Frontal cortex-driven glycinergic inhibition of the intralaminar thalamus

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Contents

1 Firing rate of IL neurons during glycinergic fiber activation

In these experiments glycinergic fibers were photactivated while the firing rate of individual IL neurons was recorded. Some of the IL cells had very low baseline activity. In order to increase the firing rate of the IL neurons and to detect the effect of the glycinergic fiber activation a small tail pinch was applied. The firing rate of the recorded IL cells decreased during the glycinergic fiber activation.

1.1 Loading data

Loading AP and stimuli times from *stimulus* and from *baseline* data to **IL_stim_firing** and to **IL_baseline_firing** tables:

```
IL_stim_firing <- CreateRecTibble(AP_times = read_csv(file.path("data",
    "IL_MFR", "stimulus", "AP_times.csv")),
    stim_times = read_csv(file.path("data",
        "IL_MFR", "stimulus", "stim_times.csv")))
IL_stim_firing %>% head()
```

```
## # A tibble: 6 x 7
##   file_name animal_id signal_type unit_id signal_time stim_freq
##   <chr>     <chr>     <chr>         <dbl>       <dbl> <chr>
## 1 cell01_0~ not spec~ AP                1      0.0376 no value
## 2 cell01_0~ not spec~ AP                1      0.0644 no value
## 3 cell01_0~ not spec~ AP                1      0.0903 no value
## 4 cell01_0~ not spec~ AP                1      0.147  no value
## 5 cell01_0~ not spec~ AP                1      0.200  no value
## 6 cell01_0~ not spec~ AP                1      0.239  no value
## # ... with 1 more variable: available_freqs <chr>
```

```
IL_baseline_firing <- CreateRecTibble(AP_times = read_csv(file.path("data",
    "IL_MFR", "baseline", "AP_times.csv")),
    stim_times = read_csv(file.path("data",
        "IL_MFR", "baseline", "stim_times.csv")))
IL_stim_firing %>% head()
```

```
## # A tibble: 6 x 7
##   file_name animal_id signal_type unit_id signal_time stim_freq
##   <chr>     <chr>     <chr>         <dbl>       <dbl> <chr>
## 1 cell01_0~ not spec~ AP                1      0.0376 no value
## 2 cell01_0~ not spec~ AP                1      0.0644 no value
## 3 cell01_0~ not spec~ AP                1      0.0903 no value
## 4 cell01_0~ not spec~ AP                1      0.147  no value
## 5 cell01_0~ not spec~ AP                1      0.200  no value
## 6 cell01_0~ not spec~ AP                1      0.239  no value
## # ... with 1 more variable: available_freqs <chr>
```

1.2 Summary information

Summary information of the *stimulus* and *baseline* recording files:

- Variables:
  - file names (*file_name*)
  - number of channels in the raw recording files (*No_ch*)
  - number of APs (*No_AP_unit*, *No_AP_unit2*)
  - number of stimulus trains (*No_Stim*)
  - LFP sampling rate (*samp_rate_lfp*)
  - unit sampling rate (*samp_rate_unit*)
  - length of the recording (*rec_length*)
  - length of the stimulus trains (*No_trains*)
  - Are the lengths of the stimulus trains equal in the recording (*train_length_equal*)

  - starting time of the stimulus trains (*train_start*)
  - ending time of the stimulus trains (*train_end*)

CELL_INFO table to store the cell categories. It was created manually using the information from the summary excel table (*Glicy_juxta-fm_exp_records_injection_sum.xls*)

- Variables
  - cell identification (*cell_id*). To find the recording file use the summary excel table
  - file names (*file_name*)
  - spontaneously active cells (*bl_activity*)
  - induced firing (*pinch*)
  - individually identified neurons (*ident*)
  - control cells (*control*)

1.3 Calculations

1.3.1 Firing rates

b_d_a_MFR: Calculating the number of APs -using a custom made function (*BDACalculator*)- before during and after the stimulus trains (*b_d_a_MFR*).

```
b_d_a_MFR <- lapply(CELL_INFO$cell_id,
    BDACalculator, data = IL_stim_firing) %>%
    bind_rows() %>% mutate(FR = No_AP/train_length) %>%
    dplyr::group_by(stim_cond,
        cell_id) %>% summarise(MFR = mean(FR))
```

```
## Warning: `as.tibble()` is deprecated, use `as_tibble()` (but mind the new semantics).
## This warning is displayed once per session.
```

sd_mean_isi: Calculating the baseline MFR of the recorded IL cells from the *IL_baseline_firing* table using a custom made function (*SDMeanISI*). The results are stored in the *sd_mean_isi* table.

1.3.2 Ranks (strength of inhibition)

cellranks: Calculating ranks based on the activity change from "*baseline*" to "*during stimulus*". If the activity change is negative (decreased MFR) the asigned rank is negative, if it is positive (increased MFR) the assigned rank is positive.

Calculating the firing rate change during stimulus (photoactivation of the glycinergic fibers) compared to baseline:

$$\textbf{activity\_change} = \frac{during\_MFR - base\_MFR}{base\_MFR} * 100$$

```
cellranks <- b_d_a_MFR %>% group_by(stim_cond) %>%
    mutate(base_MFR = sd_mean_isi$MFR) %>%
    mutate(activity_change = ((MFR -
        base_MFR)/base_MFR * 100) %>%
        round(2)) %>% dplyr::filter(stim_cond ==
    "d") %>% mutate(change_rank = ifelse(activity_change >
    0, rank(activity_change), -rank(-activity_change))) %>%
    ungroup() %>% left_join(CELL_INFO %>%
    select(cell_id, control, pinch),
    by = "cell_id")
cellranks
```

```
## # A tibble: 29 x 8
##    stim_cond cell_id   MFR base_MFR activity_change change_rank control
##    <fct>     <chr>   <dbl>    <dbl>           <dbl>       <dbl> <lgl>
##  1 d         cell01  5.34    25.4            -79.0          -18 FALSE
##  2 d         cell02  5.86     8.04           -27.1          -12 FALSE
##  3 d         cell03  0.300    0.311           -3.44          -8 FALSE
##  4 d         cell04  0.162    1.03           -84.2          -21 FALSE
##  5 d         cell05  0.729    2.23           -67.4          -16 FALSE
##  6 d         cell06  2.54    13.8            -81.6          -20 FALSE
##  7 d         cell07  0.223    1.12           -80.0          -19 FALSE
##  8 d         cell08  7.97     1.74           357.            28 FALSE
##  9 d         cell09  0.688    1.59           -56.7          -14 FALSE
## 10 d         cell10  4.25     5.08           -16.3          -10 FALSE
## # ... with 19 more rows, and 1 more variable: pinch <lgl>
```

cellranks_before_stim: Calculating ranks based on the activity change from "*before stimulus*" to "*during stimulus*". If the activity change is negative (decreased MFR) the asigned rank is negative, if it is positive (increased MFR) the assigned rank is positive.

Calculating the firing rate change during stimulus (photoactivation of the glycinergic fibers) compared to before stimulus:

$$\textbf{activity\_change} = \frac{during\_MFR - before\_MFR}{before\_MFR} * 100$$

```
cellranks_before_stim <- b_d_a_MFR %>%
    spread(key = stim_cond, value = MFR) %>%
    mutate(activity_change = ((d -
        b)/b * 100) %>% round(2)) %>%
```

```
    mutate(change_rank = ifelse(activity_change >
        0, rank(activity_change),
        -rank(-activity_change))) %>%
    left_join(CELL_INFO %>% select(cell_id,
        control, pinch), by = "cell_id")
cellranks_before_stim
```

```
## # A tibble: 29 x 8
##    cell_id      b     d      a activity_change change_rank control pinch
##    <chr>    <dbl> <dbl>  <dbl>           <dbl>       <dbl> <lgl>   <lgl>
##  1 cell01  14.5   5.34  22.3            -63.2          -13 FALSE   FALSE
##  2 cell02   8.27  5.86   5.36           -29.1           -8 FALSE   TRUE
##  3 cell03   2.38  0.300  0.526          -87.4          -21 FALSE   TRUE
##  4 cell04   3.89  0.162  3.60           -95.8          -26 FALSE   TRUE
##  5 cell05   5.10  0.729  2.17           -85.7          -20 FALSE   TRUE
##  6 cell06  16.5   2.54  18.1            -84.6          -18 FALSE   FALSE
##  7 cell07   0.668 0.223  0.526          -66.7          -15 FALSE   FALSE
##  8 cell08  12.5   7.97  12.1            -36.5           -9 FALSE   FALSE
##  9 cell09   0.708 0.688  0.749           -2.86          -5 FALSE   TRUE
## 10 cell10   9.52  4.25   6.53           -55.4          -10 FALSE   TRUE
## # ... with 19 more rows
```

1.3.3 Data to plot

TO_PLOT: Combining *b_d_a_MFR* (firing rate of 29 IL neurons b/d/a stim) with *sd_mean_isi* table (baseline firing rate of the same 29 neurons), joining with CELL_INFO containing important information of the cells (baseline activity, identified, pinched, control) and with *cellranks* containing the ranks asigned to each cells based on the changes in MFR during the stimulus compared to baseline.

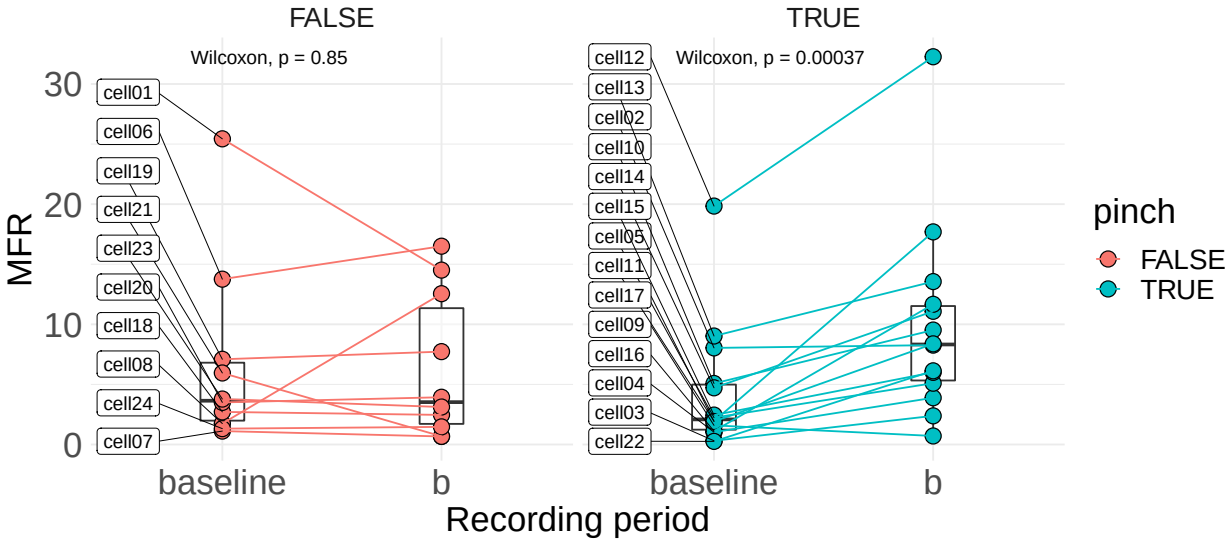
```
TO_PLOT <- bind_rows(sd_mean_isi %>%
    select(MFR, cell_id, stim_cond),
    b_d_a_MFR) %>% left_join(CELL_INFO %>%
    select(-file_name), by = "cell_id") %>%
    left_join(cellranks %>% select(cell_id,
        change_rank, activity_change),
        by = "cell_id")

datatable(TO_PLOT, caption = "TO_PLOT table",
    rownames = TRUE, options = list(pageLength = 50,
        scrollX = T, scrollY = "500px",
        dom = "t"))
```

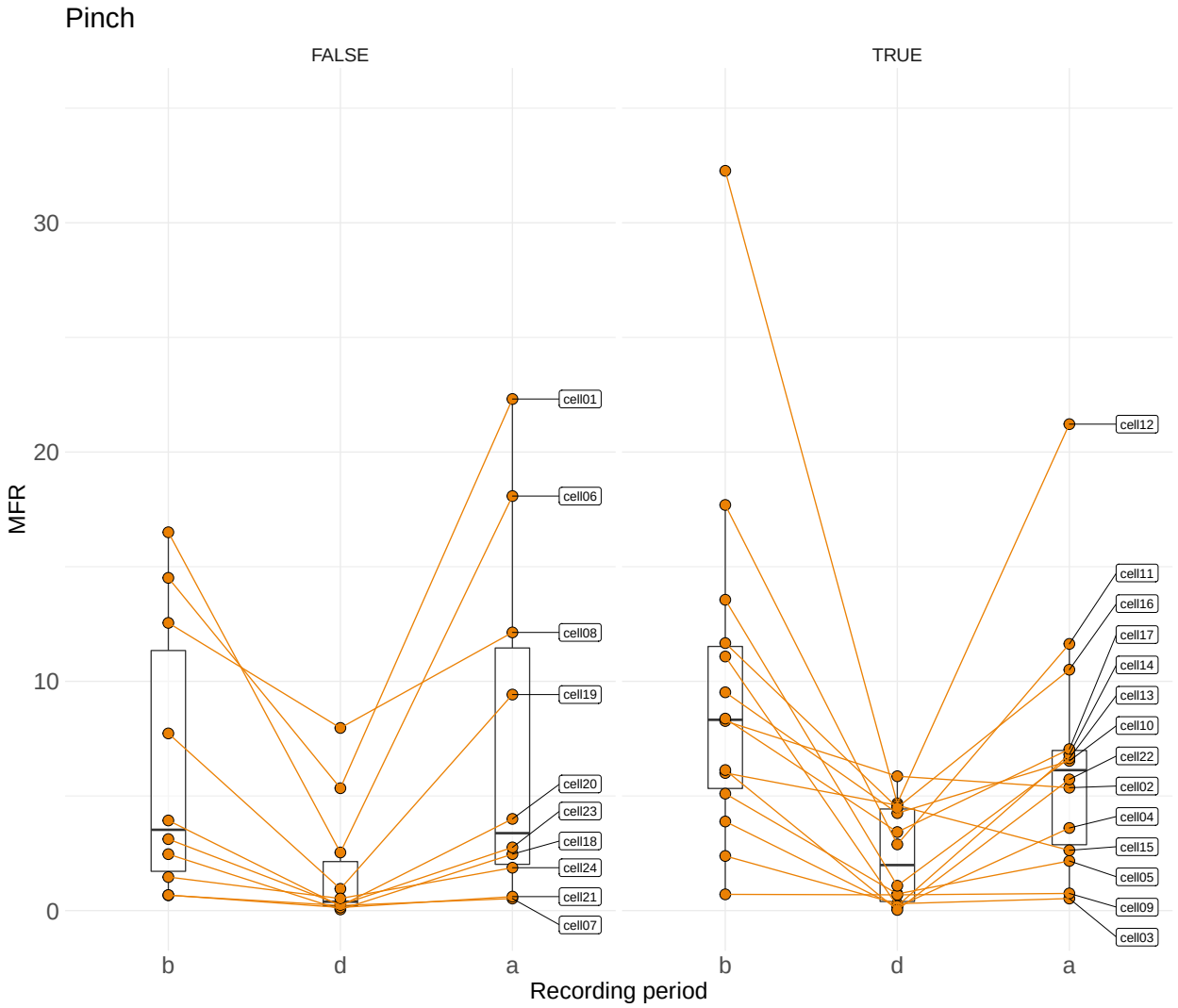
1.4 Plotting

1.4.1 Baseline vs. "before" stimulus activity

Comparison of baseline and "before" stimulus firing rates in the case of spontaneously active and sponteneously inactive (pinch) neurons. Spontaneously inactive neurons showed significantly higher MFR before stiulus compared to baseline.

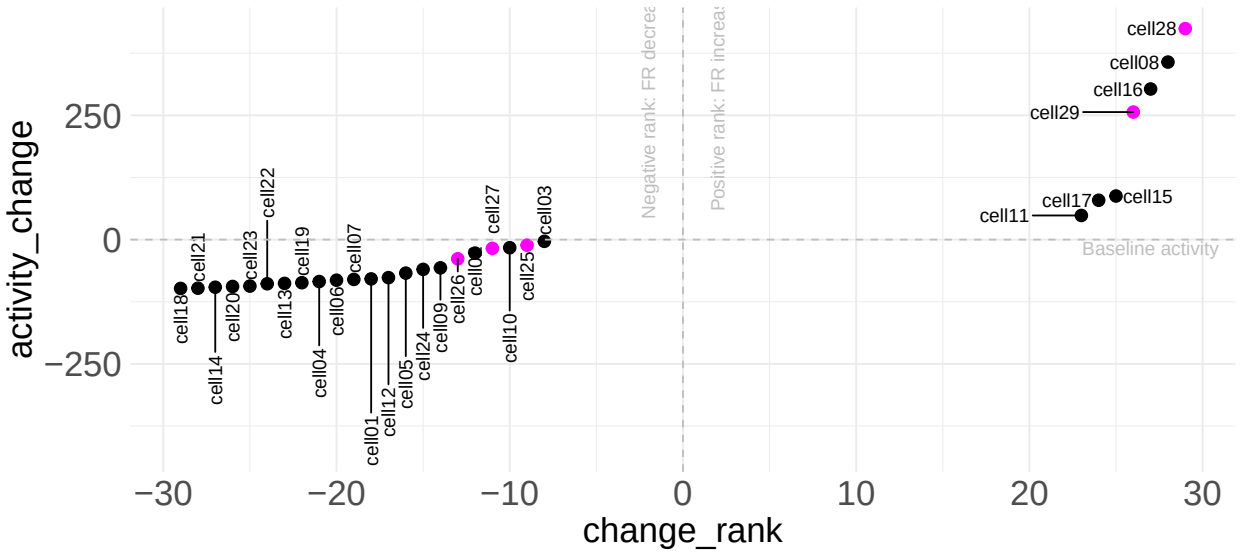


1.4.2 MFR before, during and after stimulus

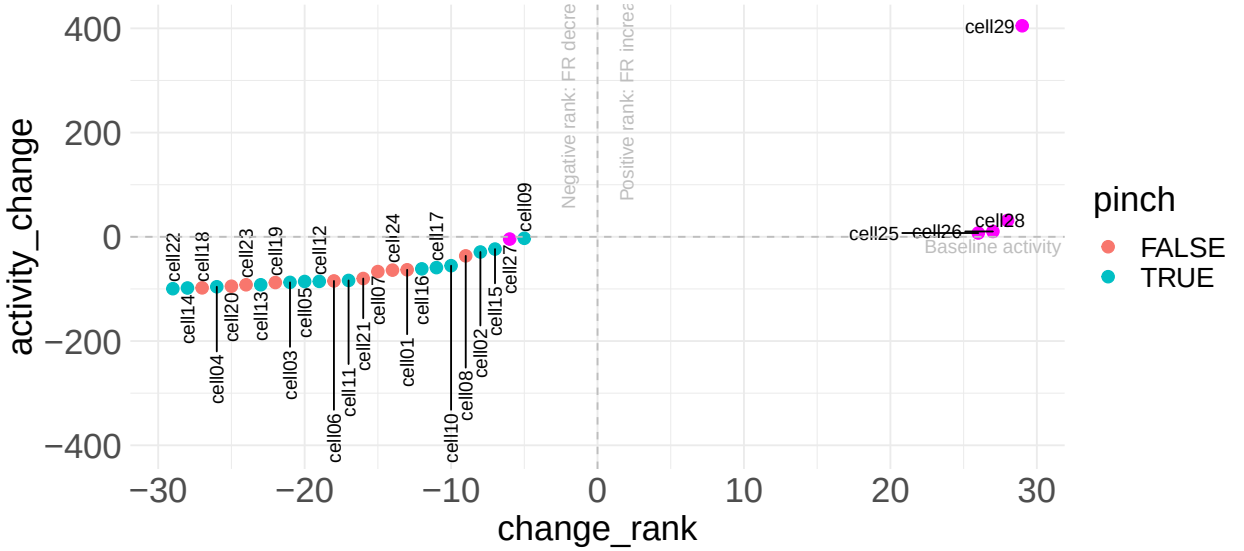


1.4.3 Strength of inhibition

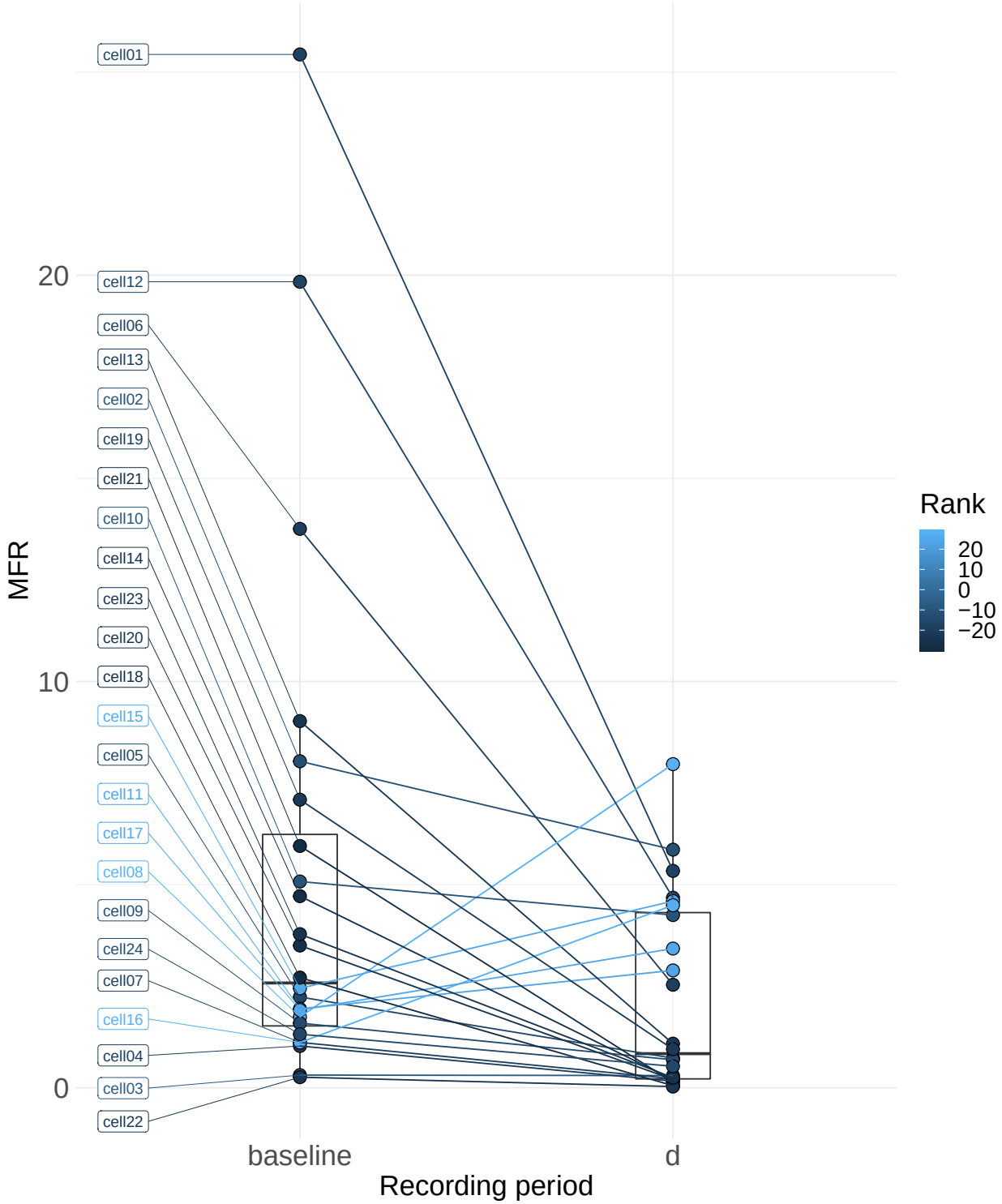
Firing rate change **during** stimulus (photoactivation of the glycinergic fibers) compared to **baseline**:



Firing rate change **during** stimulus (photoactivation of the glycinergic fibers) compared to **before** stimulus:



Plotting the change in MFR from "*baseline*" to "*during stimulus*". Coloring based on the strength of the inhibition (*rank*)


cell01
cell12
cell06
cell13
cell02
cell19
cell21
cell10
cell14
cell23
cell20
cell18
cell15
cell05
cell11
cell17
cell08
cell09
cell24
cell07
cell16
cell04
cell03
cell22
20
10
0
MFR
baseline
d
Recording period
Rank
20
10
0
−10
−20

2 Activity of PRF glycinergic cells during PFC photoactivation

- List of tibbles used to store data:
  - RECORDINGS tibble: stores AP and stim time stamps, number of stimuli in each train, stimulus frequency categories (eg. 8 10 and 12 Hz belong to 10 Hz category)
  - STIM_RESULTS: stores the data for PSTHs

```
### adding stimulus number within
### train
RECORDINGS <- RECORDINGS %>% mutate(stim_number = 0)

### calculating stimulus number
### within train
initial_value <- RECORDINGS$stim_freq[1] %>%
    `comment<-`("First value of stim_freq variable. When it changes stimulus counting re

stim_counter <- 1 %>% `comment<-`("Counts stimuli in a train")
index <- 1 %>% `comment<-`("Tracks the position (index) of stim_freq")

RECORDINGS$stim_number[1] <- stim_counter
repeat {
    if (RECORDINGS$stim_freq[index +
        1] == initial_value) {
        RECORDINGS$stim_number[index +
            1] <- stim_counter +
            1
        stim_counter <- stim_counter +
            1
        index <- index + 1
    } else {
        initial_value <- RECORDINGS$stim_freq[index +
            1]
        stim_counter <- 1
        RECORDINGS$stim_number[index +
            1] <- stim_counter
        index <- index + 1
    }

    if (index == length(RECORDINGS$stim_number)) {
        break
    }
```

```
}
```

3 Spontaneous desynchronization of the FC slow oscillation

```
file_to_load <- file_list[[1]]
filename <- as.character(substring(file_to_load,
    1, nchar(file_to_load) - 4))
raw.rec <- readMat(file.path("data",
    file_to_load))

### takes the first AP (first
### row) and tells the index of
### point with the max value
points_to_peak <- which(raw.rec$ap[,
    , 1]$values[1, ] == max(raw.rec$ap[,
    , 1]$values[1, ])) %>% as.numeric()

### time of the peak of the APs
### after its first point
raw.rec$ap[, , 1]$interval * points_to_peak
```

```
##          [,1]
## [1,] 0.00055
```

```
ap <- raw.rec$ap[, , 1]$times %>%
    as.double()
ap_peaks <- tibble(peak_times = (ap +
    c(raw.rec$ap[, , 1]$interval *
        points_to_peak)))
```

——- insert code here ———

(spont_desynchron_analysis.R), 7 recordings