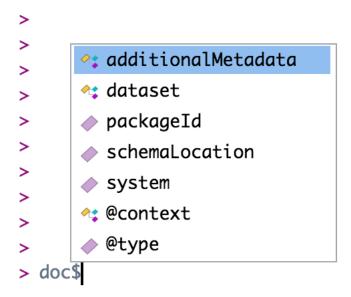
Navigate through EML

The first task when editing an EML file is navigating the EML file. An EML file is organized in a structure that contains many lists nested within other lists. The function View allows you to get a crude view of an EML file in the viewer. It can be useful for exploring the file.

```
# Need to be in this member node to explore file
 d1c test <- dataone::D1Client("STAGING", "urn:node:mnTestARCTIC")</pre>
 doc <- read eml(getObject(d1c test@mn,</pre>
                                    "urn:uuid:558eabf1-1e91-4881-8ba3-ef8684d8f6a1"))
 View(doc)
odoc 🕤
                         list [7] (S3: emld, list)
                                                    List of length 7
 @context
                         list [7]
                                                    List of length 7
                         character [1]
                                                    'EML'
    @type
 additionalMetadata
                         list [1]
                                                    List of length 1
 dataset
                         list [14]
                                                    List of length 14
                                                    'doi:10.18739/A2FS1H'
    packageld
                         character [1]
                         character [1]
    schemaLocation
                                                    'eml://ecoinformatics.org/eml-2.1.1 eml.xsd'
    system
                         character [1]
                                                    'https://arcticdata.io'
```

The complex EML document is represented in R as as series of named, nested lists. We use lists all the time in R! A data.frame is one example of a special kind of list that we use all the time. You may be familiar with the syntax dataframe\$column_name which allows us to select a particular column of a data.frame. Under the hood, a data.frame is a named list of vectors with the same length. You select one of those vectors using the \$ operator, which is called the "list selector operator."

Just like you navigate in a data.frame, you can use the \$ operator to navigate through the EML structure. The \$ operator allows you to go deeper into the EML structure and to see what elements are nested within other elements. However, you have to tell R where you want to go in the structure when you use the \$ symbol. For example, if you want to view the dataset element of your EML you would use the command doc\$dataset. If you want to view the creators of your data set you would use doc\$dataset\$creator. Note here that creator is contained within dataset. If you aren't sure where you want to go, hit the tab button on your keyboard after typing \$ and a list of available elements in the structure will appear (e.g., doc\$<TAB>):



Note that if you hit tab, and nothing pops up, this most likely implies that you are trying to go into an EML element that can take a series items. For example doc\$dataset\$creator\$<TAB> will not show a pop-up menu. This is because creator is a series-type object (i.e. you can have multiple creators). If you want to go deeper into creator, you first must tell R which creator you are interested in. Do this by writing [[i]] first where i is the index of the creator you are concerned with. For example, if you want to look at the first creator i = 1. Now doc\$dataset\$creator[[1]]\$<TAB> will give you many more options. Note, an empty autocomplete result sometimes means you have reached the end of a branch in the EML structure.

At this point stop and take a deep breath. The key takeaway is that EML is a hierarchical tree structure. The best way to get familiar with it is to explore the structure. Try entering doc\$dataset into your console, and print it. Now make the search more specific, for instance: doc\$dataset\$abstract.