

Exercices on session *Tidyverse* 2/2

For all the following exercises, use functions from the tidyverse, and pipes, whenever possible.

BCI tree count

You are going to work on data from trees in Barro Colorado Island. These data are available in the package *vegan*, and are called *BCI*.

- Load the data (don't forget to look at the metadata in the help of the package).
- Get an overview of the data and check their class.
- Transform the data to a tibble.

Transform the dataset

- Add a column with the plot ID (from BCI_1 to BCI_...) (and check what you have done).
- Create a tibble with the data in a long format, to have one row per species and plot as follow:

```
# A tibble: 11,250 x 3
  plot_ID gen_sp      abund
  <chr>   <chr>      <int>
1 BCI_1  Abarema.macradenia      0
2 BCI_1  Vachellia.melanoceras    0
3 BCI_1  Acalypha.diversifolia    0
4 BCI_1  Acalypha.macrostachya    0
5 BCI_1  Adelia.triloba          0
6 BCI_1  Aegiphila.panamensis     0
```

```

7 BCI_1 Alchornea.costaricensis 2
8 BCI_1 Alchornea.latifolia 0
9 BCI_1 Alibertia.edulis 0
10 BCI_1 Allophylus.psilospermus 0
# i 11,240 more rows

```

- Check the dimension of this new table (try to do it using a test).
- We now want to add a column for the genus and species name.
 - Let's do it with the function *separate* (don't replace the initial data, store the result in a new object).

Warning: Expected 2 pieces. Additional pieces discarded in 11250 rows [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, ...].

- We get a warning message... It is not very explicit... Let's have a look at the full species name. For that, display the species list. Can we separate the column *gen_sp* based on the separator "." ? Why?
- We want to keep only the characters that are before the second dot (so the genus and the species, removing the variety and subspecies). Let's split the *gen_sp* column by the separator ".". We want to get a matrix with a column by string separated by ".". **NB:** if you say that you want to split by ".", this will be interpreted as "any character", so you need to write "\\." instead.
- Let's keep only the two first columns of this matrix and bind these columns to the long dataset.

New names:

```

* `` -> `...4`
* `` -> `...5`

```

- Rename the two new columns to have this:

```

# A tibble: 11,250 x 5
  plot_ID gen_sp      abund genus species
  <chr>   <chr>    <int> <chr>   <chr>
1 BCI_1 Abarema.macradenia 0 Abarema macradenia
2 BCI_1 Vachellia.melanoceras 0 Vachellia melanoceras
3 BCI_1 Acalypha.diversifolia 0 Acalypha diversifolia
4 BCI_1 Acalypha.macrostachya 0 Acalypha macrostachya
5 BCI_1 Adelia.triloba 0 Adelia triloba

```

```

6 BCI_1    Aegiphila.panamensis      0 Aegiphila  panamensis
7 BCI_1    Alchornea.costaricensis 2 Alchornea  costaricensis
8 BCI_1    Alchornea.latifolia    0 Alchornea  latifolia
9 BCI_1    Alibertia.edulis      0 Alibertia  edulis
10 BCI_1   Allophylus.psilospermus 0 Allophylus psilospermus
# i 11,240 more rows

```

- Get rid of the rows with an abundance of zero.

Add environmental data

- Let's now add some environmental data from the dataset *BCI.env*. Load it and transform it to a tibble.
- Add a column with the plot ID (from BCI_1 to BCI_...)
- Reorder the levels of *Habitat* from the one with the most plots to the one with the least plots. There is a function for this, it is called *fec_infreq*.
- Add a column called *EnvHet_cat* taking the following values:
 - *low* when the environmental heterogeneity is lower than 0.08
 - *medium* when the environmental heterogeneity is between 0.08 and 0.49
 - *high* when the environmental heterogeneity is higher than 0.49
- Join the variable *Habitat* and *EnvHet_cat* to the long dataset of abundance (make sure you use the appropriate join function).

For next time

- Install the following package from CRAN: *patchwork*