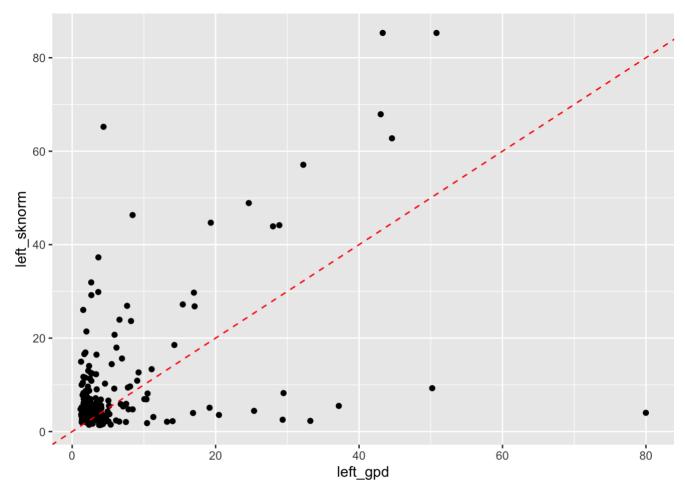
GPD vs Skew Normal

```
library(eva)
library(tidyverse)
library(katlabutils)
library(cowplot)
library(ggplot2)
# should work under low moi folder
q < -0.96
samples <- 5e5
working_dir <- getwd()</pre>
# get the file path for gpd parameters
subDir <- sprintf("figures/power_exploration/tail_prob_%d_resamples_%.2f_percentile",</pre>
samples, q)
param <- read.csv(sprintf("%s/param.csv", file.path(working_dir, subDir)))</pre>
gpd_param <- t(matrix(as.numeric(unlist(param[,-1])), nrow = 6, ncol = 660))</pre>
gpd param <- as.data.frame(gpd param)</pre>
colnames(gpd param) <- c("location", "scale", "shape", "statistic", "p-value", "p-val</pre>
ue ratio")
p_value_ratio_gpd <- gpd_param$`p-value ratio`</pre>
# check if the inf value corresponds to bumpy distribution
# bumpy: 56, 143, 169, 175, 177, 185, 191, 198, 213, 236, 241, 243
# nonbumpy: 327, 325, 324
# both bumpy: 191
sort(which(p_value_ratio_gpd == Inf), decreasing = TRUE)
```

[1] 657 655 654 528 521 515 243 241 236 213 191 177 175 169 143 56

```
# get the file path for skew normal parameter
subDir <- sprintf("figures/power exploration/sknorm tail prob %d resamples %.2f perce</pre>
ntile", samples, q)
param <- read.csv(sprintf("%s/param.csv", file.path(working dir, subDir)))</pre>
sknorm param <- t(matrix(as.numeric(unlist(param[,-1])), nrow = 6, ncol = 660))</pre>
sknorm param <- as.data.frame(sknorm param)</pre>
colnames(sknorm param) <- c("location", "scale", "shape", "statistic", "p-value", "p-</pre>
value ratio")
p value ratio sknorm <- sknorm param$`p-value ratio`</pre>
# compare left tail case
left gpd ratio <- p value ratio gpd[1:330]</pre>
left sknorm ratio <- p value ratio sknorm[1:330]</pre>
# leave the large value out
large leftgpd id <- which(left gpd ratio > 100)
large leftsknorm id <- which(left sknorm ratio > 100)
large left id <- c(large leftgpd id, large leftsknorm id)</pre>
# infinite value id
Inf_left_id <- which(left_gpd_ratio == "Inf")</pre>
# exclude the infinite value id and large value id
excl id <- c(Inf left id, large left id)</pre>
left comparison <- data.frame(left gpd = left gpd ratio[-excl id],</pre>
                                left_sknorm = left_sknorm_ratio[-excl_id])
left comparison |>
  ggplot(aes(x = left_gpd, y = left_sknorm)) +
  geom point() +
  geom abline(linetype = "dashed", color = "red")
```



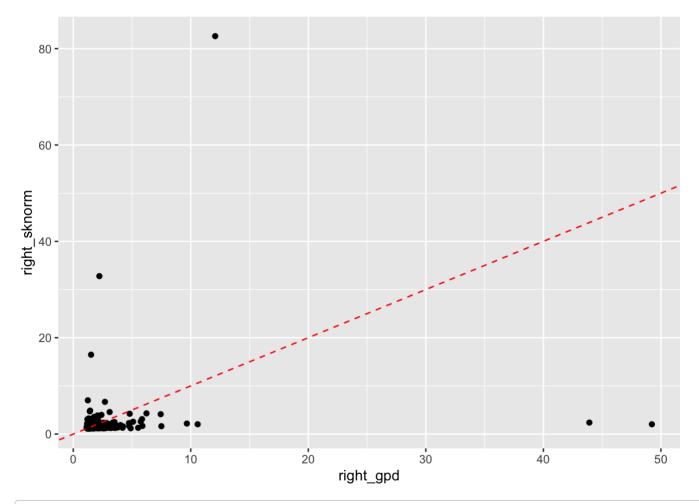
no of gpd bigger than sknorm for left tail
length(which(left_gpd_ratio > left_sknorm_ratio))

[1] 97

length(which(left_sknorm_ratio > left_gpd_ratio))

[1] 233

```
# compare right tail case
right_gpd_ratio <- p_value_ratio_gpd[331:660]</pre>
right sknorm ratio <- p value ratio sknorm[331:660]</pre>
# leave the large value out
large_rightgpd_id <- which(right_gpd_ratio > 100)
large rightsknorm id <- which(right sknorm ratio > 100)
large_right_id <- c(large_rightgpd_id, large_rightsknorm_id)</pre>
# infinite value id
Inf right id <- which(right gpd ratio == "Inf")</pre>
# exclude the infinite value id and large value id
excl id <- c(Inf right id, large right id)</pre>
right comparison <- data.frame(right gpd = right gpd ratio[-excl id],
                                right_sknorm = right_sknorm_ratio[-excl_id])
right comparison |>
  ggplot(aes(x = right_gpd, y = right_sknorm)) +
  geom_point() +
  geom abline(linetype = "dashed", color = "red")
```



```
# no of gpd bigger than sknorm for left tail
length(which(right_gpd_ratio > right_sknorm_ratio))
```

```
## [1] 224
```

length(which(right_sknorm_ratio > right_gpd_ratio))

[1] 106

GoF comparison
gpd_gof <- gpd_param\$`p-value`
sknorm_gof <- sknorm_param\$`p-value`

no of significance in terms of gof test for left/right tail.
length(which(gpd_gof[1:330] > sknorm_gof[1:330]))

[1] 241

length(which(gpd_gof[331:660] > sknorm_gof[331:660]))

[1] 295