CytoGLMM

GENERATED DATA

```r
set.seed(23)
df <- generate_data()
df

protein_names <- names(df)[3:12]
df %<>% dplyr:: mutate_at(protein_names, function(x) asinh(x/5))
glmm_fit <- CytoGLMM::cytoglmm(df,
                               protein_names = protein_names,
                               condition = "condition",
                               group = "donor",
                               num_cores=1)
glmm_fit
plot(glmm_fit)
summary(glmm_fit)
summary(glmm_fit) %>% dplyr::filter(pvalues_adj < 0.05)


glm_fit <- CytoGLMM::cytoglm(df,
                             protein_names = protein_names,
                             condition = "condition",
                             group = "donor",
                             num_boot = 1000)
glm_fit
summary(glm_fit)
```

TRY WITH PBMC DATA

```r
data(PBMC_panel, PBMC_md, PBMC_fs)
sce_pbmc <- prepData(PBMC_fs, PBMC_panel, PBMC_md, transform=T)

runCytoGLMM(sce_pbmc, "condition", "patient_id")
```

TRY WITH PLATELETS DATA (DUAL TRIPLE THERAPY)

```r
sce_platelets <- readRDS("/Users/lisiarend/Desktop/Uni/Master/SysBioMed/CyTOF/cytof/data/platelets_small
sce_platelets

runCytoGLMM(sce_platelets, "platelets", "patient_id")
```

```r
## SAMPLE PLATELETS DATA
ei_platelets <- ei(sce_platelets)
ei_platelets$platelets <- sample(ei_platelets$platelets)
platelets <- rep(ei_platelets$platelets, times = as.numeric(ei_platelets$n_cells))
data$condition <- platelets

glmm_fit <- CytoGLMM:: cytoglmm(data,
                                protein_names = marker_names,
                                condition = "condition",
                                group = "donor")
summary(glmm_fit)
results <- summary(glmm_fit)
p.adjust(results$pvalues_unadj, method = "BH")
```

COVID DATA

```r
panel <-
  read_excel(
    "/Users/lisiarend/Desktop/Uni/Master/SysBioMed/CyTOF/extdata/Covid/panel_umap.xlsx"
  )

md <-
  read_excel(
    "/Users/lisiarend/Desktop/Uni/Master/SysBioMed/CyTOF/extdata/Covid/meta_11vs8.xlsx"
  )

exp <-
  list.files(
    "/Users/lisiarend/Desktop/Uni/Master/SysBioMed/CyTOF/extdata/Covid/FlowRepository_FR-FCM-Z2MT_files
    pattern = "\\.fcs$",
    full.names = T
  )

sce_covid <-
  prepData(
    exp,
    panel,
    md,
    transform = TRUE,
    md_cols = list(
      file = "file_name",
      id = "sample_id",
      factors = c("covid","patient_id", "platelets")
    )
  )

# read in sce_covid
sce_covid <- readRDS("/nfs/home/students/l.arend/data/covid/sce_covid")

marker_names <- rowData(sce_covid)$marker_name
marker_names <- sapply(marker_names, function(marker) {
  gsub("[^[:alnum:]]", "", marker)
```
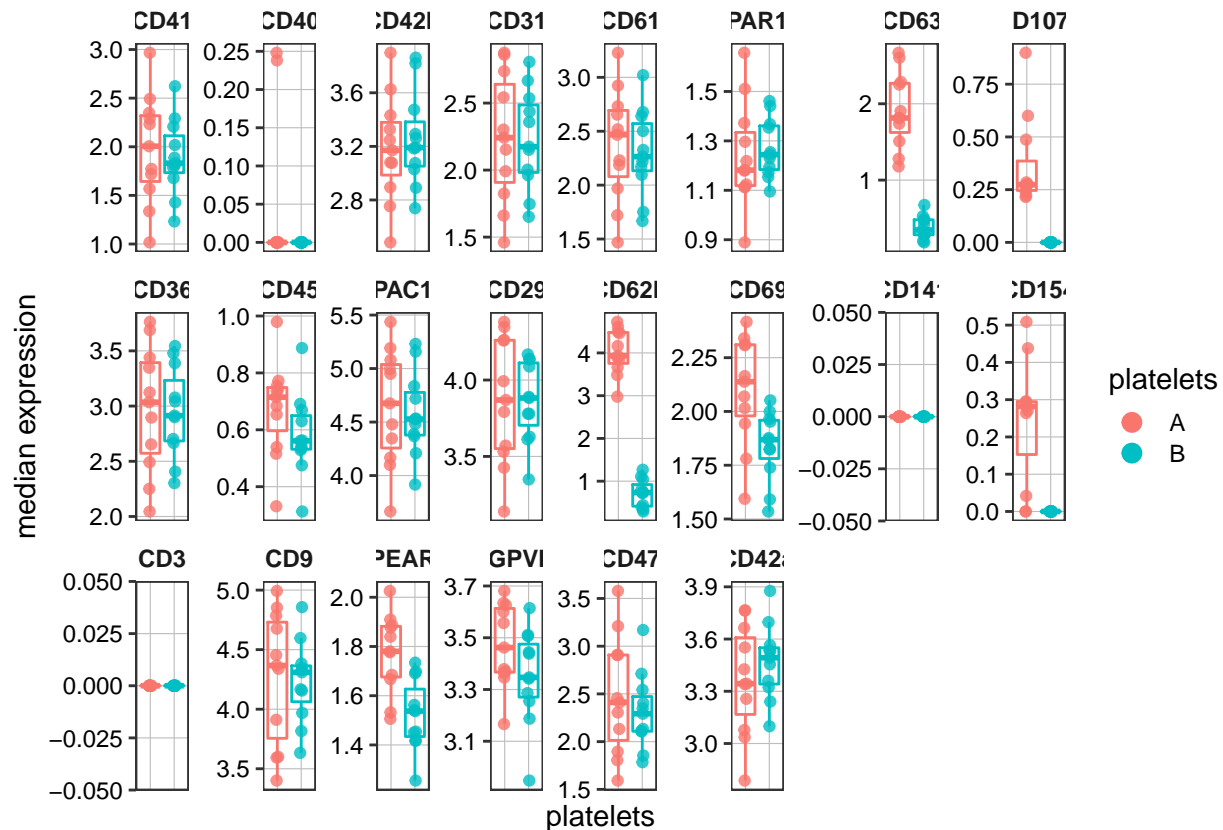
```
})
```

Activated vs. baseline in healthy patients

```
# filter SCE
sce_healthy <- filterSCE(sce_covid, covid == "healthy")

# plot boxplots
CATALYST::plotPbExprs(sce_healthy, k = "all", features = NULL , color_by = "platelets",  ncol=8, facet_
```



```
# run cytoglmm
runCytoGLMM(sce_healthy, "platelets", "patient_id")
```
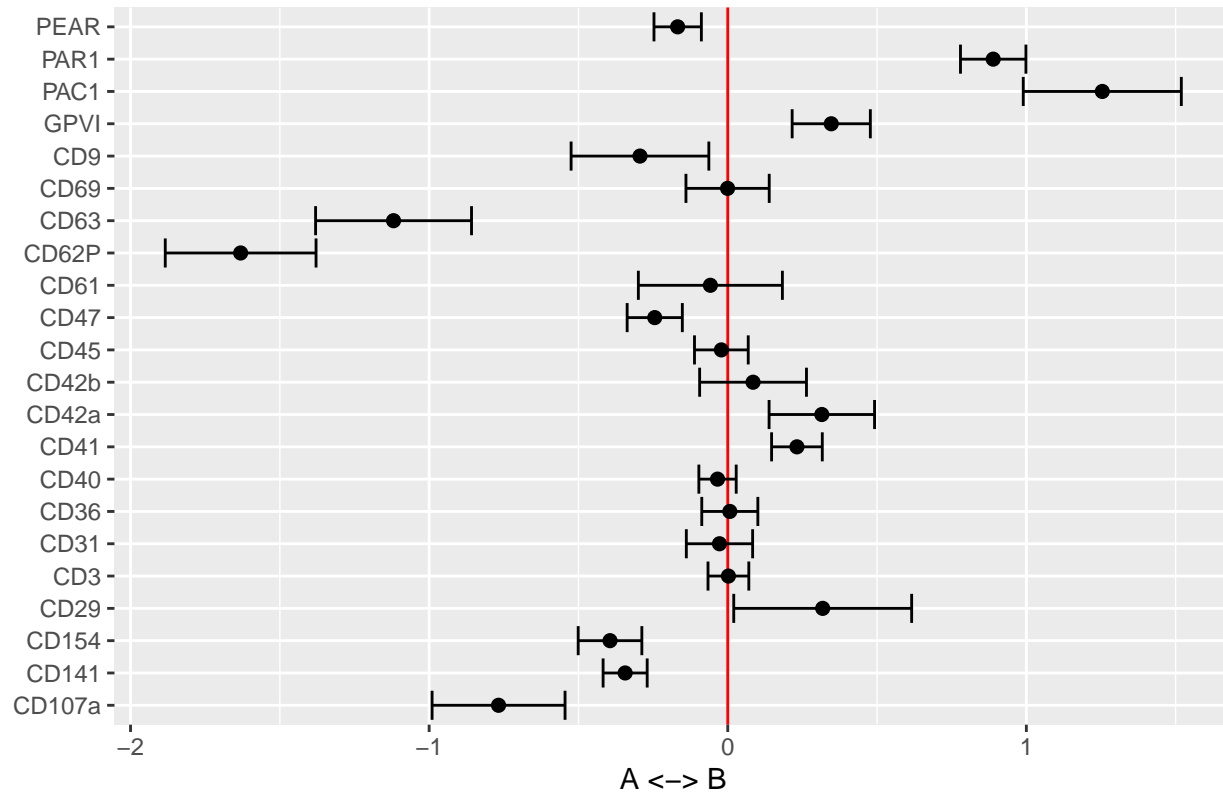
```
## Warning in moment.est.cov.reducer(cov.info, diagcov, cov.rank.warn,
## cov.psd.warn): moment-based covariance matrix estimate is not positive semi-
## definite; using projection
```

```
## # A tibble: 22 x 3
##     protein_name pvalues_unadj pvalues_adj
##     <chr>                <dbl>       <dbl>
## 1 PAR1              6.09e-57    1.34e-55
## 2 CD62P             9.37e-37    1.03e-35
## 3 PAC1              1.56e-20    1.14e-19
## 4 CD141             7.27e-20    4.00e-19
## 5 CD63              4.40e-17    1.93e-16
## 6 CD154             4.24e-13    1.56e-12
## 7 CD107a            1.42e-11    4.45e-11
```

```
##  8 CD41           8.88e- 8    2.44e- 7
##  9 GPVI           2.12e- 7    4.71e- 7
## 10 CD47           2.14e- 7    4.71e- 7
## # ... with 12 more rows

## Warning: `as.tibble()` is deprecated as of tibble 2.0.0.
## Please use `as_tibble()` instead.
## The signature and semantics have changed, see `?as_tibble`.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_warnings()` to see where this warning was generated.
```
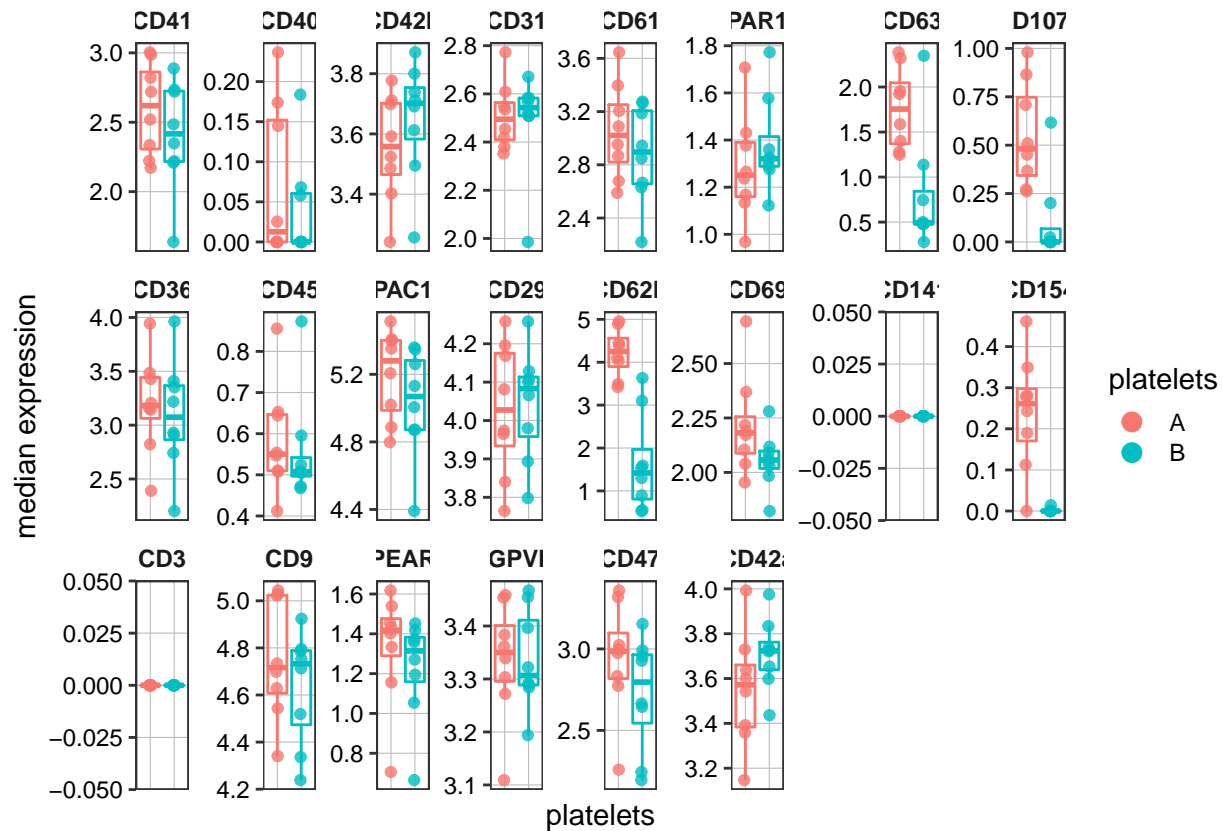

Activated vs. baseline in covid patients

```
# filter SCE
sce_patients <- filterSCE(sce_covid, covid == "patient")

# plot boxplots
CATALYST::plotPbExprs(sce_patients, k = "all", features = NULL , color_by = "platelets",  ncol=8, facet_
```
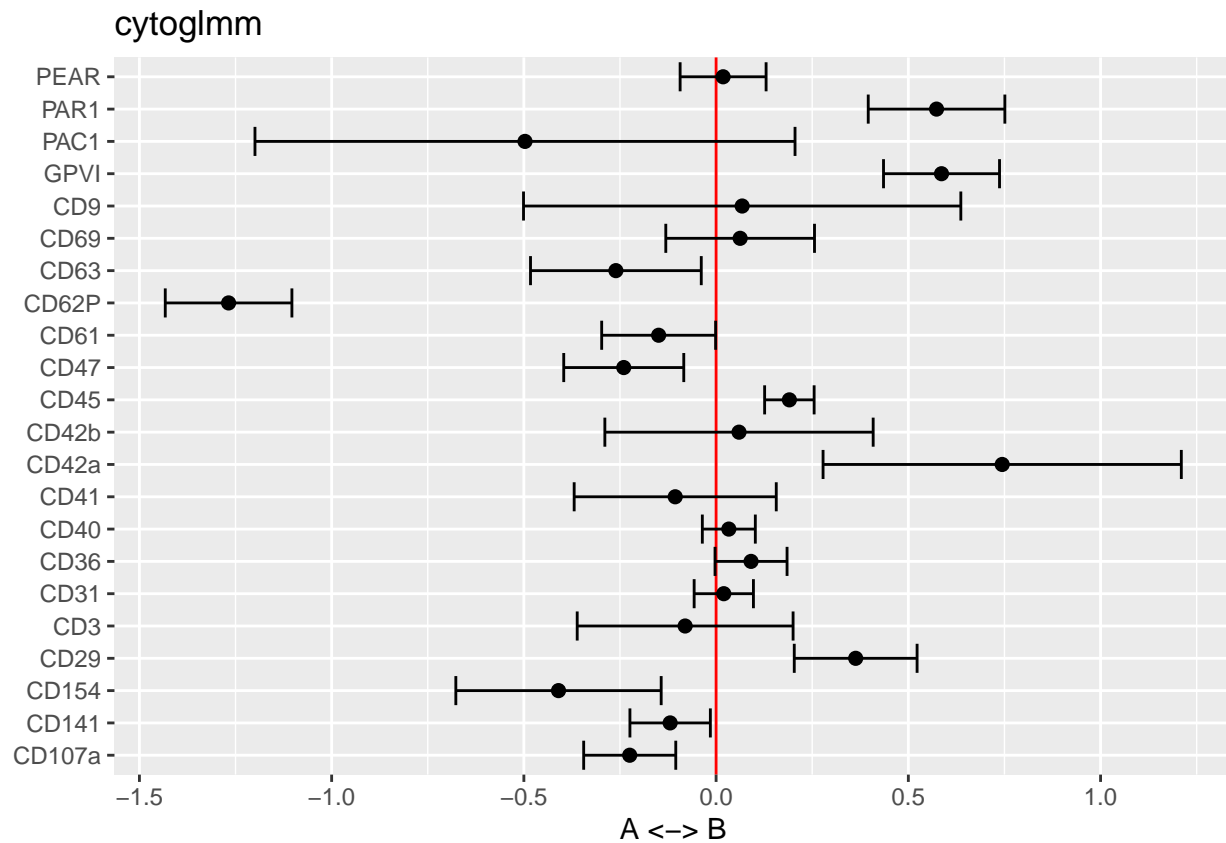
```r
# run cytoGLMM
runCytoGLMM(sce_patients, "platelets", "patient_id")
```

```
## Warning in moment.est.cov.reducer(cov.info, diagcov, cov.rank.warn,
## cov.psd.warn): moment-based covariance matrix estimate is not positive semi-
## definite; using projection

## # A tibble: 22 x 3
##    protein_name pvalues_unadj pvalues_adj
##    <chr>                <dbl>       <dbl>
##  1 CD62P             1.90e-51    4.19e-50
##  2 GPVI              2.62e-14    2.88e-13
##  3 PAR1              2.53e-10    1.86e- 9
##  4 CD45              6.50e- 9    3.58e- 8
##  5 CD29              8.45e- 6    3.72e- 5
##  6 CD107a            2.36e- 4    8.67e- 4
##  7 CD42a             1.75e- 3    5.49e- 3
##  8 CD47              2.56e- 3    6.42e- 3
##  9 CD154             2.63e- 3    6.42e- 3
## 10 CD63              2.14e- 2    4.71e- 2
## # ... with 12 more rows
```
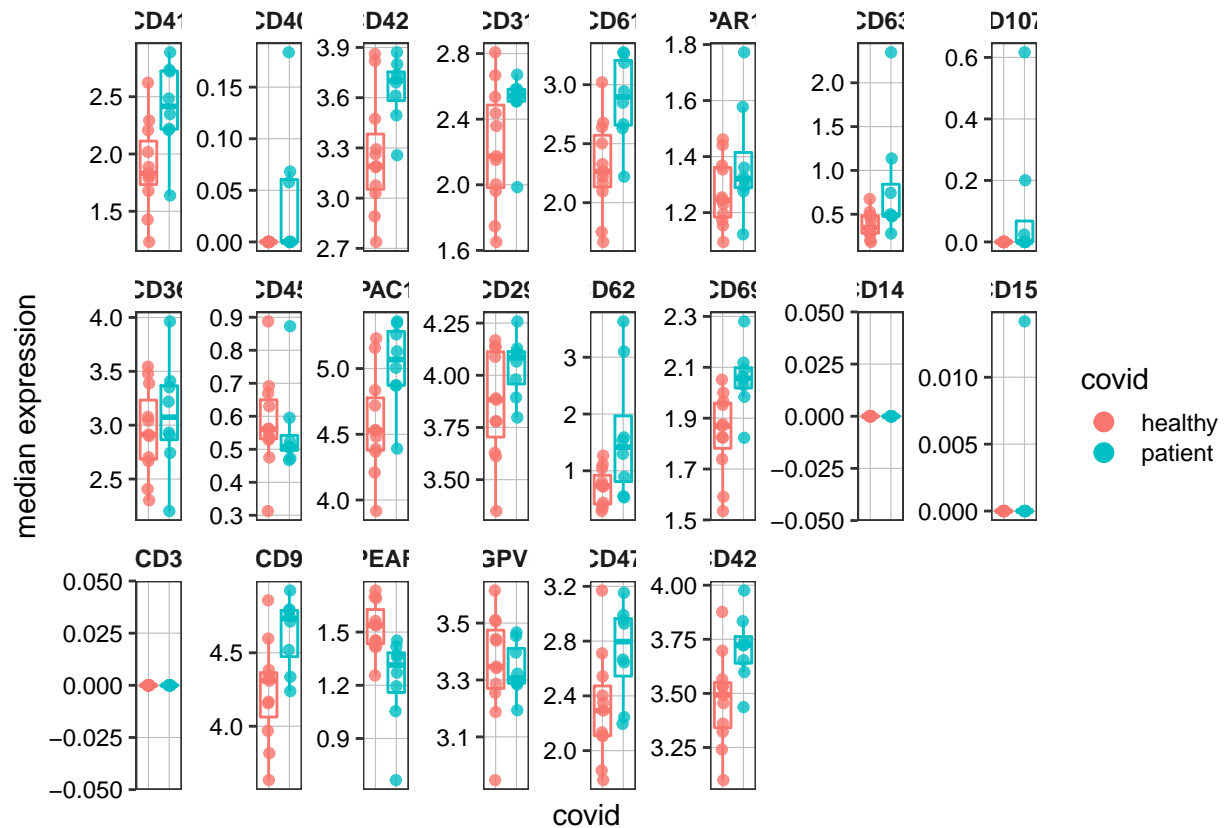
cytoglmm

Healthy vs. covid in non-stimulated platelets

```r
# filter SCE
sce_baseline <- filterSCE(sce_covid, platelets == "B")

# plot boxplots
CATALYST::plotPbExprs(sce_baseline, k = "all", features = NULL , color_by = "covid",  ncol=8, facet_by =
```
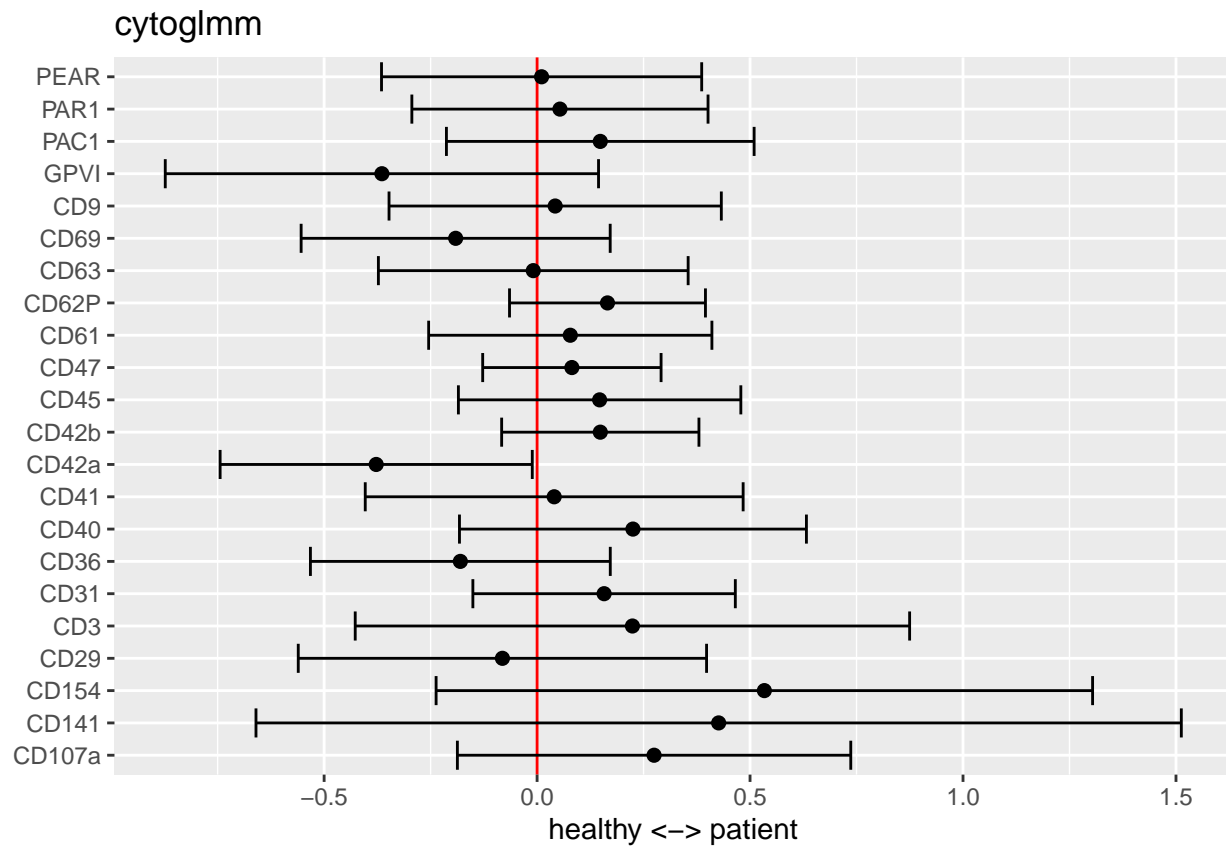
```r
# run cytoGLMM
runCytoGLMM(sce_baseline, "covid", "patient_id")
```

```
## Warning in moment.est.cov.reducer(cov.info, diagcov, cov.rank.warn,
## cov.psd.warn): moment-based covariance matrix estimate is not positive semi-
## definite; using projection

## # A tibble: 22 x 3
##    protein_name pvalues_unadj pvalues_adj
##    <chr>                <dbl>       <dbl>
##  1 CD42a               0.0434       0.697
##  2 CD62P               0.159        0.697
##  3 GPVI                0.160        0.697
##  4 CD154               0.175        0.697
##  5 CD42b               0.209        0.697
##  6 CD107a              0.244        0.697
##  7 CD40                0.279        0.697
##  8 CD69                0.302        0.697
##  9 CD36                0.316        0.697
## 10 CD31                0.317        0.697
## # ... with 12 more rows
```
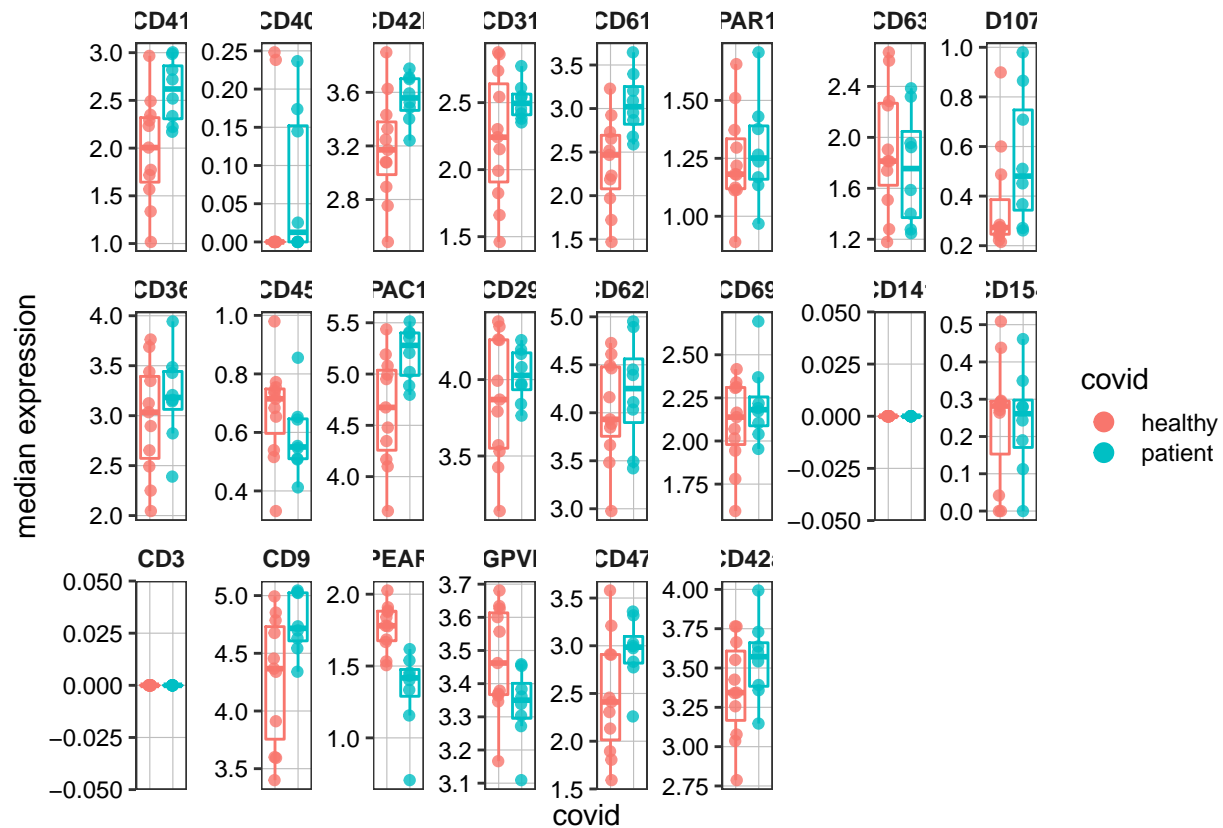
Healthy vs. covid in stimulated platelets

```r
# filter SCE
sce_activated <- filterSCE(sce_covid, platelets == "A")

# plot boxplots
CATALYST::plotPbExprs(sce_activated, k = "all", features = NULL , color_by = "covid",  ncol=8, facet_by
```

```
# run cytoGLMM
runCytoGLMM(sce_activated, "covid", "patient_id")
```

```
## Warning in moment.est.cov.reducer(cov.info, diagcov, cov.rank.warn,
## cov.psd.warn): moment-based covariance matrix estimate is not positive semi-
## definite; using projection
```

```
## # A tibble: 22 x 3
##    protein_name pvalues_unadj pvalues_adj
##    <chr>                <dbl>       <dbl>
##  1 CD42b               0.0364       0.757
##  2 CD36                0.147        0.757
##  3 GPVI                0.173        0.757
##  4 CD61                0.202        0.757
##  5 PAR1                0.229        0.757
##  6 CD42a               0.229        0.757
##  7 CD47                0.278        0.757
##  8 CD29                0.322        0.757
##  9 CD40                0.361        0.757
## 10 CD154               0.389        0.757
## # ... with 12 more rows
```

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healthy <-> patient