

# Genepar: Pain & Medication Use

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## Data Summary

Data structure:

```
# load data:
df <- readRDS("./genepar/GENEPAR1.RDS")
# select relevant variables:
df <- df[,c(1:3,7,9:12,62,78:82)]; glimpse(df)
```

```
## Rows: 982
## Columns: 14
## $ ID          <chr> "000715", "002163", "002666", "002716", "003768", "0041~
## $ DIAGNOSIS   <fct> Lower Back Pain, Neuropathic Pain, Neuropathic Pain, Ne~
## $ SEX         <fct> Female, Male, Male, Female, Male, Male, Male, Female, F~
## $ CLINIC      <fct> CHUM, MUHC, MUHC, HDL, HDL, CHUM, CHUS, CHUM, HDL, CHUM~
## $ AGE         <dbl> 52, 25, 60, 52, 36, 60, NA, 45, 37, 36, 52, 40, 55, 47,~
## $ BMI         <dbl> 19, 25, 28, 27, 29, 27, 23, 22, 29, 20, 32, 24, 27, 20,~
## $ PAIN_BASELINE <dbl> 7, 8, 6, 6, 8, 6, NA, 2, 8, 2, 4, 8, 7, 8, 5, 7, 5, 5, ~
## $ PAIN_FOLLOW_UP <dbl> 9, 7, 4, 3, 3, 1, 9, 2, 7, 1, 4, 8, 8, 8, 1, 10, 6, 3, ~
## $ SCORE_DN4    <dbl> 6, 6, 4, 3, 1, 0, 3, 4, 4, 7, 3, 6, 6, 4, 2, 2, 5, 5, 2~
## $ ACETAMINOPHEN <fct> 1, 0, 1, 0, 0, 1, NA, NA, 0, 1, 0, 1, 1, 0, NA, 0, 0, 0~
## $ GABA_ANALOGS <fct> 0, 0, 0, 1, 0, 1, NA, NA, 0, 1, 1, 1, 1, 0, NA, 0, 0, 0~
## $ OPIOIDS      <fct> 1, 0, 0, 0, 1, 1, NA, NA, 1, 0, 1, 1, 0, 1, NA, 0, 0, 1~
## $ NSAIDS       <fct> 0, 0, 1, 0, 0, 1, NA, NA, 1, 0, 1, 1, 1, 0, NA, 0, 0, 0~
## $ OTHER        <fct> 1, 1, 0, 0, 0, 0, NA, NA, 1, 0, 1, 1, 0, 1, NA, 1, 1, 1~
```

Table 1: Summary of all continuous variables

Variable	DIAGNOSIS	N	Missing	Mean	SD	Min	Median	Max	p.value
AGE	LBP	500	9	54.9	10.6	23	56	75	<0.001
	NP	470	3	51.6	11.4	18	52	77	
BMI	LBP	509	0	28.1	6.3	11	27	51	0.300
	NP	473	0	27.7	6.4	13	27	60	
PAIN_BASELINE	LBP	500	9	6.7	1.9	0	7	10	0.300
	NP	470	3	6.5	1.9	0	7	10	
PAIN_FOLLOW_UP	LBP	501	8	5.7	2.3	0	6	10	0.700
	NP	465	8	5.8	2.4	0	6	10	
SCORE_DN4	LBP	509	0	3.3	1.9	0	3	7	<0.001
	NP	473	0	3.9	1.9	0	4	7	

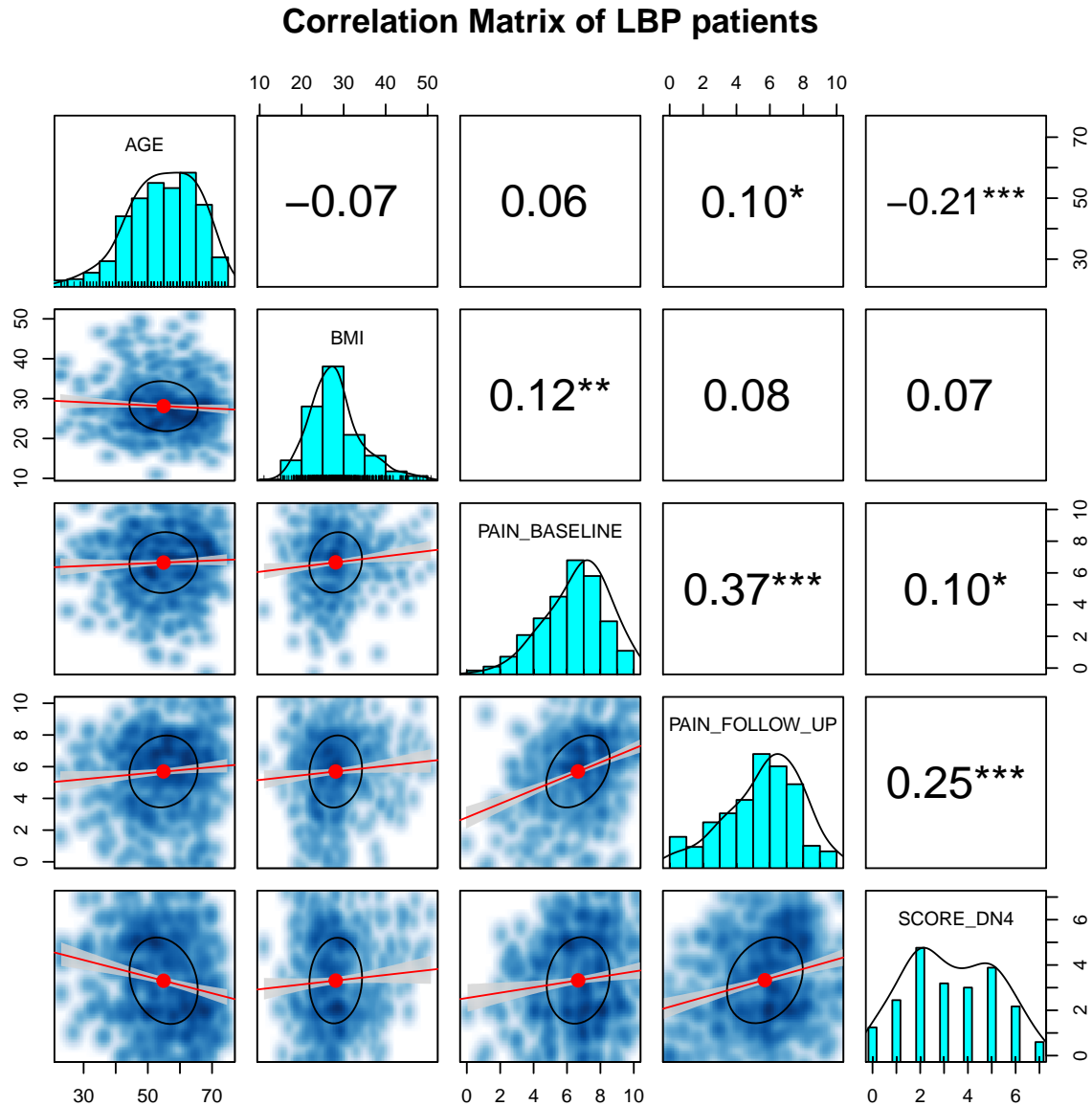
**Summary of continuous variables:**

```

dt <- summarize(df, type = "numeric", group = "DIAGNOSIS")
dt <- as.data.frame(dt)
row.names(dt) <- NULL
names(dt)[1] <- "Variable"
dt <- dt[,-c(3,6,9,11,13,15)]
dt$DIAGNOSIS[dt$DIAGNOSIS == "Lower Back Pain"] <- "LBP"
dt$DIAGNOSIS[dt$DIAGNOSIS == "Neuropathic Pain"] <- "NP"
kbl(dt, booktabs = T, caption = "Summary of all continuous variables", format="latex") %>%
kable_styling(latex_options = "scale_down")

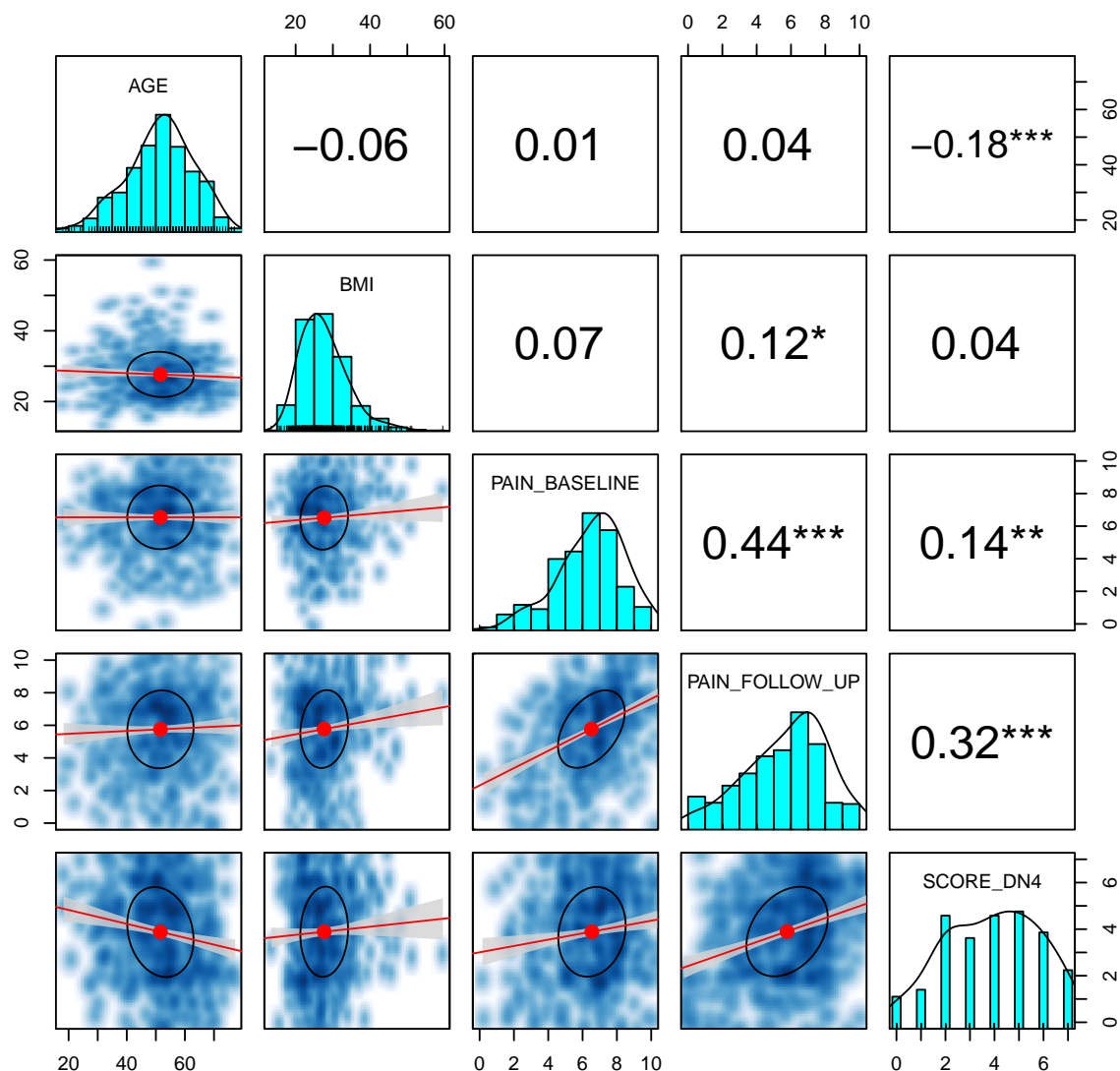
```

```
# correlation plots:
df1 <- df[df$DIAGNOSIS == "Lower Back Pain",c(3,5:9)]
pairs.panels(df1[, -1],
             method = "pearson", stars=T, lm = T, ci = T, jiggle = T, smoother = T, density = T, ellipses=T,
             main = "Correlation Matrix of LBP patients")
```



```
df1 <- df[df$DIAGNOSIS == "Neuropathic Pain",c(3,5:9)]
pairs.panels(df1[, -1],
             method = "pearson", stars=T, lm = T, ci = T, jiggle = T, smoother = T, density = T, ellipses=T,
             main = "Correlation Matrix of NP patients")
```

## Correlation Matrix of NP patients



Summary of categorical variables:

```
dt <- summarize(df[, -4], type = "factor", group = "DIAGNOSIS")
dt <- as.data.frame(dt)
dt <- dt[, -c(3, 6, 9)]
names(dt) <- c("Variable", "Level", "N_LBP", "%_LBP", "N_NP", "%_NP", "p.value")
kbl(dt, booktabs = T, caption = "Summary of all categorical variables", format = "latex") %>%
kable_styling(latex_options = "scale_down")
```

Table 2: Summary of all categorical variables

Variable	Level	N_LBP	%_LBP	N_NP	%_NP	p.value
SEX	Female	276	54.2	308	65.1	0.001
	Male	233	45.8	165	34.9	
ACETAMINOPHEN	0	200	39.3	180	38.1	0.192
	1	223	43.8	165	34.9	
	<Missing>	86	16.9	128	27.1	
GABA_ANALOGS	0	234	46.0	192	40.6	0.942
	1	189	37.1	153	32.3	
	<Missing>	86	16.9	128	27.1	
OPIOIDS	0	224	44.0	201	42.5	0.145
	1	199	39.1	144	30.4	
	<Missing>	86	16.9	128	27.1	
NSAIDS	0	230	45.2	227	48.0	0.001
	1	193	37.9	118	24.9	
	<Missing>	86	16.9	128	27.1	
OTHER	0	250	49.1	179	37.8	0.049
	1	173	34.0	166	35.1	
	<Missing>	86	16.9	128	27.1	

## Statistical modeling

### 1. Mixed effects model (LBP)

```
# models
dt <- df %>% dplyr::filter(DIAGNOSIS == "Lower Back Pain") %>%
  dplyr::select(PAIN_BASELINE, PAIN_FOLLOW_UP, ACETAMINOPHEN, GABA_ANALOGS,
    NSAIDS, OPIOIDS, OTHER, AGE, SEX, BMI, CLINIC)
m1ac <- lmer(PAIN_FOLLOW_UP ~ AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE + ACETAMINOPHEN,
  data = dt)
m1gb <- lmer(PAIN_FOLLOW_UP ~ GABA_ANALOGS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE,
  data = dt)
m1op <- lmer(PAIN_FOLLOW_UP ~ OPIOIDS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE,
  data = dt)
m1ns <- lmer(PAIN_FOLLOW_UP ~ NSAIDS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE,
  data = dt)
export_summs(m1ac, m1gb, m1op, m1ns, scale = T,
  error_format = "[{conf.low}, {conf.high}]") %>%
  kbl(booktabs = T, digits = 4, caption = "LBP models", format="latex") %>%
  kable_styling(latex_options = "scale_down")
```

Table 3: LBP models

[illegible]

```
plot_summs(m1ac, m1gb, m1op, m1ns, scale = T, plot.distributions = T)
```

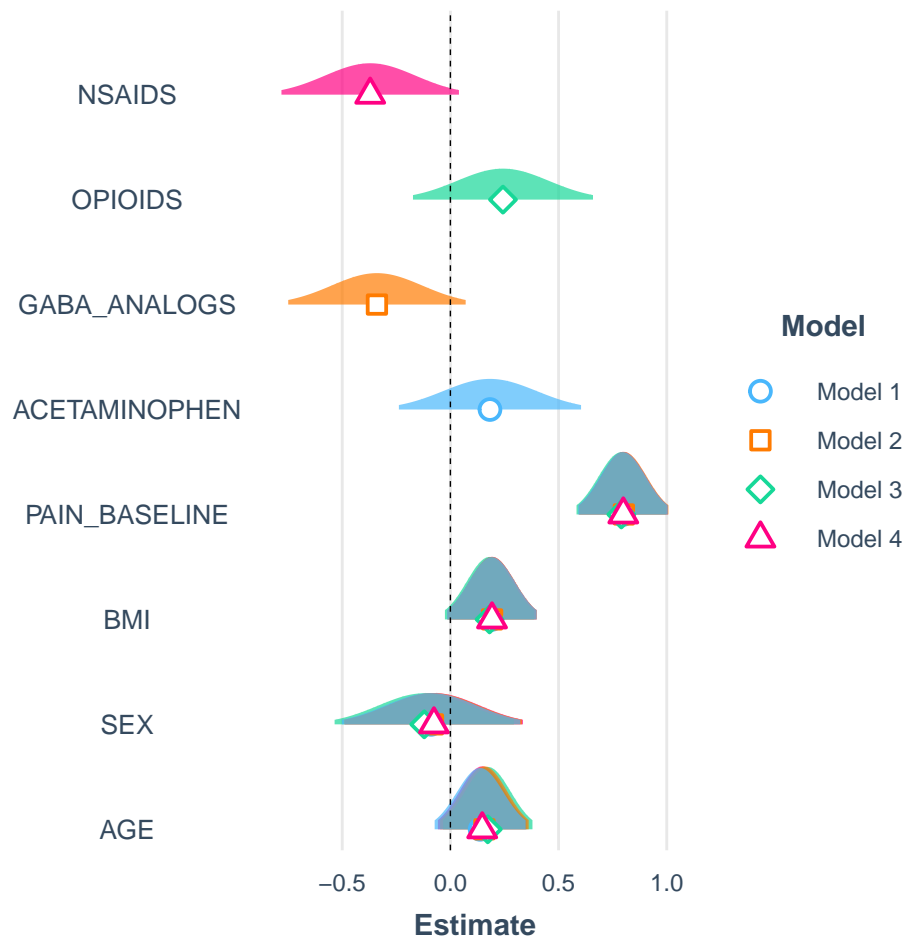
$$\text{follow-up LBP} \sim \text{Drug} + \text{baseline LBP} + \text{age} + \text{sex} + \text{BMI} + (1 \mid \text{clinic})$$


Table 4: NP models

[illegible]

## 2. Mixed effects model (NP)

```
dt <- df %>% dplyr::filter(DIAGNOSIS == "Neuropathic Pain") %>%
  dplyr::select(PAIN_BASELINE, PAIN_FOLLOW_UP, ACETAMINOPHEN, GABA_ANALOGS,
    NSAIDS, OPIOIDS, OTHER, AGE, SEX, BMI, CLINIC)
m1ac <- lmer(PAIN_FOLLOW_UP ~ AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE + ACETAMINOPHEN,
  data = dt)
m1gb <- lmer(PAIN_FOLLOW_UP ~ GABA_ANALOGS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE,
  data = dt)
m1op <- lmer(PAIN_FOLLOW_UP ~ OPIOIDS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE,
  data = dt)
m1ns <- lmer(PAIN_FOLLOW_UP ~ NSAIDS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE,
  data = dt)
export_summs(m1ac, m1gb, m1op, m1ns, scale = T,
  error_format = "[{conf.low}, {conf.high}]") %>%
  kbl(booktabs = T, digits = 4, caption = "NP models", format="latex") %>%
  kable_styling(latex_options = "scale_down")
```

```
plot_sums(m1ac, m1gb, m1op, m1ns, scale = T, plot.distributions = T)
```

$$\text{follow-up NP} \sim \text{Drug} + \text{baseline NP} + \text{age} + \text{sex} + \text{BMI} + (1 \mid \text{clinic})$$



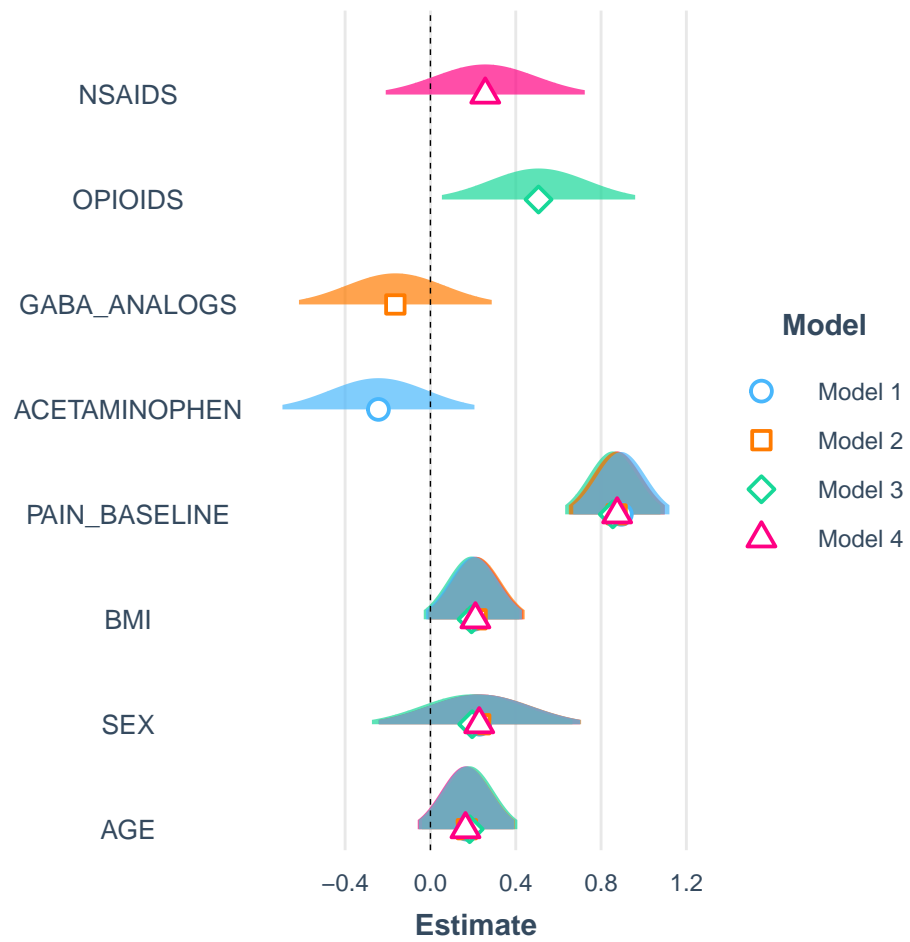


Table 5: DN4 corrected LBP models

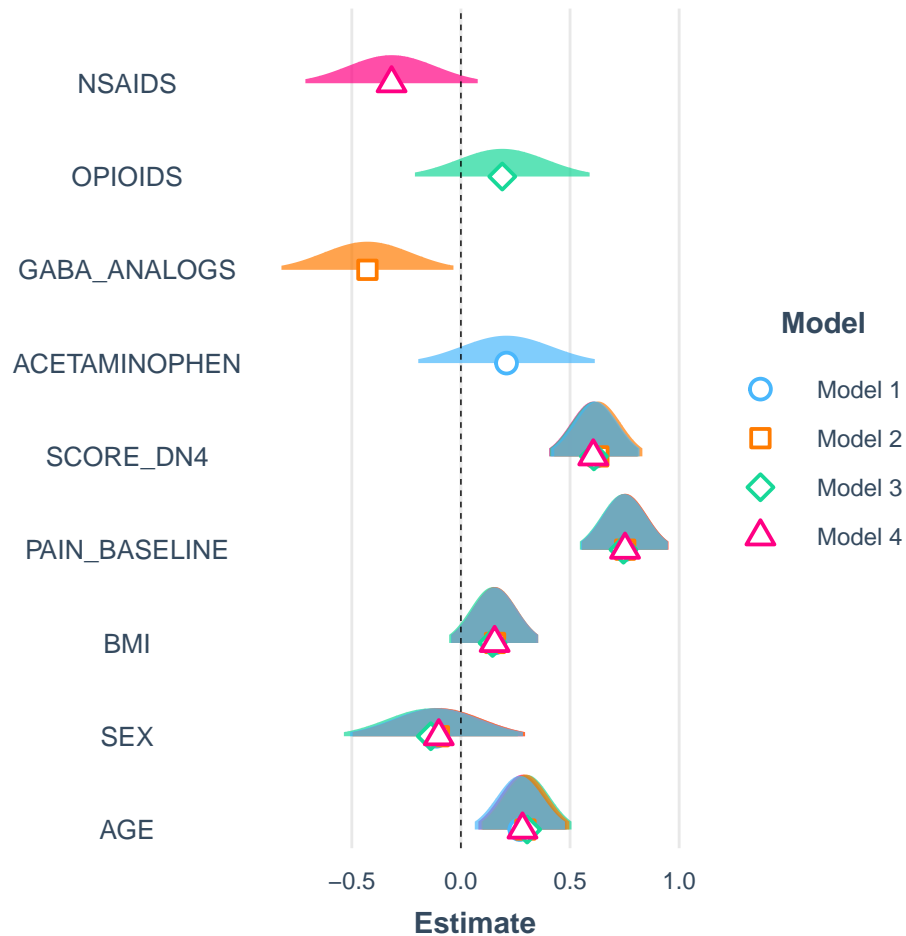
	Report 1	Report 2	Report 3	Report 4	Report 5
1	1	1	1	1	1
2	2	2	2	2	2
3	3	3	3	3	3
4	4	4	4	4	4
5	5	5	5	5	5
6	6	6	6	6	6
7	7	7	7	7	7
8	8	8	8	8	8
9	9	9	9	9	9
10	10	10	10	10	10
11	11	11	11	11	11
12	12	12	12	12	12
13	13	13	13	13	13
14	14	14	14	14	14
15	15	15	15	15	15
16	16	16	16	16	16
17	17	17	17	17	17
18	18	18	18	18	18
19	19	19	19	19	19
20	20	20	20	20	20
21	21	21	21	21	21
22	22	22	22	22	22
23	23	23	23	23	23
24	24	24	24	24	24
25	25	25	25	25	25
26	26	26	26	26	26
27	27	27	27	27	27
28	28	28	28	28	28
29	29	29	29	29	29
30	30	30	30	30	30
31	31	31	31	31	31
32	32	32	32	32	32
33	33	33	33	33	33
34	34	34	34	34	34
35	35	35	35	35	35
36	36	36	36	36	36
37	37	37	37	37	37
38	38	38	38	38	38
39	39	39	39	39	39
40	40	40	40	40	40
41	41	41	41	41	41
42	42	42	42	42	42
43	43	43	43	43	43
44	44	44	44	44	44
45	45	45	45	45	45
46	46	46	46	46	46
47	47	47	47	47	47
48	48	48	48	48	48
49	49	49	49	49	49
50	50	50	50	50	50
51	51	51	51	51	51
52	52	52	52	52	52
53	53	53	53	53	53
54	54	54	54	54	54
55	55	55	55	55	55
56	56	56	56	56	56
57	57	57	57	57	57
58	58	58	58	58	58
59	59	59	59	59	59
60	60	60	60	60	60
61	61	61	61	61	61
62	62	62	62	62	62
63	63	63	63	63	63
64	64	64	64	64	64
65	65	65	65	65	65
66	66	66	66	66	66
67	67	67	67	67	67
68	68	68	68	68	68
69	69	69	69	69	69
70	70	70	70	70	70
71	71	71	71	71	71
72	72	72	72	72	72
73	73	73	73	73	73
74	74	74	74	74	74
75	75	75	75	75	75
76	76	76	76	76	76
77	77	77	77	77	77
78	78	78	78	78	78
79	79	79	79	79	79
80	80	80	80	80	80
81	81	81	81	81	81
82	82	82	82	82	82
83	83	83	83	83	83
84	84	84	84	84	84
85	85	85	85	85	85
86	86	86	86	86	86
87	87	87	87	87	87
88	88	88	88	88	88
89	89	89	89	89	89
90	90	90	90	90	90
91	91	91	91	91	91
92	92	92	92	92	92
93	93	93	93	93	93
94	94	94	94	94	94
95	95	95	95	95	95
96	96	96	96	96	96
97	97	97	97	97	97
98	98	98	98	98	98
99	99	99	99	99	99
100	100	100	100	100	100

### 3. DN4 score corrected mixed effects model (LBP)

```
dt <- df %>% dplyr::filter(DIAGNOSIS == "Lower Back Pain") %>%
  dplyr::select(PAIN_BASELINE, PAIN_FOLLOW_UP, SCORE_DN4, ACETAMINOPHEN, GABA_ANALOGS,
    NSAIDS, OPIOIDS, OTHER, AGE, SEX, BMI, CLINIC)
m1ac <- lmer(PAIN_FOLLOW_UP ~ AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE + SCORE_DN4 + ACETAMINOPHEN,
  data = dt)
m1gb <- lmer(PAIN_FOLLOW_UP ~ GABA_ANALOGS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE + SCORE_DN4,
  data = dt)
m1op <- lmer(PAIN_FOLLOW_UP ~ OPIOIDS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE + SCORE_DN4,
  data = dt)
m1ns <- lmer(PAIN_FOLLOW_UP ~ NSAIDS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE + SCORE_DN4,
  data = dt)
export_summs(m1ac, m1gb, m1op, m1ns, scale = T,
  error_format = "[{conf.low}, {conf.high}]") %>%
  kbl(booktabs = T, digits = 4, caption = "DN4 corrected LBP models", format="latex") %>%
  kable_styling(latex_options = "scale_down")
```

```
plot_summs(m1ac, m1gb, m1op, m1ns, scale = T, plot.distributions = T)
```

$$\text{follow-up LBP} \sim \text{Drug} + \text{baseline LBP} + \text{DN4 score} + \text{age} + \text{sex} + \text{BMI} + (1 \mid \text{clinic})$$



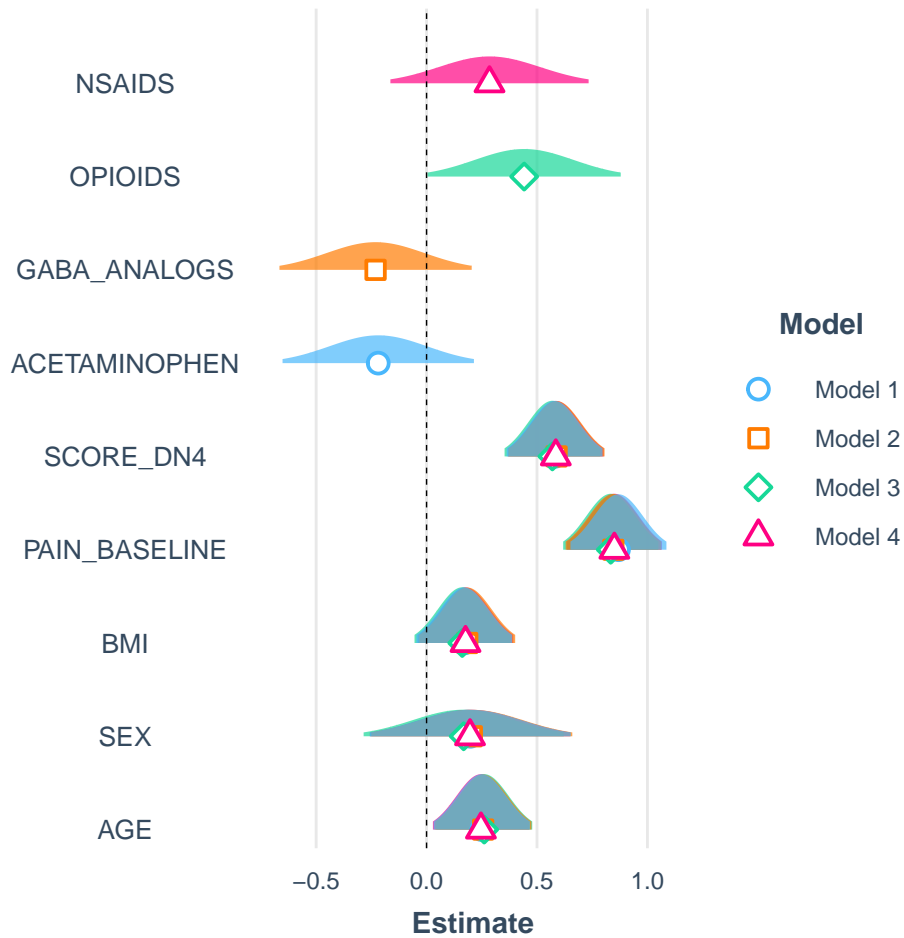
#### 4. DN4 score corrected mixed effects model (NP)

```
dt <- df %>% dplyr::filter(DIAGNOSIS == "Neuropathic Pain") %>%
  dplyr::select(PAIN_BASELINE, PAIN_FOLLOW_UP, SCORE_DN4, ACETAMINOPHEN, GABA_ANALOGS,
    NSAIDS, OPIOIDS, OTHER, AGE, SEX, BMI, CLINIC)
m1ac <- lmer(PAIN_FOLLOW_UP ~ AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE + SCORE_DN4 + ACETAMINOPHEN,
  data = dt)
m1gb <- lmer(PAIN_FOLLOW_UP ~ GABA_ANALOGS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE + SCORE_DN4,
  data = dt)
m1op <- lmer(PAIN_FOLLOW_UP ~ OPIOIDS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE + SCORE_DN4,
  data = dt)
m1ns <- lmer(PAIN_FOLLOW_UP ~ NSAIDS + AGE + SEX + BMI + (1 | CLINIC) + PAIN_BASELINE + SCORE_DN4,
  data = dt)
export_summs(m1ac, m1gb, m1op, m1ns, scale = T,
  error_format = "[{conf.low}, {conf.high}]") %>%
  kbl(booktabs = T, digits = 4, caption = "DN4 corrected NP models", format="latex") %>%
  kable_styling(latex_options = "scale_down")
```

Table 6: DN4 corrected NP models

[illegible]

```
plot_summs(m1ac, m1gb, m1op, m1ns, scale = T, plot.distributions = T)
```

$$\text{follow-up NP} \sim \text{Drug} + \text{baseline NP} + \text{age} + \text{sex} + \text{BMI} + (1 \mid \text{clinic})$$


## Session Information

```
sessionInfo()
```

```
## R version 4.0.5 (2021-03-31)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.2 LTS
##
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.9.0
## LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.9.0
##
## locale:
##  [1] LC_CTYPE=en_CA.UTF-8          LC_NUMERIC=C
##  [3] LC_TIME=en_CA.UTF-8          LC_COLLATE=en_CA.UTF-8
##  [5] LC_MONETARY=en_CA.UTF-8      LC_MESSAGES=en_CA.UTF-8
##  [7] LC_PAPER=en_CA.UTF-8         LC_NAME=C
##  [9] LC_ADDRESS=C                 LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_CA.UTF-8   LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
##  [1] psych_2.1.6      jtools_2.1.3      kableExtra_1.3.4  data.table_1.14.0
##  [5] effects_4.2-0    knitr_1.31         lme4_1.1-27.1     Matrix_1.3-2
##  [9] papeR_1.0-5      xtable_1.8-4      car_3.0-10        carData_3.0-4
## [13] forcats_0.5.1    stringr_1.4.0     dplyr_1.0.5       purrr_0.3.4
## [17] readr_1.4.0      tidyr_1.1.3       tibble_3.1.1      ggplot2_3.3.3
## [21] tidyverse_1.3.0
##
## loaded via a namespace (and not attached):
##  [1] nlme_3.1-152      pbkrtest_0.5.1     fs_1.5.0           lubridate_1.7.10
##  [5] webshot_0.5.2     insight_0.14.2     gmodels_2.18.1     httr_1.4.2
##  [9] tools_4.0.5       backports_1.2.1    utf8_1.2.1         R6_2.5.0
## [13] KernSmooth_2.23-18 DBI_1.1.1          colorspace_2.0-0    nnet_7.3-15
## [17] withr_2.4.2       mnormt_2.0.2       tidysselect_1.1.1   curl_4.3
## [21] compiler_4.0.5    cli_2.5.0          rvest_1.0.0         xml2_1.3.2
## [25] labeling_0.4.2    scales_1.1.1       systemfonts_1.0.1   digest_0.6.27
## [29] foreign_0.8-81    minqa_1.2.4        rmarkdown_2.7       svglite_2.0.0
## [33] rio_0.5.26        pkgconfig_2.0.3    htmltools_0.5.1.1   dbplyr_2.1.0
## [37] rlang_0.4.10      readxl_1.3.1       rstudioapi_0.13     farver_2.1.0
## [41] generics_0.1.0    jsonlite_1.7.2     broom.mixed_0.2.7    gtools_3.8.2
## [45] zip_2.1.1         huxtable_5.4.0     magrittr_2.0.1      Rcpp_1.0.6
## [49] munsell_0.5.0     fansi_0.4.2        abind_1.4-5         lifecycle_1.0.0
## [53] stringi_1.5.3     yaml_2.2.1         MASS_7.3-53.1       ggstance_0.3.5
## [57] grid_4.0.5        parallel_4.0.5     gdata_2.18.0        crayon_1.4.1
## [61] lattice_0.20-41   haven_2.4.1        splines_4.0.5       pander_0.6.4
## [65] hms_1.0.0         tmvnsim_1.0-2      pillar_1.6.0        boot_1.3-27
## [69] reprex_1.0.0      glue_1.4.2         evaluate_0.14       mitools_2.4
## [73] modelr_0.1.8      vctrs_0.3.8        nloptr_1.2.2.2      cellranger_1.1.0
## [77] gtable_0.3.0      assertthat_0.2.1   xfun_0.22           openxlsx_4.2.3
## [81] broom_0.7.8       survey_4.0         viridisLite_0.4.0   survival_3.2-10
```

```
## [85] ellipsis_0.3.2
```