

# Showcase some database functionality

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## Intro

Not much here yet, only some quick commands.

```
library(Norimon)

## Loading required package: rlang
##
## Attaching package: 'rlang'
## The following objects are masked from 'package:purrr':
##
##   %%, flatten, flatten_chr, flatten_dbl, flatten_int, flatten_lgl,
##   flatten_raw, invoke, splice

connect_to_insect_db()

require(DBI)
require(dplyr)
locations <- tbl(
  con,
  Id(
    schema = "locations",
    table = "localities"
  )
)

locations

## # Source:   table<"locations"."localities"> [?? x 9]
## # Database: postgres [jens.astrom@ninradardata01.nina.no:5432/insect_monitoring]
##   id          local~1 habit~2 regio~3 ano_f~4 ssbid geom  set_p~5 md_fl~6
##   <chr>        <chr>   <chr>   <chr>   <chr>   <int> <pq_> <pq_gm> <chr>
## 1 9a74225c-c6ac-46~ Semi-n~ Semi-n~ Østlan~ <NA>    2e13 0103~ NA      ins_01~
## 2 d0d007d1-f49f-44~ Semi-n~ Semi-n~ Østlan~ <NA>    2e13 0103~ NA      ins_01~
```

```
## 3 5a41b127-ee5b-48~ Semi-n~ Semi-n~ Østlan~ <NA>      2e13 0103~ NA      ins_01~
## 4 8fcaafbe-fc15-43~ Semi-n~ Semi-n~ Østlan~ <NA>      2e13 0103~ NA      ins_01~
## 5 2c93ae8c-ea17-41~ Semi-n~ Semi-n~ Østlan~ <NA>      2e13 0103~ NA      ins_01~
## 6 0b6c2f31-9bc8-4e~ Semi-n~ Semi-n~ Trønede~ ANO4819  2e13 0103~ NA      INS_00~
## 7 16b4dc4a-596d-49~ Semi-n~ Semi-n~ Trønede~ ANO8007  2e13 0103~ NA      INS_00~
## 8 7dfa552d-b519-41~ Semi-n~ Semi-n~ Trønede~ ANO4343  2e13 0103~ NA      INS_00~
## 9 f7ca5476-7ef1-48~ Semi-n~ Semi-n~ Trønede~ ANO0930  2e13 0103~ NA      INS_00~
## 10 a50d1be8-ac65-43~ Semi-n~ Semi-n~ Trønede~ ANO3940  2e13 0103~ NA      INS_00~
## # ... with more rows, and abbreviated variable names 1: locality,
## #   2: habitat_type, 3: region_name, 4: ano_flate_id, 5: set_point,
## #   6: md_flate_id
```

```
require(sf)
```

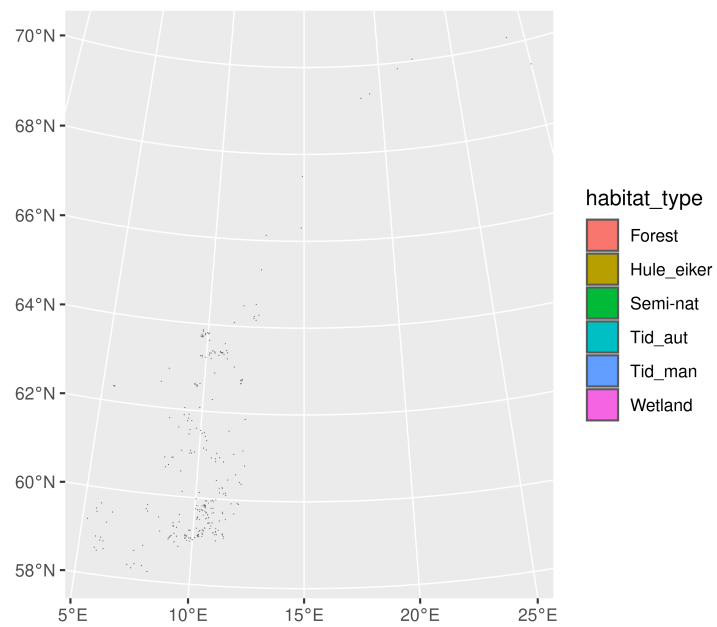
```
## Loading required package: sf
```

```
## Linking to GEOS 3.10.2, GDAL 3.4.3, PROJ 8.2.0; sf_use_s2() is TRUE
```

```
locations_sf <- read_sf(
  con,
  Id(
    schema = "locations",
    table = "localities"
  )
)
```

```
require(ggplot2)
```

```
ggplot(locations_sf) +
  geom_sf(aes(fill = habitat_type))
```



## New locality function

```
insect_localities_sf <- get_localities()
```

```
insect_localities <- get_localities(as_sf = FALSE)
```