

Indicateurs de la Biodiversité

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Chapter 1

Dependencies

```
library(rcoleo)  
library(tidyverse)  
library(lubridate)
```


Chapter 2

Download data

The only point here is to demonstrate the workflow for downloading data

```
# On retire les cellules (classe sf) depuis l'API
cells <- rcoleo::sf_cells()
obs <- rcoleo::get_obs()
sites_dl <- rcoleo::sf_sites()

# until there is a better way to obtain the data and parse the result (perhaps
# in the form of a convenience function in rcoleo) we do this:

obs_df <- obs[[1]] %>% map("body") %>% map_df(~ select(.x, -closed_at))

all_obs <- obs_df %>%
  select(cell_code, site_code, date_obs, type,
         taxa = obs_species.taxa_name,
         var = obs_species.variable,
         val = obs_species.value) %>%
  mutate(date_obs = lubridate::ymd(date_obs),
         # convert cover into pres/abs (right?)
         count = if_else(var == "recouvrement", 1, val))

# CELLULES: On compte le nombre d'observation/nombre espece par type, année et cellule
obs_cells <- all_obs %>%
  group_by(cell_code, date_obs, type) %>%
  summarise(n = sum(count)) %>%
  ungroup

sp_cells <- all_obs %>%
  select(cell_code, date_obs, type, taxa) %>%
  distinct() %>%
```

```

group_by(cell_code, date_obs, type) %>%
  summarise(n = n()) %>%
  ungroup

# CAMPAGNES
sites <- sites_dl %>%
  select(site_code, off_station_code_id,
         type_milieu = type, geometry, site_id = id)

# On prépare les jeux de données pour chacun des types de campagnes

all_obs_con <- all_obs %>%
  filter(taxa != "inconnu")

microfaunes <- subset(all_obs_con, type == "insectes_sol")
papillons <- subset(all_obs_con, type == "papilionidés")
odonates <- subset(all_obs_con, type == "odonates")
vegetation <- subset(all_obs_con, type == "végétation")

```

2.0.1 overall summary

```

all_obs_con %>%
  group_by(type) %>%
  summarize(sites = n_distinct(site_code),
            cells = n_distinct(cell_code),
            taxa = n_distinct(taxa))

## `summarise()` ungrouping output (override with `.groups` argument)

## # A tibble: 4 x 4
##   type      sites cells taxa
##   <chr>    <int> <int> <int>
## 1 insectes_sol    13    13    37
## 2 odonates        12    10    35
## 3 papilionidés    14    11    26
## 4 végétation      26    11   170

```

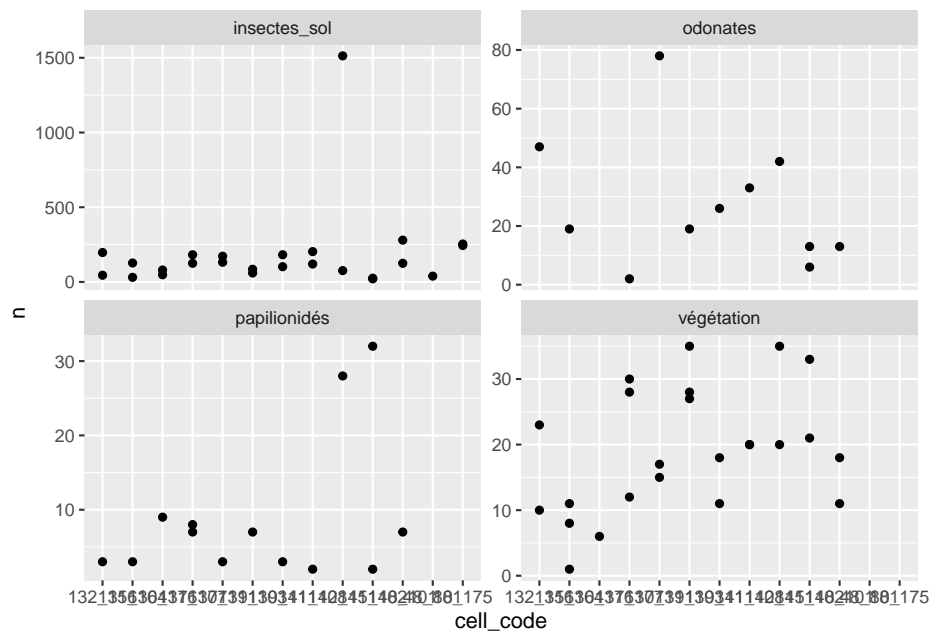

Chapter 3

Sites

Summary data about the different sites

```
obs_cells %>%  
  ggplot(aes(x = cell_code, y = n)) + geom_point() +  
  facet_wrap(~type, scales = "free_y")
```

Warning: Removed 1 rows containing missing values (geom_point).



Chapter 4

Odonate communities

```
# confirm that the only variable recorded here is "abondance"
odonates$var %>% unique %>% {stopifnot(. == "abondance")}

odonates %>%
  glimpse %>%
  {all.equal(.$count, .$val)}

## Rows: 151
## Columns: 8
## $ cell_code <chr> "135_104", "135_104", "135_104", "135_104", "135_104", "1...
## $ site_code <chr> "135_104_H01", "135_104_H01", "135_104_H01", "135_104_H01...
## $ date_obs <date> 2016-06-23, 2016-06-23, 2016-06-23, 2016-06-23, 2016-06-...
## $ type <chr> "odonates", "odonates", "odonates", "odonates", "odonates...
## $ taxa <chr> "Leucorrhinia hudsonica", "Nehalennia gracilis", "Gomphus...
## $ var <chr> "abondance", "abondance", "abondance", "abondance", "abon...
## $ val <dbl> 2, 1, 1, 1, 1, 1, 1, 2, 1, 1, 2, 4, 1, 10, 1, 30, 5, 20, ...
## $ count <dbl> 2, 1, 1, 1, 1, 1, 1, 2, 1, 1, 2, 4, 1, 10, 1, 30, 5, 20, ...

## [1] TRUE

## are sites nested in cells?

odonates %>%
  select(site_code, cell_code) %>% distinct %>%
  group_by(cell_code) %>% tally

## # A tibble: 10 x 2
##   cell_code      n
##   <chr>      <int>
## 1 132_116        1
```

```
## 2 135_104      1
## 3 137_107      1
## 4 137_111      1
## 5 139_103      1
## 6 139_111      1
## 7 141_108      1
## 8 142_111      2
## 9 145_102      2
## 10 148_101     1
```

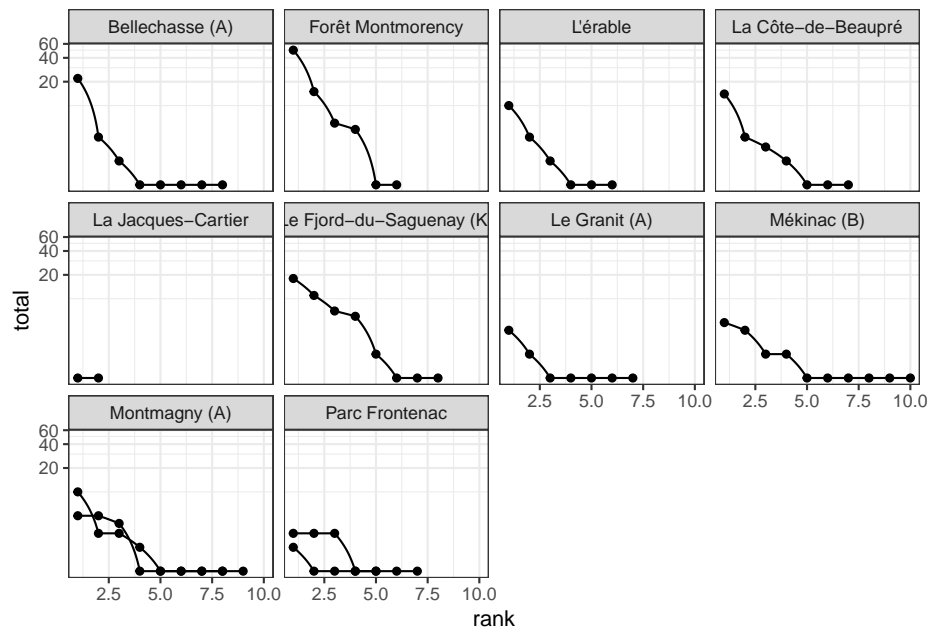
```
# yes, sometimes there are sites within cells!
```

```
rank_abundance <- odonates %>%
  left_join(select(cells, cell_code, name)) %>%
  group_by(cell_code, name, site_code, taxa) %>%
  summarize(total = sum(count)) %>%
  mutate(rank = row_number(desc(total)))
```

```
## Joining, by = "cell_code"
```

```
## `summarise()` regrouping output by 'cell_code', 'name', 'site_code' (override with `group_by()`)
```

```
rank_abundance %>%
  ggplot(aes(x = rank, y = total, group = site_code)) +
  geom_point() +
  geom_line() +
  facet_wrap(~name) +
  coord_trans(y = "log") +
  theme_bw()
```



4.1 Questions

Some sites appear to count **individuals**, not species? why is that?

```
odonates %>%
  left_join(select(cells, cell_code, name)) %>%
  filter(name %>% stringr::str_detect("Parc|-de-")) %>%
  select(name, site_code, taxa, val) %>% knitr::kable(.)
```

```
## Joining, by = "cell_code"
```

name	site_code	taxa	val
La Côte-de-Beaupré	139_111_H01	Leucorrhinia glacialis	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Enallagma ebrium	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Nehalennia irene	1
La Côte-de-Beaupré	139_111_H01	Leucorrhinia proxima	1
La Côte-de-Beaupré	139_111_H01	Dorocordulia libera	1
La Côte-de-Beaupré	139_111_H01	Enallagma ebrium	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Somatochlora franklini	1
La Côte-de-Beaupré	139_111_H01	Enallagma ebrium	1
La Côte-de-Beaupré	139_111_H01	Ladona julia	1
La Côte-de-Beaupré	139_111_H01	Enallagma ebrium	1
La Côte-de-Beaupré	139_111_H01	Leucorrhinia proxima	1
La Côte-de-Beaupré	139_111_H01	Leucorrhinia proxima	1
La Côte-de-Beaupré	139_111_H01	Nehalennia irene	1
Parc Frontenac	145_102_H01	Nehalennia gracilis	1
Parc Frontenac	145_102_H01	Leucorrhinia proxima	1
Parc Frontenac	145_102_H01	Nannothemis bella	1
Parc Frontenac	145_102_H01	Nannothemis bella	1
Parc Frontenac	145_102_H01	Nehalennia gracilis	1
Parc Frontenac	145_102_H01	Nannothemis bella	1
Parc Frontenac	145_102_H01	Nehalennia irene	1
Parc Frontenac	145_102_H01	Nehalennia irene	1
Parc Frontenac	145_102_H01	Nehalennia gracilis	1
Parc Frontenac	145_102_H01	Enallagma boreale	1
Parc Frontenac	145_102_H01	Leucorrhinia patricia	1
Parc Frontenac	145_102_H01	Nehalennia irene	1
Parc Frontenac	145_102_H01	Leucorrhinia glacialis	1
Parc Frontenac	145_102_H02	Nehalennia irene	1
Parc Frontenac	145_102_H02	Celithemis elisa	1
Parc Frontenac	145_102_H02	Nehalennia irene	1
Parc Frontenac	145_102_H02	Leucorrhinia proxima	1
Parc Frontenac	145_102_H02	Ischnura posita	1
Parc Frontenac	145_102_H02	Enallagma ebrium	1

Chapter 5

Soil invertebrates

```
# confirm that the only variable recorded here is "abondance"
microfaunes$var %>% unique %>% {stopifnot(. == "abondance")}
```

```
## are sites nested in cells?
```

```
microfaunes %>%
  select(site_code, cell_code) %>% distinct %>%
  group_by(cell_code) %>% tally
```

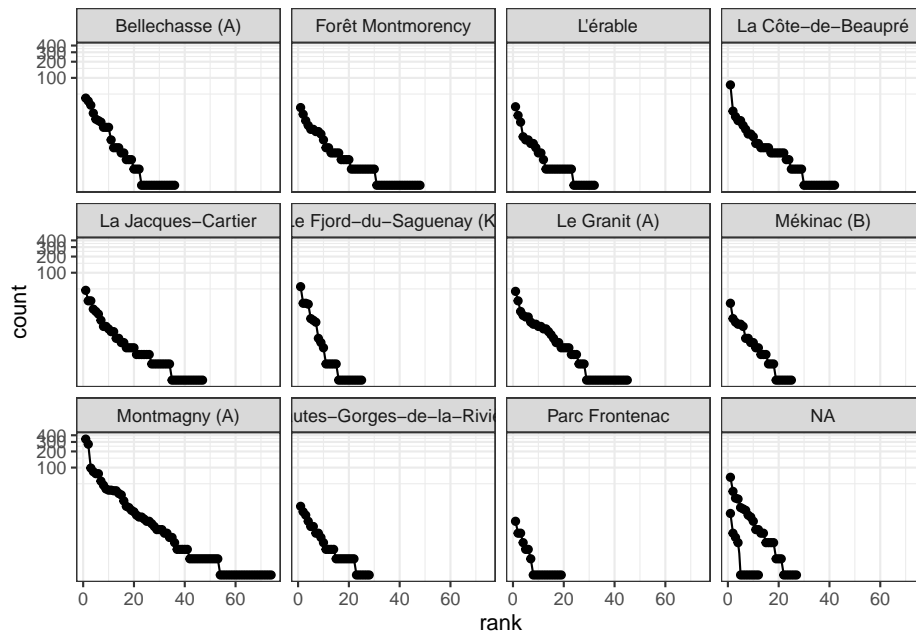
```
## # A tibble: 13 x 2
##   cell_code      n
##   <chr>      <int>
## 1 132_116        1
## 2 135_104        1
## 3 136_116        1
## 4 137_107        1
## 5 137_111        1
## 6 139_103        1
## 7 139_111        1
## 8 141_108        1
## 9 142_111        1
## 10 145_102        1
## 11 148_101        1
## 12 48_181         1
## 13 80_175         1
```

```
# no, here we have one survey per cell
```

```
rank_abundance <- microfaunes %>%
  filter(val>0) %>%
  left_join(select(cells, cell_code, name)) %>%
  group_by(cell_code, name, site_code) %>%
  mutate(rank = row_number(desc(count)))

## Joining, by = "cell_code"

rank_abundance %>%
  ggplot(aes(x = rank, y = count, group = site_code)) +
  geom_point() +
  geom_line() +
  facet_wrap(~name) +
  coord_trans(y = "log") +
  theme_bw()
```



5.1 Questions

Why are some site names NA? do those sites not have names?

Should 0 values be uploaded into Coleo?