" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T125" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: Striatal" ## [1] "Start position: 5724" ## [1] "End position: 5732" ## [1] "Index to bngs: 127" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T127" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 5810" ## [1] "End position: 5815" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T126" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 5778" ## [1] "End position: 5786" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 128" ## [1] "Anaphor:" ## [1] "Filename: myfilename"

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- file:///Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/TRANSLATOR-Coreference-Resolution.html

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[1] "Label: CL:0000540" ## [1] "Covered text: neurons" ## [1] "Start position: 6772" ## [1] "End position: 6779" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T146" ## [1] "Label: CL:0000540" ## [1] "Covered text: neurons" ## [1] "Start position: 6734" ## [1] "End position: 6741" ## [1] "Index to bngs: 148" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T148" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 6917" ## [1] "End position: 6921" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T147" ## [1] "Label: CL:0000540" ## [1] "Covered text: neurons" ## [1] "Start position: 6772" ## [1] "End position: 6779" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 149" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T149" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 6980" ## [1] "End position: 6988" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T148" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 6917" ## [1] "End position: 6921" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 150" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T150" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuronal" ## [1] "Start position: 7009"

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- file:///Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/TRANSLATOR-Coreference-Resolution.html

[1] "ID: T158" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 7659" ## [1] "End position: 7666" ## [1] "anaphor semantic class: NCBITaxon:33208" ## [1] "candidate semantic class: NCBITaxon:33208" ## [1] "Semantic match! NCBITaxon:33208 NCBITaxon:33208" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T159" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 7885" ## [1] "End position: 7892" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T158" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 7659" ## [1] "End position: 7666" ## [1] "Index to bngs: 160" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T160" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 7893" ## [1] "End position: 7898" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T159" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 7885" ## [1] "End position: 7892" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: NCBITaxon:33208" ## [1] "Index to bngs: 161" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T161" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 7936" ## [1] "End position: 7944" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T160" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain"

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[1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T170" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 8442" ## [1] "End position: 8449" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T169" ## [1] "Label: SO:0000704" ## [1] "Covered text: genetically" ## [1] "Start position: 8413" ## [1] "End position: 8424" ## [1] "anaphor semantic class: NCBITaxon:33208" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 171" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T171" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 8566" ## [1] "End position: 8571" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T170" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 8442" ## [1] "End position: 8449" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: NCBITaxon:33208" ## [1] "Index to bngs: 172" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T172" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 8607" ## [1] "End position: 8615" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T171" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 8566" ## [1] "End position: 8571" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 173" ## [1] "Anaphor:"

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## [1] "ID: T173"
## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatal"
## [1] "Start position: 8651"
## [1] "End position: 8659"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T172"
## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatal"
## [1] "Start position: 8607"
## [1] "End position: 8615"
## [1] "anaphor semantic class: UBERON:0002435"
## [1] "candidate semantic class: UBERON:0002435"
## [1] "Semantic match! UBERON:0002435 UBERON:0002435"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T173"
## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatal"
## [1] "Start position: 8651"
## [1] "End position: 8659"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T172"
## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatal"
## [1] "Start position: 8607"
## [1] "End position: 8615"
## [1] "Index to bngs: 174"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T174"
## [1] "Label: CL:0002613"
## [1] "Covered text: striatal neuron"
## [1] "Start position: 8651"
## [1] "End position: 8666"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T173"
## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatal"
## [1] "Start position: 8651"
## [1] "End position: 8659"
## [1] "anaphor semantic class: CL:0002613"
## [1] "candidate semantic class: UBERON:0002435"
## [1] "Index to bngs: 175"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T175"
## [1] "Label: UBERON:0002435"
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[1] "Covered text: striatal" ## [1] "Start position: 8714" ## [1] "End position: 8722" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T174" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neuron" ## [1] "Start position: 8651" ## [1] "End position: 8666" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 176" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T176" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neuron" ## [1] "Start position: 8714" ## [1] "End position: 8729" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T175" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 8714" ## [1] "End position: 8722" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 177" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T177" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 8970" ## [1] "End position: 8978" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T176" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neuron" ## [1] "Start position: 8714" ## [1] "End position: 8729" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 178" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T178" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brains"

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[1] "End position: 9059" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T180" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neuron" ## [1] "Start position: 9010" ## [1] "End position: 9025" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 182" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T182" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neuron" ## [1] "Start position: 9051" ## [1] "End position: 9066" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T181" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 9051" ## [1] "End position: 9059" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 183" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T183" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 9131" ## [1] "End position: 9139" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T182" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neuron" ## [1] "Start position: 9051" ## [1] "End position: 9066" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 184" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T184" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 9156" ## [1] "End position: 9161"

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## [1] "Label: UBERON:0002435"
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## [1] "End position: 9386"
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## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatal"
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## [1] "End position: 9438"
## [1] "Candidate:"
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## [1] "ID: T189"
## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatal"
## [1] "Start position: 9378"
## [1] "End position: 9386"
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## [1] "Label: CL:0002613"
## [1] "Covered text: striatal neuron"
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## [1] "End position: 9445"
## [1] "Candidate:"
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## [1] "ID: T190"
## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatal"
## [1] "Start position: 9430"
## [1] "End position: 9438"
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## [1] "candidate semantic class: UBERON:0002435"
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## [1] "Anaphor:"
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## [1] "ID: T192"
## [1] "Label: UBERON:0000955"
## [1] "Covered text: brain"
## [1] "Start position: 9576"
## [1] "End position: 9581"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T191"
## [1] "Label: CL:0002613"
## [1] "Covered text: striatal neuron"
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file:///Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/TRANSLATOR-Coreference-Resolution.html

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## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatal"
## [1] "Start position: 13186"
## [1] "End position: 13194"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T227"
## [1] "Label: GO:0065007"
## [1] "Covered text: control"
## [1] "Start position: 13151"
## [1] "End position: 13158"
## [1] "anaphor semantic class: UBERON:0002435"
## [1] "candidate semantic class: GO:0065007"
## [1] "Index to bngs: 229"
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## [1] "ID: T229"
## [1] "Label: UBERON:0002435"
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## [1] "End position: 13264"
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## [1] "ID: T228"
## [1] "Label: UBERON:0002435"
## [1] "Covered text: striatal"
## [1] "Start position: 13186"
## [1] "End position: 13194"
## [1] "anaphor semantic class: UBERON:0002435"
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## [1] "Covered text: striatal"
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[1] "Semantic match! CL:0000540 CL:0000540" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T252" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 15216" ## [1] "End position: 15222" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T251" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 15169" ## [1] "End position: 15175" ## [1] "Index to bngs: 253" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T253" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 15336" ## [1] "End position: 15344" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T252" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 15216" ## [1] "End position: 15222" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 254" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T254" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 15391" ## [1] "End position: 15396" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T253" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 15336" ## [1] "End position: 15344" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 255" ## [1] "Anaphor:" ## [1] "Filename: myfilename"

- ## [1] "ID: T255" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 15565" ## [1] "End position: 15573" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T254" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 15391" ## [1] "End position: 15396" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 256" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T256" ## [1] "Label: GO:0065007" ## [1] "Covered text: controlling" ## [1] "Start position: 15664" ## [1] "End position: 15675" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T255" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 15565" ## [1] "End position: 15573" ## [1] "anaphor semantic class: GO:0065007" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 257" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T257" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 15676" ## [1] "End position: 15684" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T256" ## [1] "Label: GO:0065007" ## [1] "Covered text: controlling" ## [1] "Start position: 15664" ## [1] "End position: 15675" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: GO:0065007" ## [1] "Index to bngs: 258" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T258"
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[1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neuron" ## [1] "Start position: 15676" ## [1] "End position: NA" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T257" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 15676" ## [1] "End position: 15684" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 259" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T259" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: Striatal" ## [1] "Start position: 15723" ## [1] "End position: 15731" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T258" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neuron" ## [1] "Start position: 15676" ## [1] "End position: NA" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 260" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T260" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 15762" ## [1] "End position: 15767" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T259" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: Striatal" ## [1] "Start position: 15723" ## [1] "End position: 15731" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 261" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T261" ## [1] "Label: UBERON:0002435"

[1] "Covered text: striatal" ## [1] "Start position: 15837" ## [1] "End position: 15845" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T260" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 15762" ## [1] "End position: 15767" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 262" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T262" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neuron" ## [1] "Start position: 15837" ## [1] "End position: NA" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T261" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 15837" ## [1] "End position: 15845" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 263" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T263" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 15895" ## [1] "End position: 15899" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T262" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neuron" ## [1] "Start position: 15837" ## [1] "End position: NA" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 264" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T264" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain"

[1] "Start position: 15937" ## [1] "End position: 15942" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T263" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 15895" ## [1] "End position: 15899" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 265" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T265" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 16065" ## [1] "End position: 16070" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T264" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 15937" ## [1] "End position: 15942" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 266" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T266" ## [1] "Label: UBERON:0005382" ## [1] "Covered text: dorsal striatum" ## [1] "Start position: 16127" ## [1] "End position: 16142" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T265" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 16065" ## [1] "End position: 16070" ## [1] "anaphor semantic class: UBERON:0005382" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 267" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T267" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 16154"

[1] "End position: 16159" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T266" ## [1] "Label: UBERON:0005382" ## [1] "Covered text: dorsal striatum" ## [1] "Start position: 16127" ## [1] "End position: 16142" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0005382" ## [1] "Index to bngs: 268" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T268" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 16202" ## [1] "End position: 16205" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T267" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 16154" ## [1] "End position: 16159" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 269" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T269" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 16262" ## [1] "End position: 16270" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T268" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 16202" ## [1] "End position: 16205" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 270" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T270" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 16292" ## [1] "End position: 16297"

[1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T269" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 16262" ## [1] "End position: 16270" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 271" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T271" ## [1] "Label: SO:0000771" ## [1] "Covered text: OTL" ## [1] "Start position: 16359" ## [1] "End position: 16362" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T270" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 16292" ## [1] "End position: 16297" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 272" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T272" ## [1] "Label: CL:0000540" ## [1] "Covered text: neurons" ## [1] "Start position: 16399" ## [1] "End position: 16406" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T271" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 16359" ## [1] "End position: 16362" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 273" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T273" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 16414" ## [1] "End position: 16422" ## [1] "Candidate:"

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[1] "Filename: myfilename" ## [1] "ID: T272" ## [1] "Label: CL:0000540" ## [1] "Covered text: neurons" ## [1] "Start position: 16399" ## [1] "End position: 16406" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 274" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T274" ## [1] "Label: UBERON:0001017" ## [1] "Covered text: CNS" ## [1] "Start position: 16513" ## [1] "End position: 16516" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T273" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 16414" ## [1] "End position: 16422" ## [1] "anaphor semantic class: UBERON:0001017" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 275" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T275" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 16588" ## [1] "End position: 16596" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T274" ## [1] "Label: UBERON:0001017" ## [1] "Covered text: CNS" ## [1] "Start position: 16513" ## [1] "End position: 16516" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0001017" ## [1] "Index to bngs: 276" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T276" ## [1] "Label: UBERON:0001017" ## [1] "Covered text: CNS" ## [1] "Start position: 16630" ## [1] "End position: 16633" ## [1] "Candidate:" ## [1] "Filename: myfilename"

- ## [1] "ID: T275" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 16588" ## [1] "End position: 16596" ## [1] "anaphor semantic class: UBERON:0001017" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 277" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T277" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 16649" ## [1] "End position: 16657" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T276" ## [1] "Label: UBERON:0001017" ## [1] "Covered text: CNS" ## [1] "Start position: 16630" ## [1] "End position: 16633" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0001017" ## [1] "Index to bngs: 278" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T278" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neurons" ## [1] "Start position: 16649" ## [1] "End position: NA" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T277" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 16649" ## [1] "End position: 16657" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 279" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T279" ## [1] "Label: CHEBI:15355" ## [1] "Covered text: cholinergic" ## [1] "Start position: 16658" ## [1] "End position: 16669" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T278"

[1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neurons" ## [1] "Start position: 16649" ## [1] "End position: NA" ## [1] "anaphor semantic class: CHEBI:15355" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 280" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T280" ## [1] "Label: CL:0000108" ## [1] "Covered text: cholinergic neurons" ## [1] "Start position: 16658" ## [1] "End position: 16677" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T279" ## [1] "Label: CHEBI:15355" ## [1] "Covered text: cholinergic" ## [1] "Start position: 16658" ## [1] "End position: 16669" ## [1] "anaphor semantic class: CL:0000108" ## [1] "candidate semantic class: CHEBI:15355" ## [1] "Index to bngs: 281" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T281" ## [1] "Label: CHEBI:5613" ## [1] "Covered text: haloperidol" ## [1] "Start position: 16806" ## [1] "End position: 16817" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T280" ## [1] "Label: CL:0000108" ## [1] "Covered text: cholinergic neurons" ## [1] "Start position: 16658" ## [1] "End position: 16677" ## [1] "anaphor semantic class: CHEBI:5613" ## [1] "candidate semantic class: CL:0000108" ## [1] "Index to bngs: 282" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T282" ## [1] "Label: CL:0000120" ## [1] "Covered text: granule cell" ## [1] "Start position: 16855" ## [1] "End position: 16867" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T281" ## [1] "Label: CHEBI:5613"

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## [1] "Covered text: haloperidol"
## [1] "Start position: 16806"
## [1] "End position: 16817"
## [1] "anaphor semantic class: CL:0000120"
## [1] "candidate semantic class: CHEBI:5613"
## [1] "Index to bngs: 283"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T283"
## [1] "Label: UBERON:0005381"
## [1] "Covered text: granule cell layer of ... dentate gyrus"
## [1] "Start position: 16855"
## [1] "End position: NA"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T282"
## [1] "Label: CL:0000120"
## [1] "Covered text: granule cell"
## [1] "Start position: 16855"
## [1] "End position: 16867"
## [1] "anaphor semantic class: UBERON:0005381"
## [1] "candidate semantic class: CL:0000120"
## [1] "Index to bngs: 284"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T284"
## [1] "Label: NCBITaxon:10088"
## [1] "Covered text: mice"
## [1] "Start position: 16954"
## [1] "End position: 16958"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T283"
## [1] "Label: UBERON:0005381"
## [1] "Covered text: granule cell layer of ... dentate gyrus"
## [1] "Start position: 16855"
## [1] "End position: NA"
## [1] "anaphor semantic class: NCBITaxon:10088"
## [1] "candidate semantic class: UBERON:0005381"
## [1] "Index to bngs: 285"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T285"
## [1] "Label: CL:0000540"
## [1] "Covered text: neuron"
## [1] "Start position: 17065"
## [1] "End position: 17071"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T284"
## [1] "Label: NCBITaxon:10088"
## [1] "Covered text: mice"
```

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## [1] "Start position: 16954"
## [1] "End position: 16958"
## [1] "anaphor semantic class: CL:0000540"
## [1] "candidate semantic class: NCBITaxon:10088"
## [1] "Index to bngs: 286"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T286"
## [1] "Label: CL:0000598"
## [1] "Covered text: pyramidal ... cell"
## [1] "Start position: 17097"
## [1] "End position: NA"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T285"
## [1] "Label: CL:0000540"
## [1] "Covered text: neuron"
## [1] "Start position: 17065"
## [1] "End position: 17071"
## [1] "anaphor semantic class: CL:0000598"
## [1] "candidate semantic class: CL:0000540"
## [1] "Index to bngs: 287"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T287"
## [1] "Label: UBERON:0002313"
## [1] "Covered text: pyramidal ... cell layers of ... hippocampus"
## [1] "Start position: 17097"
## [1] "End position: NA"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T286"
## [1] "Label: CL:0000598"
## [1] "Covered text: pyramidal ... cell"
## [1] "Start position: 17097"
## [1] "End position: NA"
## [1] "anaphor semantic class: UBERON:0002313"
## [1] "candidate semantic class: CL:0000598"
## [1] "Index to bngs: 288"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T288"
## [1] "Label: UBERON:0002304"
## [1] "Covered text: dentate cell layers of ... hippocampus"
## [1] "Start position: 17111"
## [1] "End position: NA"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T287"
## [1] "Label: UBERON:0002313"
## [1] "Covered text: pyramidal ... cell layers of ... hippocampus"
## [1] "Start position: 17097"
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[1] "End position: NA" ## [1] "anaphor semantic class: UBERON:0002304" ## [1] "candidate semantic class: UBERON:0002313" ## [1] "Index to bngs: 289" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T289" ## [1] "Label: CL:0000120" ## [1] "Covered text: Granule cell" ## [1] "Start position: 17156" ## [1] "End position: 17168" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T288" ## [1] "Label: UBERON:0002304" ## [1] "Covered text: dentate cell layers of ... hippocampus" ## [1] "Start position: 17111" ## [1] "End position: NA" ## [1] "anaphor semantic class: CL:0000120" ## [1] "candidate semantic class: UBERON:0002304" ## [1] "Index to bngs: 290" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T290" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 17234" ## [1] "End position: 17238" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T289" ## [1] "Label: CL:0000120" ## [1] "Covered text: Granule cell" ## [1] "Start position: 17156" ## [1] "End position: 17168" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: CL:0000120" ## [1] "Index to bngs: 291" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T291" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 17343" ## [1] "End position: 17347" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T290" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 17234" ## [1] "End position: 17238"

[1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Semantic match! NCBITaxon:10088 NCBITaxon:10088" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T291" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 17343" ## [1] "End position: 17347" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T290" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 17234" ## [1] "End position: 17238" ## [1] "Index to bngs: 292" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T292" ## [1] "Label: UBERON:0001016" ## [1] "Covered text: nervous system" ## [1] "Start position: 17426" ## [1] "End position: 17440" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T291" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 17343" ## [1] "End position: 17347" ## [1] "anaphor semantic class: UBERON:0001016" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 293" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T293" ## [1] "Label: UBERON:0009050" ## [1] "Covered text: nucleus of ... solitary tract" ## [1] "Start position: 17455" ## [1] "End position: NA" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T292" ## [1] "Label: UBERON:0001016" ## [1] "Covered text: nervous system" ## [1] "Start position: 17426" ## [1] "End position: 17440" ## [1] "anaphor semantic class: UBERON:0009050" ## [1] "candidate semantic class: UBERON:0001016" ## [1] "Index to bngs: 294"

[1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T294" ## [1] "Label: UBERON:0018545" ## [1] "Covered text: spinal nucleus of ... bulbocavernosus" ## [1] "Start position: 17495" ## [1] "End position: NA" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T293" ## [1] "Label: UBERON:0009050" ## [1] "Covered text: nucleus of ... solitary tract" ## [1] "Start position: 17455" ## [1] "End position: NA" ## [1] "anaphor semantic class: UBERON:0018545" ## [1] "candidate semantic class: UBERON:0009050" ## [1] "Index to bngs: 295" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T295" ## [1] "Label: UBERON:0001792" ## [1] "Covered text: retinal ganglion" ## [1] "Start position: 17543" ## [1] "End position: 17559" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T294" ## [1] "Label: UBERON:0018545" ## [1] "Covered text: spinal nucleus of ... bulbocavernosus" ## [1] "Start position: 17495" ## [1] "End position: NA" ## [1] "anaphor semantic class: UBERON:0001792" ## [1] "candidate semantic class: UBERON:0018545" ## [1] "Index to bngs: 296" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T296" ## [1] "Label: CL:0000740" ## [1] "Covered text: retinal ganglion cells" ## [1] "Start position: 17543" ## [1] "End position: 17565" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T295" ## [1] "Label: UBERON:0001792" ## [1] "Covered text: retinal ganglion" ## [1] "Start position: 17543" ## [1] "End position: 17559" ## [1] "anaphor semantic class: CL:0000740" ## [1] "candidate semantic class: UBERON:0001792" ## [1] "Index to bngs: 297" ## [1] "Anaphor:"

[1] "Filename: myfilename" ## [1] "ID: T297" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 17646" ## [1] "End position: 17652" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T296" ## [1] "Label: CL:0000740" ## [1] "Covered text: retinal ganglion cells" ## [1] "Start position: 17543" ## [1] "End position: 17565" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: CL:0000740" ## [1] "Index to bngs: 298" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T298" ## [1] "Label: UBERON:0001017" ## [1] "Covered text: CNS" ## [1] "Start position: 17667" ## [1] "End position: 17670" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T297" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 17646" ## [1] "End position: 17652" ## [1] "anaphor semantic class: UBERON:0001017" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 299" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T299" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 17674" ## [1] "End position: 17678" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T298" ## [1] "Label: UBERON:0001017" ## [1] "Covered text: CNS" ## [1] "Start position: 17667" ## [1] "End position: 17670" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: UBERON:0001017" ## [1] "Index to bngs: 300" ## [1] "Anaphor:" ## [1] "Filename: myfilename"

[1] "ID: T300" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 17752" ## [1] "End position: 17760" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T299" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 17674" ## [1] "End position: 17678" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 301" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T301" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 17974" ## [1] "End position: 17980" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T300" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 17752" ## [1] "End position: 17760" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 302" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T302" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 18045" ## [1] "End position: 18053" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T301" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 17974" ## [1] "End position: 17980" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 303" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T303"

- ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neuron" ## [1] "Start position: 18045" ## [1] "End position: NA" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T302" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 18045" ## [1] "End position: 18053" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 304" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T304" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 18121" ## [1] "End position: 18127" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T303" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal ... neuron" ## [1] "Start position: 18045" ## [1] "End position: NA" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 305" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T305" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 18153" ## [1] "End position: 18159" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T304" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 18121" ## [1] "End position: 18127" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: CL:0000540" ## [1] "Semantic match! CL:0000540 CL:0000540" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T305" ## [1] "Label: CL:0000540"
- file:///Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/TRANSLATOR-Coreference-Resolution.html

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[1] "Covered text: neuron" ## [1] "Start position: 18153" ## [1] "End position: 18159" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T304" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 18121" ## [1] "End position: 18127" ## [1] "Index to bngs: 306" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T306" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuronal" ## [1] "Start position: 18305" ## [1] "End position: 18313" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T305" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 18153" ## [1] "End position: 18159" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: CL:0000540" ## [1] "Semantic match! CL:0000540 CL:0000540" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T306" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuronal" ## [1] "Start position: 18305" ## [1] "End position: 18313" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T305" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 18153" ## [1] "End position: 18159" ## [1] "Index to bngs: 307" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T307" ## [1] "Label: UBERON:0002304" ## [1] "Covered text: dentate gyrus cell layers of ... hippocampus" ## [1] "Start position: 18337" ## [1] "End position: NA" ## [1] "Candidate:" ## [1] "Filename: myfilename"

```
## [1] "ID: T306"
## [1] "Label: CL:0000540"
## [1] "Covered text: neuronal"
## [1] "Start position: 18305"
## [1] "End position: 18313"
## [1] "anaphor semantic class: UBERON:0002304"
## [1] "candidate semantic class: CL:0000540"
## [1] "Index to bngs: 308"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T308"
## [1] "Label: NCBITaxon:10088"
## [1] "Covered text: mouse"
## [1] "Start position: 18398"
## [1] "End position: 18403"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T307"
## [1] "Label: UBERON:0002304"
## [1] "Covered text: dentate gyrus cell layers of ... hippocampus"
## [1] "Start position: 18337"
## [1] "End position: NA"
## [1] "anaphor semantic class: NCBITaxon:10088"
## [1] "candidate semantic class: UBERON:0002304"
## [1] "Index to bngs: 309"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T309"
## [1] "Label: CL:0000598"
## [1] "Covered text: pyramidal cell"
## [1] "Start position: 18476"
## [1] "End position: 18490"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T308"
## [1] "Label: NCBITaxon:10088"
## [1] "Covered text: mouse"
## [1] "Start position: 18398"
## [1] "End position: 18403"
## [1] "anaphor semantic class: CL:0000598"
## [1] "candidate semantic class: NCBITaxon:10088"
## [1] "Index to bngs: 310"
## [1] "Anaphor:"
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## [1] "Label: UBERON:0000119"
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## [1] "Candidate:"
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- ## [1] "Label: CL:0000598" ## [1] "Covered text: pyramidal cell" ## [1] "Start position: 18476" ## [1] "End position: 18490" ## [1] "anaphor semantic class: UBERON:0000119" ## [1] "candidate semantic class: CL:0000598" ## [1] "Index to bngs: 311" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T311" ## [1] "Label: CL:0000120" ## [1] "Covered text: granule cell" ## [1] "Start position: 18543" ## [1] "End position: 18555" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T310" ## [1] "Label: UBERON:0000119" ## [1] "Covered text: cell layers" ## [1] "Start position: 18486" ## [1] "End position: 18497" ## [1] "anaphor semantic class: CL:0000120" ## [1] "candidate semantic class: UBERON:0000119" ## [1] "Index to bngs: 312" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T312" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 18696" ## [1] "End position: 18701" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T311" ## [1] "Label: CL:0000120" ## [1] "Covered text: granule cell" ## [1] "Start position: 18543" ## [1] "End position: 18555" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: CL:0000120" ## [1] "Index to bngs: 313" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T313" ## [1] "Label: GO:0065007" ## [1] "Covered text: govern" ## [1] "Start position: 18752" ## [1] "End position: 18758" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T312" ## [1] "Label: NCBITaxon:10088"
- file: ///Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/TRANSLATOR-Coreference-Resolution.html (Control of the Control of

[1] "Covered text: mouse" ## [1] "Start position: 18696" ## [1] "End position: 18701" ## [1] "anaphor semantic class: GO:0065007" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 314" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T314" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuronal" ## [1] "Start position: 18784" ## [1] "End position: 18792" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T313" ## [1] "Label: GO:0065007" ## [1] "Covered text: govern" ## [1] "Start position: 18752" ## [1] "End position: 18758" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: GO:0065007" ## [1] "Index to bngs: 315" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T315" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 18804" ## [1] "End position: 18810" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T314" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuronal" ## [1] "Start position: 18784" ## [1] "End position: 18792" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: CL:0000540" ## [1] "Semantic match! CL:0000540 CL:0000540" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T315" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 18804" ## [1] "End position: 18810" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T314" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuronal"

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## [1] "End position: 19520"
## [1] "Candidate:"
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## [1] "ID: T326"
## [1] "Label: SO:0000771"
## [1] "Covered text: QTL"
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## [1] "Label: CL:0002613"
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## [1] "End position: 19528"
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## [1] "Covered text: brain"
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## [1] "End position: 19555"
## [1] "Candidate:"
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## [1] "ID: T328"
## [1] "Label: CL:0002613"
## [1] "Covered text: striatal neurons"
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[1] "Filename: myfilename" ## [1] "ID: T334" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulates" ## [1] "Start position: 19936" ## [1] "End position: 19945" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: GO:0065007" ## [1] "Index to bngs: 336" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T336" ## [1] "Label: SO:0001026" ## [1] "Covered text: genome" ## [1] "Start position: 19969" ## [1] "End position: 19975" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T335" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 19946" ## [1] "End position: 19954" ## [1] "anaphor semantic class: SO:0001026" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 337" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T337" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 20085" ## [1] "End position: 20093" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T336" ## [1] "Label: SO:0001026" ## [1] "Covered text: genome" ## [1] "Start position: 19969" ## [1] "End position: 19975" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: SO:0001026" ## [1] "Index to bngs: 338" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T338" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neurons" ## [1] "Start position: 20085" ## [1] "End position: 20101" ## [1] "Candidate:" ## [1] "Filename: myfilename"

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- file:///Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/TRANSLATOR-Coreference-Resolution.html

[1] "Covered text: striatum" ## [1] "Start position: 20344" ## [1] "End position: 20352" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 345" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T345" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 20551" ## [1] "End position: 20556" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T344" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: Mouse" ## [1] "Start position: 20545" ## [1] "End position: 20550" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 346" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T346" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 20731" ## [1] "End position: 20734" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T345" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 20551" ## [1] "End position: 20556" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 347" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T347" ## [1] "Label: SO:0000704" ## [1] "Covered text: gene" ## [1] "Start position: 20841" ## [1] "End position: 20845" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T346" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL"

[1] "Start position: 20731" ## [1] "End position: 20734" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 348" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T348" ## [1] "Label: SO:0001023" ## [1] "Covered text: allele" ## [1] "Start position: 20890" ## [1] "End position: 20896" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T347" ## [1] "Label: SO:0000704" ## [1] "Covered text: gene" ## [1] "Start position: 20841" ## [1] "End position: 20845" ## [1] "anaphor semantic class: SO:0001023" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 349" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T349" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 20925" ## [1] "End position: 20928" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T348" ## [1] "Label: SO:0001023" ## [1] "Covered text: allele" ## [1] "Start position: 20890" ## [1] "End position: 20896" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: SO:0001023" ## [1] "Index to bngs: 350" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T350" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 21050" ## [1] "End position: 21055" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T349" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 20925"

[1] "End position: 20928" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 351" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T351" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTLs" ## [1] "Start position: 21092" ## [1] "End position: 21096" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T350" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 21050" ## [1] "End position: 21055" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 352" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T352" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 21168" ## [1] "End position: 21173" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T351" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTLs" ## [1] "Start position: 21092" ## [1] "End position: 21096" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 353" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T353" ## [1] "Label: NCBITaxon:9606" ## [1] "Covered text: human" ## [1] "Start position: 21178" ## [1] "End position: 21183" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T352" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 21168" ## [1] "End position: 21173"

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[1] "candidate semantic class: GO:0010467" ## [1] "Index to bngs: 357" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T357" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 21276" ## [1] "End position: 21284" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T356" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 21266" ## [1] "End position: 21271" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 358" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T358" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTLs" ## [1] "Start position: 21325" ## [1] "End position: 21329" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T357" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 21276" ## [1] "End position: 21284" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 359" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T359" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 21409" ## [1] "End position: 21412" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T358" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTLs" ## [1] "Start position: 21325" ## [1] "End position: 21329" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: SO:0000771"

[1] "Semantic match! SO:0000771 SO:0000771" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T359" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 21409" ## [1] "End position: 21412" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T358" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTLs" ## [1] "Start position: 21325" ## [1] "End position: 21329" ## [1] "Index to bngs: 360" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T360" ## [1] "Label: SO:0000018" ## [1] "Covered text: cluster of linked genes" ## [1] "Start position: 21435" ## [1] "End position: 21458" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T359" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 21409" ## [1] "End position: 21412" ## [1] "anaphor semantic class: SO:0000018" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 361" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T361" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 21538" ## [1] "End position: 21545" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T360" ## [1] "Label: SO:0000018" ## [1] "Covered text: cluster of linked genes" ## [1] "Start position: 21435" ## [1] "End position: 21458" ## [1] "anaphor semantic class: NCBITaxon:33208" ## [1] "candidate semantic class: SO:0000018" ## [1] "Index to bngs: 362" ## [1] "Anaphor:" ## [1] "Filename: myfilename"

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- ## [1] "Label: GO:0007420" ## [1] "Covered text: brain development" ## [1] "Start position: 21709" ## [1] "End position: 21726" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T364" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 21709" ## [1] "End position: 21714" ## [1] "anaphor semantic class: GO:0007420" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 366" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T366" ## [1] "Label: PR:000008241" ## [1] "Covered text: Grk2" ## [1] "Start position: 21744" ## [1] "End position: 21748" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T365" ## [1] "Label: GO:0007420" ## [1] "Covered text: brain development" ## [1] "Start position: 21709" ## [1] "End position: 21726" ## [1] "anaphor semantic class: PR:000008241" ## [1] "candidate semantic class: GO:0007420" ## [1] "Index to bngs: 367" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T367" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 21806" ## [1] "End position: 21811" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T366" ## [1] "Label: PR:000008241" ## [1] "Covered text: Grk2" ## [1] "Start position: 21744" ## [1] "End position: 21748" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: PR:000008241" ## [1] "Index to bngs: 368" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T368" ## [1] "Label: GO:0065007"

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## [1] "Covered text: modulating"
## [1] "Start position: 21846"
## [1] "End position: 21856"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T367"
## [1] "Label: SO:0000704"
## [1] "Covered text: genes"
## [1] "Start position: 21806"
## [1] "End position: 21811"
## [1] "anaphor semantic class: GO:0065007"
## [1] "candidate semantic class: SO:0000704"
## [1] "Index to bngs: 369"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T369"
## [1] "Label: http://purl.obolibrary.org/obo/MONDO_0007739"
## [1] "Covered text: Huntington disease"
## [1] "Start position: 21857"
## [1] "End position: 21875"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T368"
## [1] "Label: GO:0065007"
## [1] "Covered text: modulating"
## [1] "Start position: 21846"
## [1] "End position: 21856"
## [1] "anaphor semantic class: http://purl.obolibrary.org/obo/MONDO_0007739"
## [1] "candidate semantic class: GO:0065007"
## [1] "Index to bngs: 370"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T370"
## [1] "Label: NCBITaxon:10088"
## [1] "Covered text: mouse"
## [1] "Start position: 21889"
## [1] "End position: 21894"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T369"
## [1] "Label: http://purl.obolibrary.org/obo/MONDO 0007739"
## [1] "Covered text: Huntington disease"
## [1] "Start position: 21857"
## [1] "End position: 21875"
## [1] "anaphor semantic class: NCBITaxon:10088"
## [1] "candidate semantic class: http://purl.obolibrary.org/obo/MONDO 0007739"
## [1] "Index to bngs: 371"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T371"
## [1] "Label: GO:0045202"
## [1] "Covered text: synaptic"
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[1] "Start position: 21958" ## [1] "End position: 21966" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T370" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mouse" ## [1] "Start position: 21889" ## [1] "End position: 21894" ## [1] "anaphor semantic class: GO:0045202" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 372" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T372" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 21983" ## [1] "End position: 21991" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T371" ## [1] "Label: GO:0045202" ## [1] "Covered text: synaptic" ## [1] "Start position: 21958" ## [1] "End position: 21966" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: GO:0045202" ## [1] "Index to bngs: 373" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T373" ## [1] "Label: SO:0000704" ## [1] "Covered text: gene" ## [1] "Start position: 22006" ## [1] "End position: 22010" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T372" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 21983" ## [1] "End position: 21991" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 374" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T374" ## [1] "Label: PR:000010184" ## [1] "Covered text: Macs" ## [1] "Start position: 22050"

[1] "End position: 22054" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T373" ## [1] "Label: SO:0000704" ## [1] "Covered text: gene" ## [1] "Start position: 22006" ## [1] "End position: 22010" ## [1] "anaphor semantic class: PR:000010184" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 375" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T375" ## [1] "Label: SO:0000704" ## [1] "Covered text: gene" ## [1] "Start position: 22060" ## [1] "End position: 22064" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T374" ## [1] "Label: PR:000010184" ## [1] "Covered text: Macs" ## [1] "Start position: 22050" ## [1] "End position: 22054" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: PR:000010184" ## [1] "Index to bngs: 376" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T376" ## [1] "Label: MOP:0000124" ## [1] "Covered text: myristoylated" ## [1] "Start position: 22078" ## [1] "End position: 22091" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T375" ## [1] "Label: SO:0000704" ## [1] "Covered text: gene" ## [1] "Start position: 22060" ## [1] "End position: 22064" ## [1] "anaphor semantic class: MOP:0000124" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 377" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T377" ## [1] "Label: PR:000010184" ## [1] "Covered text: myristoylated alanine-rich C kinase substrate" ## [1] "Start position: 22078" ## [1] "End position: 22123"

[1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T376" ## [1] "Label: MOP:0000124" ## [1] "Covered text: myristoylated" ## [1] "Start position: 22078" ## [1] "End position: 22091" ## [1] "anaphor semantic class: PR:000010184" ## [1] "candidate semantic class: MOP:0000124" ## [1] "Index to bngs: 378" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T378" ## [1] "Label: PR:000010184" ## [1] "Covered text: MARCKS" ## [1] "Start position: 22125" ## [1] "End position: 22131" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T377" ## [1] "Label: PR:000010184" ## [1] "Covered text: myristoylated alanine-rich C kinase substrate" ## [1] "Start position: 22078" ## [1] "End position: 22123" ## [1] "anaphor semantic class: PR:000010184" ## [1] "candidate semantic class: PR:000010184" ## [1] "Semantic match! PR:000010184 PR:000010184" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T378" ## [1] "Label: PR:000010184" ## [1] "Covered text: MARCKS" ## [1] "Start position: 22125" ## [1] "End position: 22131" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T377" ## [1] "Label: PR:000010184" ## [1] "Covered text: myristoylated alanine-rich C kinase substrate" ## [1] "Start position: 22078" ## [1] "End position: 22123" ## [1] "Index to bngs: 379" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T379" ## [1] "Label: CHEBI:36357" ## [1] "Covered text: molecule" ## [1] "Start position: 22147" ## [1] "End position: 22155" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T378"

[1] "Label: PR:000010184" ## [1] "Covered text: MARCKS" ## [1] "Start position: 22125" ## [1] "End position: 22131" ## [1] "anaphor semantic class: CHEBI:36357" ## [1] "candidate semantic class: PR:000010184" ## [1] "Index to bngs: 380" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T380" ## [1] "Label: UBERON:0001893" ## [1] "Covered text: cerebral" ## [1] "Start position: 22172" ## [1] "End position: 22180" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T379" ## [1] "Label: CHEBI:36357" ## [1] "Covered text: molecule" ## [1] "Start position: 22147" ## [1] "End position: 22155" ## [1] "anaphor semantic class: UBERON:0001893" ## [1] "candidate semantic class: CHEBI:36357" ## [1] "Index to bngs: 381" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T381" ## [1] "Label: GO:0021537" ## [1] "Covered text: cerebral development" ## [1] "Start position: 22172" ## [1] "End position: 22192" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T380" ## [1] "Label: UBERON:0001893" ## [1] "Covered text: cerebral" ## [1] "Start position: 22172" ## [1] "End position: 22180" ## [1] "anaphor semantic class: GO:0021537" ## [1] "candidate semantic class: UBERON:0001893" ## [1] "Index to bngs: 382" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T382" ## [1] "Label: PR:000010184" ## [1] "Covered text: MARCKS" ## [1] "Start position: 22194" ## [1] "End position: 22200" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T381" ## [1] "Label: GO:0021537"

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## [1] "Covered text: cerebral development"
## [1] "Start position: 22172"
## [1] "End position: 22192"
## [1] "anaphor semantic class: PR:000010184"
## [1] "candidate semantic class: GO:0021537"
## [1] "Index to bngs: 383"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T383"
## [1] "Label: NCBITaxon:10088"
## [1] "Covered text: mice"
## [1] "Start position: 22211"
## [1] "End position: 22215"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T382"
## [1] "Label: PR:000010184"
## [1] "Covered text: MARCKS"
## [1] "Start position: 22194"
## [1] "End position: 22200"
## [1] "anaphor semantic class: NCBITaxon:10088"
## [1] "candidate semantic class: PR:000010184"
## [1] "Index to bngs: 384"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T384"
## [1] "Label: http://purl.obolibrary.org/obo/MONDO 0009022"
## [1] "Covered text: agenesis of corpus callosum"
## [1] "Start position: 22254"
## [1] "End position: NA"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T383"
## [1] "Label: NCBITaxon:10088"
## [1] "Covered text: mice"
## [1] "Start position: 22211"
## [1] "End position: 22215"
## [1] "anaphor semantic class: http://purl.obolibrary.org/obo/MONDO 0009022"
## [1] "candidate semantic class: NCBITaxon:10088"
## [1] "Index to bngs: 385"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T385"
## [1] "Label: UBERON:0002336"
## [1] "Covered text: corpus callosum"
## [1] "Start position: 22270"
## [1] "End position: 22285"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T384"
## [1] "Label: http://purl.obolibrary.org/obo/MONDO 0009022"
## [1] "Covered text: agenesis of corpus callosum"
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## [1] "Start position: 22254"
## [1] "End position: NA"
## [1] "anaphor semantic class: UBERON:0002336"
## [1] "candidate semantic class: http://purl.obolibrary.org/obo/MONDO_0009022"
## [1] "Index to bngs: 386"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T386"
## [1] "Label: UBERON:0001890"
## [1] "Covered text: forebrain"
## [1] "Start position: 22311"
## [1] "End position: 22320"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T385"
## [1] "Label: UBERON:0002336"
## [1] "Covered text: corpus callosum"
## [1] "Start position: 22270"
## [1] "End position: 22285"
## [1] "anaphor semantic class: UBERON:0001890"
## [1] "candidate semantic class: UBERON:0002336"
## [1] "Index to bngs: 387"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T387"
## [1] "Label: UBERON:0001950"
## [1] "Covered text: neocortical"
## [1] "Start position: 22352"
## [1] "End position: 22363"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T386"
## [1] "Label: UBERON:0001890"
## [1] "Covered text: forebrain"
## [1] "Start position: 22311"
## [1] "End position: 22320"
## [1] "anaphor semantic class: UBERON:0001950"
## [1] "candidate semantic class: UBERON:0001890"
## [1] "Index to bngs: 388"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T388"
## [1] "Label: PR:000010185"
## [1] "Covered text: MARCKS-related protein"
## [1] "Start position: 22387"
## [1] "End position: 22409"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T387"
## [1] "Label: UBERON:0001950"
## [1] "Covered text: neocortical"
## [1] "Start position: 22352"
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[1] "End position: 22363" ## [1] "anaphor semantic class: PR:000010185" ## [1] "candidate semantic class: UBERON:0001950" ## [1] "Index to bngs: 389" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T389" ## [1] "Label: SO:0000704" ## [1] "Covered text: gene" ## [1] "Start position: 22410" ## [1] "End position: 22414" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T388" ## [1] "Label: PR:000010185" ## [1] "Covered text: MARCKS-related protein" ## [1] "Start position: 22387" ## [1] "End position: 22409" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: PR:000010185" ## [1] "Index to bngs: 390" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T390" ## [1] "Label: GO:0010467" ## [1] "Covered text: expressed" ## [1] "Start position: 22418" ## [1] "End position: 22427" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T389" ## [1] "Label: SO:0000704" ## [1] "Covered text: gene" ## [1] "Start position: 22410" ## [1] "End position: 22414" ## [1] "anaphor semantic class: GO:0010467" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 391" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T391" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 22435" ## [1] "End position: 22443" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T390" ## [1] "Label: GO:0010467" ## [1] "Covered text: expressed" ## [1] "Start position: 22418" ## [1] "End position: 22427"

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[1] "candidate semantic class: GO:0007420" ## [1] "Index to bngs: 395" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T395" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 22513" ## [1] "End position: 22516" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T394" ## [1] "Label: NCBITaxon:10114" ## [1] "Covered text: rat" ## [1] "Start position: 22482" ## [1] "End position: 22485" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: NCBITaxon:10114" ## [1] "Index to bngs: 396" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T396" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulating" ## [1] "Start position: 22517" ## [1] "End position: 22527" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T395" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 22513" ## [1] "End position: 22516" ## [1] "anaphor semantic class: GO:0065007" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 397" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T397" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 22528" ## [1] "End position: 22536" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T396" ## [1] "Label: GO:0065007" ## [1] "Covered text: modulating" ## [1] "Start position: 22517" ## [1] "End position: 22527" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: GO:0065007"

- ## [1] "Index to bngs: 398" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T398" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neuron" ## [1] "Start position: 22528" ## [1] "End position: 22543" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T397" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 22528" ## [1] "End position: 22536" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 399" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T399" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 22625" ## [1] "End position: 22630" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T398" ## [1] "Label: CL:0002613" ## [1] "Covered text: striatal neuron" ## [1] "Start position: 22528" ## [1] "End position: 22543" ## [1] "anaphor semantic class: SO:0000704" ## [1] "candidate semantic class: CL:0002613" ## [1] "Index to bngs: 400" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T400" ## [1] "Label: UBERON:0001893" ## [1] "Covered text: telencephalic" ## [1] "Start position: 22693" ## [1] "End position: 22706" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T399" ## [1] "Label: SO:0000704" ## [1] "Covered text: genes" ## [1] "Start position: 22625" ## [1] "End position: 22630" ## [1] "anaphor semantic class: UBERON:0001893" ## [1] "candidate semantic class: SO:0000704" ## [1] "Index to bngs: 401"
- file:///Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/TRANSLATOR-Coreference-Resolution.html

[1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T401" ## [1] "Label: GO:0021537" ## [1] "Covered text: telencephalic development" ## [1] "Start position: 22693" ## [1] "End position: 22718" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T400" ## [1] "Label: UBERON:0001893" ## [1] "Covered text: telencephalic" ## [1] "Start position: 22693" ## [1] "End position: 22706" ## [1] "anaphor semantic class: GO:0021537" ## [1] "candidate semantic class: UBERON:0001893" ## [1] "Index to bngs: 402" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T402" ## [1] "Label: PR:000017268" ## [1] "Covered text: Vax1" ## [1] "Start position: 22733" ## [1] "End position: 22737" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T401" ## [1] "Label: GO:0021537" ## [1] "Covered text: telencephalic development" ## [1] "Start position: 22693" ## [1] "End position: 22718" ## [1] "anaphor semantic class: PR:000017268" ## [1] "candidate semantic class: GO:0021537" ## [1] "Index to bngs: 403" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T403" ## [1] "Label: PR:000017268" ## [1] "Covered text: Vax1" ## [1] "Start position: 22739" ## [1] "End position: 22743" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T402" ## [1] "Label: PR:000017268" ## [1] "Covered text: Vax1" ## [1] "Start position: 22733" ## [1] "End position: 22737" ## [1] "anaphor semantic class: PR:000017268" ## [1] "candidate semantic class: PR:000017268" ## [1] "Semantic match! PR:000017268 PR:000017268" ## [1] "Anaphor:"

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[1] "End position: 22969" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T411" ## [1] "Label: GO:0009790" ## [1] "Covered text: embryogenesis" ## [1] "Start position: 22936" ## [1] "End position: 22949" ## [1] "anaphor semantic class: CHEBI:36357" ## [1] "candidate semantic class: GO:0009790" ## [1] "Index to bngs: 413" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T413" ## [1] "Label: GO:0030424" ## [1] "Covered text: axon" ## [1] "Start position: 23000" ## [1] "End position: 23004" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T412" ## [1] "Label: CHEBI:36357" ## [1] "Covered text: molecule" ## [1] "Start position: 22961" ## [1] "End position: 22969" ## [1] "anaphor semantic class: GO:0030424" ## [1] "candidate semantic class: CHEBI:36357" ## [1] "Index to bngs: 414" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T414" ## [1] "Label: GO:0007411" ## [1] "Covered text: axon guidance" ## [1] "Start position: 23000" ## [1] "End position: 23013" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T413" ## [1] "Label: GO:0030424" ## [1] "Covered text: axon" ## [1] "Start position: 23000" ## [1] "End position: 23004" ## [1] "anaphor semantic class: GO:0007411" ## [1] "candidate semantic class: GO:0030424" ## [1] "Index to bngs: 415" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T415" ## [1] "Label: UBERON:0002336" ## [1] "Covered text: corpus callosum" ## [1] "Start position: 23048" ## [1] "End position: 23063"

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[1] "Covered text: basal forebrain" ## [1] "Start position: 23289" ## [1] "End position: 23304" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0002743" ## [1] "Index to bngs: 428" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T428" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 23333" ## [1] "End position: 23339" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T427" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: Brain" ## [1] "Start position: 23316" ## [1] "End position: 23321" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 429" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T429" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 23397" ## [1] "End position: 23402" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T428" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 23333" ## [1] "End position: 23339" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 430" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T430" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 23436" ## [1] "End position: 23441" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T429" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain"

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[1] "candidate semantic class: UBERON:0001017" ## [1] "Index to bngs: 433" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T433" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 23611" ## [1] "End position: 23615" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T432" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 23523" ## [1] "End position: 23528" ## [1] "anaphor semantic class: NCBITaxon:10088" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 434" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T434" ## [1] "Label: NCBITaxon:9606" ## [1] "Covered text: humans" ## [1] "Start position: 23623" ## [1] "End position: 23629" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T433" ## [1] "Label: NCBITaxon:10088" ## [1] "Covered text: mice" ## [1] "Start position: 23611" ## [1] "End position: 23615" ## [1] "anaphor semantic class: NCBITaxon:9606" ## [1] "candidate semantic class: NCBITaxon:10088" ## [1] "Index to bngs: 435" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T435" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 23707" ## [1] "End position: 23712" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T434" ## [1] "Label: NCBITaxon:9606" ## [1] "Covered text: humans" ## [1] "Start position: 23623" ## [1] "End position: 23629" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: NCBITaxon:9606"

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[1] "ID: T438" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 23883" ## [1] "End position: 23891" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T437" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 23805" ## [1] "End position: 23811" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 439" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T439" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 23913" ## [1] "End position: 23919" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T438" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 23883" ## [1] "End position: 23891" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 440" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T440" ## [1] "Label: UBERON:0000125" ## [1] "Covered text: nucleus" ## [1] "Start position: 23935" ## [1] "End position: 23942" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T439" ## [1] "Label: CL:0000540" ## [1] "Covered text: neuron" ## [1] "Start position: 23913" ## [1] "End position: 23919" ## [1] "anaphor semantic class: UBERON:0000125" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 441" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T441"

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## [1] "Label: UBERON:0002435"
## [1] "Covered text: striata"
## [1] "Start position: 24011"
## [1] "End position: 24018"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T440"
## [1] "Label: UBERON:0000125"
## [1] "Covered text: nucleus"
## [1] "Start position: 23935"
## [1] "End position: 23942"
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## [1] "candidate semantic class: UBERON:0000125"
## [1] "Index to bngs: 442"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T442"
## [1] "Label: CL:0000540"
## [1] "Covered text: neurons"
## [1] "Start position: 24058"
## [1] "End position: 24065"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T441"
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## [1] "Covered text: neurons"
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[1] "Filename: myfilename" ## [1] "ID: T506" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: Striatal" ## [1] "Start position: 29094" ## [1] "End position: 29102" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T505" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 28774" ## [1] "End position: 28782" ## [1] "Index to bngs: 507" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T507" ## [1] "Label: CL:0002613" ## [1] "Covered text: Striatal Neuron" ## [1] "Start position: 29094" ## [1] "End position: 29109" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T506" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: Striatal" ## [1] "Start position: 29094" ## [1] "End position: 29102" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 508" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T508" ## [1] "Label: CL:0002613" ## [1] "Covered text: Striatal ... Neuron" ## [1] "Start position: 29094" ## [1] "End position: NA" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T507" ## [1] "Label: CL:0002613" ## [1] "Covered text: Striatal Neuron" ## [1] "Start position: 29094" ## [1] "End position: 29109" ## [1] "anaphor semantic class: CL:0002613" ## [1] "candidate semantic class: CL:0002613" ## [1] "Semantic match! CL:0002613 CL:0002613" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T508" ## [1] "Label: CL:0002613"

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file:///Users/kevincohen/Dropbox/N-Z/translator-relation-extraction/code/TRANSLATOR-Coreference-Resolution.html

[1] "Filename: myfilename" ## [1] "ID: T513" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 29602" ## [1] "End position: 29610" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 515" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T515" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 29814" ## [1] "End position: 29822" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T514" ## [1] "Label: CL:0000540" ## [1] "Covered text: Neuron" ## [1] "Start position: 29696" ## [1] "End position: 29702" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 516" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T516" ## [1] "Label: CL:0000540" ## [1] "Covered text: neurons" ## [1] "Start position: 29889" ## [1] "End position: 29896" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T515" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 29814" ## [1] "End position: 29822" ## [1] "anaphor semantic class: CL:0000540" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 517" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T517" ## [1] "Label: UBERON:0000125" ## [1] "Covered text: nucleus" ## [1] "Start position: 29905" ## [1] "End position: 29912" ## [1] "Candidate:" ## [1] "Filename: myfilename"

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[1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: CL:0000540" ## [1] "Index to bngs: 526" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T526" ## [1] "Label: SO:0001026" ## [1] "Covered text: Genomic" ## [1] "Start position: 30776" ## [1] "End position: 30783" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T525" ## [1] "Label: SO:0000771" ## [1] "Covered text: OTL" ## [1] "Start position: 30763" ## [1] "End position: 30766" ## [1] "anaphor semantic class: SO:0001026" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 527" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T527" ## [1] "Label: UBERON:0002106" ## [1] "Covered text: spleens" ## [1] "Start position: 30807" ## [1] "End position: 30814" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T526" ## [1] "Label: SO:0001026" ## [1] "Covered text: Genomic" ## [1] "Start position: 30776" ## [1] "End position: 30783" ## [1] "anaphor semantic class: UBERON:0002106" ## [1] "candidate semantic class: SO:0001026" ## [1] "Index to bngs: 528" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T528" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 30821" ## [1] "End position: 30828" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T527" ## [1] "Label: UBERON:0002106" ## [1] "Covered text: spleens" ## [1] "Start position: 30807" ## [1] "End position: 30814" ## [1] "anaphor semantic class: NCBITaxon:33208" ## [1] "candidate semantic class: UBERON:0002106" ## [1] "Index to bngs: 529" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T529" ## [1] "Label: CHEBI:24866" ## [1] "Covered text: salt" ## [1] "Start position: 30842" ## [1] "End position: 30846" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T528" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 30821" ## [1] "End position: 30828" ## [1] "anaphor semantic class: CHEBI:24866" ## [1] "candidate semantic class: NCBITaxon:33208" ## [1] "Index to bngs: 530" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T530" ## [1] "Label: GO:0030849" ## [1] "Covered text: autosomes" ## [1] "Start position: 30918" ## [1] "End position: 30927" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T529" ## [1] "Label: CHEBI:24866" ## [1] "Covered text: salt" ## [1] "Start position: 30842" ## [1] "End position: 30846" ## [1] "anaphor semantic class: GO:0030849" ## [1] "candidate semantic class: CHEBI:24866" ## [1] "Index to bngs: 531" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T531" ## [1] "Label: GO:0000805" ## [1] "Covered text: X chromosome" ## [1] "Start position: 30936" ## [1] "End position: 30948" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T530" ## [1] "Label: GO:0030849" ## [1] "Covered text: autosomes" ## [1] "Start position: 30918" ## [1] "End position: 30927" ## [1] "anaphor semantic class: GO:0000805" ## [1] "candidate semantic class: GO:0030849"

[1] "Index to bngs: 532" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T532" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 30978" ## [1] "End position: 30985" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T531" ## [1] "Label: GO:0000805" ## [1] "Covered text: X chromosome" ## [1] "Start position: 30936" ## [1] "End position: 30948" ## [1] "anaphor semantic class: NCBITaxon:33208" ## [1] "candidate semantic class: GO:0000805" ## [1] "Index to bngs: 533" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T533" ## [1] "Label: SO:0001026" ## [1] "Covered text: genome" ## [1] "Start position: 31317" ## [1] "End position: 31323" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T532" ## [1] "Label: NCBITaxon:33208" ## [1] "Covered text: animals" ## [1] "Start position: 30978" ## [1] "End position: 30985" ## [1] "anaphor semantic class: SO:0001026" ## [1] "candidate semantic class: NCBITaxon:33208" ## [1] "Index to bngs: 534" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T534" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 31884" ## [1] "End position: 31887" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T533" ## [1] "Label: SO:0001026" ## [1] "Covered text: genome" ## [1] "Start position: 31317" ## [1] "End position: 31323" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: SO:0001026" ## [1] "Index to bngs: 535"

[1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T535" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 32034" ## [1] "End position: 32042" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T534" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTL" ## [1] "Start position: 31884" ## [1] "End position: 31887" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 536" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T536" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 32110" ## [1] "End position: 32115" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T535" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatal" ## [1] "Start position: 32034" ## [1] "End position: 32042" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 537" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T537" ## [1] "Label: SO:0000771" ## [1] "Covered text: QTLs" ## [1] "Start position: 32174" ## [1] "End position: 32178" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T536" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 32110" ## [1] "End position: 32115" ## [1] "anaphor semantic class: SO:0000771" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Index to bngs: 538" ## [1] "Anaphor:"

[1] "Filename: myfilename" ## [1] "ID: T538" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 32218" ## [1] "End position: 32226" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T537" ## [1] "Label: SO:0000771" ## [1] "Covered text: OTLs" ## [1] "Start position: 32174" ## [1] "End position: 32178" ## [1] "anaphor semantic class: UBERON:0002435" ## [1] "candidate semantic class: SO:0000771" ## [1] "Index to bngs: 539" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T539" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 32335" ## [1] "End position: 32340" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T538" ## [1] "Label: UBERON:0002435" ## [1] "Covered text: striatum" ## [1] "Start position: 32218" ## [1] "End position: 32226" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0002435" ## [1] "Index to bngs: 540" ## [1] "Anaphor:" ## [1] "Filename: myfilename" ## [1] "ID: T540" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 32448" ## [1] "End position: 32453" ## [1] "Candidate:" ## [1] "Filename: myfilename" ## [1] "ID: T539" ## [1] "Label: UBERON:0000955" ## [1] "Covered text: brain" ## [1] "Start position: 32335" ## [1] "End position: 32340" ## [1] "anaphor semantic class: UBERON:0000955" ## [1] "candidate semantic class: UBERON:0000955" ## [1] "Semantic match! UBERON:0000955 UBERON:0000955" ## [1] "Anaphor:" ## [1] "Filename: myfilename"

```
## [1] "ID: T540"
## [1] "Label: UBERON:0000955"
## [1] "Covered text: brain"
## [1] "Start position: 32448"
## [1] "End position: 32453"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T539"
## [1] "Label: UBERON:0000955"
## [1] "Covered text: brain"
## [1] "Start position: 32335"
## [1] "End position: 32340"
## [1] "Index to bngs: 541"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T541"
## [1] "Label: UBERON:0001062"
## [1] "Covered text: anatomic"
## [1] "Start position: 32955"
## [1] "End position: 32963"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T540"
## [1] "Label: UBERON:0000955"
## [1] "Covered text: brain"
## [1] "Start position: 32448"
## [1] "End position: 32453"
## [1] "anaphor semantic class: UBERON:0001062"
## [1] "candidate semantic class: UBERON:0000955"
## [1] "Index to bngs: 542"
## [1] "Anaphor:"
## [1] "Filename: myfilename"
## [1] "ID: T542"
## [1] "Label: NCBITaxon:10088"
## [1] "Covered text: mice"
## [1] "Start position: 33526"
## [1] "End position: 33530"
## [1] "Candidate:"
## [1] "Filename: myfilename"
## [1] "ID: T541"
## [1] "Label: UBERON:0001062"
## [1] "Covered text: anatomic"
## [1] "Start position: 32955"
## [1] "End position: 32963"
## [1] "anaphor semantic class: NCBITaxon:10088"
## [1] "candidate semantic class: UBERON:0001062"
## [1] ""
## [1] "FINISHED RUNNING SEMANTIC CHECKS ON FULL FILE"
## [1] ""
```

Produce output from the semantic rules

```
print("IDENT PAIRS FROM SEMANTIC RULES:")
```

```
## [1] "IDENT PAIRS FROM SEMANTIC RULES:"
```

```
# Just printing the list sucks--way too much empty space! Let's iterate over
# the list and call the pretty-print function for each pair; if I don't have
# one yet, let's write one.
#print(ident.pairs.in.list)

for (i in 1:length(ident.pairs.in.list)) {
   identPrint(ident.pair = ident.pairs.in.list[[i]])
} # close for-loop through list of IdentPairs
```

```
## [1] "IdentPair 0"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 1"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 1"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 2"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 2"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 3"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 3"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 3"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 3"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
```

```
## character(0)
## character(0)
## [1] "IdentPair 4"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 4"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 4"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 5"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 5"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 5"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 6"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 6"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 7"
## [1] "Sieve: STRING.MATCH.EXACT"
```

```
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 7"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 8"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 8"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 9"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 9"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 9"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 10"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 10"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
```

```
## [1] "IdentPair 11"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 11"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 12"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 12"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 12"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 12"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 13"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 13"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 14"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
```

```
## character(0)
## character(0)
## [1] "IdentPair 14"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 15"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 15"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 16"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 16"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 17"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 17"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 18"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 18"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
```

```
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 19"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 19"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 20"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 20"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 21"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 21"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 22"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 22"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
```

```
## [1] "IdentPair 23"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 23"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 24"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 24"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 25"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 25"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 26"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 26"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 26"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
```

```
## character(0)
## character(0)
## [1] "IdentPair 26"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 27"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 27"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 28"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 28"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 28"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: STRING.MATCH.EXACT"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: STRING.MATCH.CASE.TOGGLED"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
```

```
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
```

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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
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## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
```

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## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
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## character(0)
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
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## [1] "Antecedent: T541"
## character(0)
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
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## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
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## [1] "Antecedent: T541"
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
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## [1] "Antecedent: T541"
## character(0)
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## [1] "IdentPair 29"
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## [1] "IdentPair 29"
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
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## [1] "IdentPair 29"
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## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
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## [1] "IdentPair 29"
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
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## character(0)
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## [1] "IdentPair 29"
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## character(0)
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## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
```

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## character(0)
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
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## character(0)
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## character(0)
## character(0)
## [1] "IdentPair 29"
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```

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## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
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## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
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## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
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## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
## [1] "IdentPair 29"
## [1] "Sieve: SEMANTIC.LEAF.NODE.MATCH"
## [1] "Anaphor: T542"
## [1] "Antecedent: T541"
## character(0)
## character(0)
```

Reproducibility/Repeatability

TODO: after calling this, give the option of printing out the entire file contents for debugging/traceability purposes.

```
sessionInfo()
```

```
## R version 4.0.1 (2020-06-06)
## Platform: x86 64-apple-darwin17.0 (64-bit)
## Running under: macOS 10.16
##
## Matrix products: default
## BLAS:
           /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en US.UTF-8/en US.UTF-8/en US.UTF-8/C/en US.UTF-8/en US.UTF-8
##
## attached base packages:
## [1] stats
                 graphics grDevices utils
                                               datasets methods
                                                                   base
##
## other attached packages:
                       stringr_1.4.0
## [1] forcats_0.5.1
                                       dplyr_1.0.8
                                                       purrr 0.3.4
## [5] readr 2.1.2
                       tidyr 1.2.0
                                       tibble 3.1.6
                                                       ggplot2 3.3.5
## [9] tidyverse 1.3.1
##
## loaded via a namespace (and not attached):
   [1] tidyselect 1.1.1 xfun 0.29
                                          bslib 0.3.1
                                                           haven 2.4.3
##
## [5] colorspace 2.0-2 vctrs 0.3.8
                                          generics 0.1.2
                                                           htmltools 0.5.2
## [9] yaml 2.2.2
                         utf8 1.2.2
                                          rlang 1.0.1
                                                           jquerylib 0.1.4
## [13] pillar 1.7.0
                        withr 2.4.3
                                          glue 1.6.1
                                                           DBI 1.1.2
## [17] dbplyr 2.1.1
                        modelr 0.1.8
                                          readxl 1.3.1
                                                           lifecycle 1.0.1
## [21] cellranger 1.1.0 munsell 0.5.0
                                          gtable 0.3.0
                                                           rvest 1.0.2
## [25] evaluate 0.14
                        knitr 1.37
                                          tzdb 0.2.0
                                                           fastmap 1.1.0
## [29] fansi 1.0.2
                        broom 0.7.12
                                          Rcpp 1.0.8
                                                           backports 1.4.1
## [33] scales 1.1.1
                                                           hms 1.1.1
                         jsonlite 1.7.3
                                          fs 1.5.2
## [37] digest 0.6.29
                        stringi 1.7.6
                                          grid 4.0.1
                                                           cli 3.2.0
## [41] tools 4.0.1
                        magrittr 2.0.2
                                          sass 0.4.0
                                                           crayon 1.5.0
## [45] pkgconfig 2.0.3 ellipsis 0.3.2
                                          xml2 1.3.3
                                                           reprex 2.0.1
## [49] lubridate 1.8.0 assertthat 0.2.1 rmarkdown 2.11
                                                           httr 1.4.2
## [53] rstudioapi 0.13 R6 2.5.1
                                          compiler 4.0.1
```