

Last login: Tue May 28 19:26:02 on ttys000

RScript Analysis.R

APD_Neur

ology_MS_data.csv

```
#####  
#####
```

1. SOURCE PACKAGES AND FUNCTIONS

```
#####  
#####
```

— Attaching core tidyverse packages — tidyverse 2.0.0 —

✓ dplyr	1.1.4	✓ readr	2.1.5
✓ forcats	1.0.0	✓ stringr	1.5.1
✓ ggplot2	3.5.0	✓ tibble	3.2.1
✓ lubridate	1.9.3	✓ tidyr	1.3.1
✓ purrr	1.0.2		

— Conflicts — tidyverse_conflicts() —

✖ dplyr::filter() masks stats::filter()

✖ dplyr::lag() masks stats::lag()

i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

Loading required package: carData

Attaching package: 'car'

The following object is masked from 'package:dplyr':

recode

The following object is masked from 'package:purrr':

some

Loading required package: lattice

Attaching package: 'caret'

The following object is masked from 'package:purrr':

lift

Attaching package: 'survival'

The following object is masked from 'package:caret':

cluster

Attaching package: 'survminer'

The following object is masked from 'package:survival':

myeloma

Attaching package: 'janitor'

The following objects are masked from 'package:stats':

chisq.test, fisher.test

Attaching package: 'nlme'

The following object is masked from 'package:dplyr':

collapse

Loading required package: zoo

Attaching package: 'zoo'

The following objects are masked from 'package:base':

as.Date, as.Date.numeric

Registered S3 methods overwritten by 'fmsb':

method from

print.roc pROC

plot.roc pROC

Classes and Methods for R originally developed in the

Political Science Computational Laboratory

Department of Political Science

Stanford University (2002-2015),

by and under the direction of Simon Jackman.

hurdle and zeroinfl functions by Achim Zeileis.

#####

2. DATAFRAME LOADING

#####

```

The file: /Users/nikhilbhagwat/Desktop/7_PUBLICATIONS_ONGOING/7.1_APD_MS_2024-01
/7.1.0_Data/APD_Neurology_MS_data.csv is read into the dataframe: df
This is not a warning. as.numeric() call:
Check potential issues when using cbind:
1- duplicate column names;
2- different row numbers, etc.
[1] 67
[1] 67
[1] 67
[1] "ID"
[2] "Include_APDs"
[3] "Name"
[4] "Clinic_only"
[5] "Sex"
[6] "DOB_dd.mmmm.yy"
[7] "ID_Date_dd.mmmm.yy"
[8] "RTQUIC_2_Date_dd.mmmm.yy"
[9] "First_Visit_Date_dd.mmmm.yy"
[10] "Last_Visit_Date_dd.mmmm.yy"
[11] "ID_Age"
[12] "PPA"
[13] "Onset_type"
[14] "DX_Lifetime"
[15] "DX_Lifetime_criteria"
[16] "DX_Jabbari"
[17] "DX_APD"
[18] "Race_ethnicity"
[19] "RTQUIC_lifetime"
[20] "RTQUIC_conversion"
[21] "AD_lifetime_ATHENA"
[22] "AD_lifetime_notes"
[23] "AD_2_ATHENA"
[24] "AD_2_notes"
[25] "YKL40_2"
[26] "LP2_auton_signs"
[27] "LP2_auton_signs_n"
[28] "LP2_Light_Sensitivity"
[29] "LP2_Dysphagia"
[30] "LP2_Sexual_dysfunction"
[31] "LP2_Constipation"
[32] "LP2_Urinary"
[33] "LP2_Hyperhidrosis_Thermoregulatory_plus_other"
[34] "LP2_Orthostatism_plus_other"
[35] "LP2_Bowel_Incontinence"
[36] "LP2_RBD_plus_other"
[37] "LP2_Anosmia"
[38] "Genetics_FamilyHistory"
[39] "APOEe4_alleles"
[40] "LP2_MOCA_1year"
[41] "LP2_Cognitive_Extra"
[42] "LP2_MOCA_total_corrected"
[43] "LP2_Delusions"

```

[44] "Lifetime_Hallucinations"
[45] "LP2_gait"
[46] "LP2_falls_PI"
[47] "LP2_hypomimia"
[48] "LP2_retropulsion"
[49] "LP2_tremor"
[50] "LP2_slowness"
[51] "LP2_oculomotor"
[52] "Lifetime_oculomotor"
[53] "LP2_rigidity"
[54] "LP2_dystonia"
[55] "LP2_apraxia"
[56] "Lifetime_apraxia"
[57] "LP2_myoclonus"
[58] "LP2_alien_limb"
[59] "LP2_PSPRS"
[60] "Medication_10_Mov"
[61] "Lifetime_Dopa"
[62] "Lifetime_Dopa_responder"
[63] "Lifetime_Dopa_responder_true"
[64] "X"
[65] "X.1"
[66] "X.2"
[67] "X.3"
[68] "X.4"
[69] "X.5"
[70] "X.6"
[71] "X.7"
[72] "X.8"
[73] "X.9"
[74] "X.10"
[75] "X.11"
[76] "X.12"
[77] "X.13"
[78] "X.14"
[79] "X.15"
[80] "X.16"
[81] "X.17"
[82] "X.18"
[83] "X.19"
[84] "X.20"
[85] "X.21"
[86] "X.22"
[87] "X.23"
[88] "X.24"
[89] "X.25"
[90] "X.26"
[91] "X.27"
[92] "X.28"
[93] "DOB"
[94] "Date"
[95] "First_Visit"

```
[96] "Last_Visit"
[97] "Education"
[98] "ID_Age_TXT"
[99] "Onset_age"
[100] "Park_onset"
[101] "ptau_2"
[102] "ttau_2"
[103] "abeta_2"
[104] "ATI_2"
[105] "NFL_2"
[106] "LP2_Cognitive_Z.score"
[107] "LP2_MOCA_Z.score"
[108] "LP2_MOCA_total"
[109] "Lag_hours"
[110] "ThTmax"
```

as.factor() call:

Check potential issues when using cbind:

- 1- duplicate column names;
- 2- different row numbers, etc.

```
[1] 67
```

```
[1] 67
```

```
[1] 67
```

```
[1] "ID"
[2] "Include_APDs"
[3] "Name"
[4] "Clinic_only"
[5] "DOB_dd.mmmm.yy"
[6] "ID_Date_dd.mmmm.yy"
[7] "RTQUIC_2_Date_dd.mmmm.yy"
[8] "First_Visit_Date_dd.mmmm.yy"
[9] "Last_Visit_Date_dd.mmmm.yy"
[10] "ID_Age"
[11] "DX_Lifetime"
[12] "DX_Lifetime_criteria"
[13] "DX_Jabbari"
[14] "RTQUIC_conversion"
[15] "AD_lifetime_notes"
[16] "AD_2_ATHENA"
[17] "AD_2_notes"
[18] "YKL40_2"
[19] "LP2_auton_signs_n"
[20] "LP2_Light_Sensitivity"
[21] "LP2_Dysphagia"
[22] "LP2_Hyperhidrosis_Thermoregulatory_plus_other"
[23] "LP2_Orthostatism_plus_other"
[24] "Genetics_FamilyHistory"
[25] "LP2_MOCA_1year"
[26] "LP2_Cognitive_Extra"
[27] "LP2_MOCA_total_corrected"
[28] "LP2_Delusions"
[29] "Lifetime_Hallucinations"
[30] "LP2_hypomimia"
```

[31] "LP2_dystonia"
[32] "LP2_myoclonus"
[33] "LP2_alien_limb"
[34] "LP2_PSPRS"
[35] "Medication_10_Mov"
[36] "Lifetime_Dopa_responder"
[37] "X"
[38] "X.1"
[39] "X.2"
[40] "X.3"
[41] "X.4"
[42] "X.5"
[43] "X.6"
[44] "X.7"
[45] "X.8"
[46] "X.9"
[47] "X.10"
[48] "X.11"
[49] "X.12"
[50] "X.13"
[51] "X.14"
[52] "X.15"
[53] "X.16"
[54] "X.17"
[55] "X.18"
[56] "X.19"
[57] "X.20"
[58] "X.21"
[59] "X.22"
[60] "X.23"
[61] "X.24"
[62] "X.25"
[63] "X.26"
[64] "X.27"
[65] "X.28"
[66] "DOB"
[67] "Date"
[68] "First_Visit"
[69] "Last_Visit"
[70] "Education"
[71] "ID_Age_TXT"
[72] "Onset_age"
[73] "Park_onset"
[74] "ptau_2"
[75] "ttau_2"
[76] "abeta_2"
[77] "ATI_2"
[78] "NFL_2"
[79] "LP2_Cognitive_Z.score"
[80] "LP2_MOCA_Z.score"
[81] "LP2_MOCA_total"
[82] "Lag_hours"

```
[83] "ThTmax"
[84] "Age"
[85] "Age_Calculation_SanityCheck"
[86] "Age_cbind_SanityCheck"
[87] "Followup_duration"
[88] "LP2_Disease_Duration"
[89] "LP2_Park_duration"
[90] "Age_at_last_visit"
[91] "Duration_last_visit"
[92] "ID.factor"
[93] "Sex"
[94] "PPA"
[95] "Onset_type"
[96] "DX_APD"
[97] "Race_ethnicity"
[98] "RTQUIC_lifetime"
[99] "AD_lifetime_ATHENA"
[100] "LP2_auton_signs"
[101] "LP2_RBD_plus_other"
[102] "LP2_Anosmia"
[103] "LP2_Sexual_dysfunction"
[104] "LP2_Constipation"
[105] "LP2_Urinary"
[106] "LP2_Bowel_Incontinence"
[107] "APOEe4_alleles"
[108] "LP2_gait"
[109] "LP2_falls_PI"
[110] "LP2_retropulsion"
[111] "LP2_tremor"
[112] "LP2_slowness"
[113] "LP2_oculomotor"
[114] "Lifetime_oculomotor"
[115] "LP2_rigidity"
[116] "LP2_apraxia"
[117] "Lifetime_apraxia"
[118] "Lifetime_Dopa"
[119] "Lifetime_Dopa_responder_true"
```

Warning messages:

```
1: In lapply(X = X, FUN = FUN, ...) : NAs introduced by coercion
2: In lapply(X = X, FUN = FUN, ...) : NAs introduced by coercion
3: In lapply(X = X, FUN = FUN, ...) : NAs introduced by coercion
4: In lapply(X = X, FUN = FUN, ...) : NAs introduced by coercion
5: In lapply(X = X, FUN = FUN, ...) : NAs introduced by coercion
```

```
#####
#####
```

3. SUBSET DF FOR ASSUMPTION TESTING

```
#####
#####
```


4. COHORT CHARACTERISTICS

#####

----- GOES IN TABLE 1: DEMOGRAPHICS -----

----- GOES IN TEXT - RESULTS - COHORT CHARACTERISTICS -

COMPARISONS OF DEMOGRAPHICS FOR DX:
DX_APD n
1 CBS 39
2 PSP 28

4.1. COHORT CHARACTERISTICS: NUMERICAL VARIABLES

#####

4.1.1. AGE #

#####

----- GOES IN TABLE 1: DEMOGRAPHICS -----

----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----

----- GOES IN eTABLE 2: CBS-AD+ vs CBS-AD- -----

----- GOES IN TEXT - RESULTS - COHORT CHARACTERISTICS -

Shapiro-Wilk normality test

data: CBSdf\$Age
W = 0.97123, p-value = 0.4092

Shapiro-Wilk normality test


```
data: PSPdf$Age
W = 0.94623, p-value = 0.1591
```

F test to compare two variances

```
data: Age by DX_APD
F = 0.97338, num df = 38, denom df = 27, p-value = 0.924
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.4680448 1.9390187
sample estimates:
ratio of variances
 0.9733823
```

MEAN AGE AT LP (FOR TABLE):

```
# A tibble: 2 × 4
  DX_APD count `format(round(mean(Age, na.rm = T), 2), 2)` sd
  <chr>   <int> <chr>                                     <dbl>
1 CBS      39 65.92                                     8.58
2 PSP      28 72.51                                     8.70
  count format(round(mean(Age, na.rm = T), 2), 2) sd
1      67                                68.67 9.171745
There is a significant difference in age at LP between CBS and PSP. p-value: 0.0
03007677
0.003007677
```

```
#####
#####
#####                                4.1.2. EDUCATION                                #
#####
#####
#####
```

```
----- GOES IN TABLE 1: DEMOGRAPHICS -----
-----
```

Shapiro-Wilk normality test

```
data: CBSdf$Education
W = 0.91698, p-value = 0.009044
```

Shapiro-Wilk normality test

```
data: PSPdf$Education
W = 0.88686, p-value = 0.00678
```

```
Levene's Test for Homogeneity of Variance (center = median)
  Df F value Pr(>F)
group 1 0.3371 0.5636
```

62

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

MEDIAN EDUCATION (FOR TABLE):

```
count format(round(median(Education, na.rm = T), 2), 2) IQR min max
1      67                                     16  6  5  20
```

A tibble: 2 × 6

```
DX_APD count format(round(median(Education, na.rm = T), 2)...1 IQR min max
<chr> <int> <chr>                                     <dbl> <dbl> <dbl>
1 CBS      39 16                                     6      5    20
2 PSP      28 16                                     4.5    7    18
```

i abbreviated name: ¹ `format(round(median(Education, na.rm = T), 2), 2)`

Wilcoxon rank sum test with continuity correction

data: df\$Education by df\$DX_APD

W = 551.5, p-value = 0.478

alternative hypothesis: true location shift is not equal to 0

Warning message:

In wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...) :

cannot compute exact p-value with ties

```
#####
#####
#####                                4.1.3. ONSET & DURATION
#####
#####
#####
```

```
----- GOES IN TABLE 1: DEMOGRAPHICS -----
-----
----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----
-----
----- GOES IN eTABLE 2: CBS-AD+ vs CBS-AD- -----
-----
----- GOES IN TEXT - RESULTS - COHORT CHARACTERISTICS -
-----
```

Shapiro-Wilk normality test

data: CBSdf\$Onset_age

W = 0.95739, p-value = 0.1458

Shapiro-Wilk normality test

data: PSPdf\$Onset_age

W = 0.94965, p-value = 0.1942

Levene's Test for Homogeneity of Variance (center = median)

```

      Df F value Pr(>F)
group 1      0 0.9954
      65

```

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

A tibble: 2 × 4

```

  DX_APD count `format(round(mean(Onset_age, na.rm = T), 2), 2)` sd
  <chr>   <int> <chr>                                     <dbl>
1 CBS      39 61.36                                           8.33
2 PSP      28 66.29                                           8.33
  count format(round(mean(Onset_age, na.rm = T), 2), 2) sd
1      67                                           63.42 8.618425

```

Two Sample t-test

data: df\$Onset_age by df\$DX_APD

t = -2.3887, df = 65, p-value = 0.01982

alternative hypothesis: true difference in means between group CBS and group PSP
is not equal to 0

95 percent confidence interval:

-9.0458769 -0.8076029

sample estimates:

mean in group CBS mean in group PSP
61.35897 66.28571

Shapiro-Wilk normality test

data: CBSdf\$Park_onset

W = 0.94554, p-value = 0.06351

Shapiro-Wilk normality test

data: PSPdf\$Park_onset

W = 0.93769, p-value = 0.09654

Levene's Test for Homogeneity of Variance (center = median)

```

      Df F value Pr(>F)
group 1  0.0483 0.8267
      64

```

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

A tibble: 2 × 4

```

  DX_APD count `format(round(mean(Park_onset, na.rm = T), 2), 2)` sd
  <chr>   <int> <chr>                                     <dbl>
1 CBS      39 63.16                                           8.23
2 PSP      28 67.14                                           8.25
  count format(round(mean(Park_onset, na.rm = T), 2), 2) sd
1      67                                           64.85 8.411059

```

Two Sample t-test

```
data: df$Park_onset by df$DX_APD
t = -1.9424, df = 64, p-value = 0.05649
alternative hypothesis: true difference in means between group CBS and group PSP
is not equal to 0
95 percent confidence interval:
-8.0833861 0.1134613
sample estimates:
mean in group CBS mean in group PSP
63.15789 67.14286
```

Shapiro-Wilk normality test

```
data: CBSdf$LP2_Disease_Duration
W = 0.80147, p-value = 9.012e-06
```

Shapiro-Wilk normality test

```
data: PSPdf$LP2_Disease_Duration
W = 0.82991, p-value = 0.0003773
```

Levene's Test for Homogeneity of Variance (center = median)

```
Df F value Pr(>F)
group 1 2.9946 0.08829 .
65
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

A tibble: 2 × 6

	DX_APD	count	format(round(median(LP2_Disease_Duration, na.... ¹	IQR	min	max
	<chr>	<int>	<chr>	<dbl>	<dbl>	<dbl>
1	CBS	39	3.9	2.25	1.03	14.8
2	PSP	28	4.83	3.93	1.65	17.3

i abbreviated name:

```
# 1 `format(round(median(LP2_Disease_Duration, na.rm = T), 2), 2)`
count format(round(median(LP2_Disease_Duration, na.rm = T), 2), 2) IQR
1 67 4.1 2.847945
min max
1 1.027397 17.27123
```

Wilcoxon rank sum test with continuity correction

```
data: df$LP2_Disease_Duration by df$DX_APD
W = 409, p-value = 0.0827
alternative hypothesis: true location shift is not equal to 0
```

Warning message:

In wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...) :
cannot compute exact p-value with ties

```
#####
#####
#####                                4.1.4. COGNITIVE Z-SCORES
#####
#####
#####
#####
```

```

----- GOES IN TABLE 1: DEMOGRAPHICS -----
-----
----- GOES IN eTABLE 2: CBS-AD+ vs CBS-AD- -----
-----
----- GOES IN TEXT - RESULTS - COHORT CHARACTERISTICS -----
-----
numeric(0)
numeric(0)

```

Shapiro-Wilk normality test

```
data: CBSdf$LP2_MOCA_Z.score
W = 0.95558, p-value = 0.1802
```

Shapiro-Wilk normality test

```
data:  PSPdf$LP2_MOCA_Z.score
W = 0.88622, p-value = 0.01111
```

Levene's Test for Homogeneity of Variance (center = median)

	Df	F value	Pr(>F)
group	1	3.5999	0.06294
	56		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Warning message:

In `leveneTest.default(y = y, group = group, ...)` : group coerced to factor.

```
# A tibble: 2 x 6
```

	DX_APD	count	format(round(median(LP2_MOCA_Z.score, na.rm =... ¹	IQR	min	max
	<chr>	<int>	<chr>	<dbl>	<dbl>	<dbl>
1	CBS	39	-6.32	7.99	-18.4	-0.16
2	PSP	28	-3.1	5.09	-10.9	0.62

```
# i abbreviated name:
```

```
# 1 `format(round(median(LP2_MOCA_Z.score, na.rm = T), 2), 2)`
```

[illegible]

Wilcoxon rank sum test with continuity correction

```
data: df$LP2 MOCA Z.score by df$DX APD
```

```
W = 258, p-value = 0.01826
alternative hypothesis: true location shift is not equal to 0
```

```
Warning message:
In wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...) :
  cannot compute exact p-value with ties
```

Shapiro-Wilk normality test

```
data: CBSdf$LP2_Cognitive_Z.score
W = 0.94653, p-value = 0.06848
```

Shapiro-Wilk normality test

```
data: PSPdf$LP2_Cognitive_Z.score
W = 0.90904, p-value = 0.02506
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1  5.0982 0.02748 *
      62
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
Warning message:
In leveneTest.default(y = y, group = group, ...) : group coerced to factor.
```

Wilcoxon rank sum test with continuity correction

```
data: df$LP2_Cognitive_Z.score by df$DX_APD
W = 324, p-value = 0.0205
alternative hypothesis: true location shift is not equal to 0
```

Warning message:

```
In wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...) :
  cannot compute exact p-value with ties
```

```
count format(round(median(LP2_Cognitive_Z.score, na.rm = T), 2), 2)      IQR
1      67                                     -4.85 7.4775
```

```
      min max
```

```
1 -18.35 0.62
```

```
# A tibble: 2 × 6
```

```
DX_APD count format(round(median(LP2_Cognitive_Z.score, na.rm = T), 2), 2)      IQR      min      max
  <chr>  <int> <chr>                                     <dbl> <dbl> <dbl>
1 CBS      39 -6.32                                     8.46 -18.4 -0.16
2 PSP      28 -3.4                                      5.99 -10.9  0.62
```

```
# i abbreviated name:
```

```
# 1 `format(round(median(LP2_Cognitive_Z.score, na.rm = T), 2), 2)`
```

```
#####
#####
#####
```

4.1.5. BIOMARKERS: ABETA42

#####

----- GOES IN TABLE 1: DEMOGRAPHICS -----

[1] 1174.82

numeric(0)

	DX_APD	abeta_2
1	CBS	372.1540
2	CBS	569.8260
3	CBS	233.3620
4	PSP	530.8380
5	CBS	582.6150
6	CBS	393.9600
8	PSP	1133.5210
9	PSP	990.4640
10	PSP	157.3680
11	PSP	857.4720
12	PSP	616.0428
13	PSP	401.6630
14	PSP	423.4450
15	PSP	406.8770
16	PSP	471.8610
17	PSP	575.1950
18	PSP	353.7820
19	PSP	216.7000
20	CBS	274.8000
21	CBS	178.2770
22	CBS	557.7000
23	CBS	367.1650
24	CBS	617.5000
25	CBS	460.1000
26	CBS	314.4800
27	PSP	966.6420
28	PSP	641.7790
30	CBS	277.9730
31	PSP	814.2000
32	CBS	743.2790
33	CBS	626.6690
34	PSP	816.8230
35	PSP	669.8000
36	CBS	475.7000
37	PSP	148.4680
38	PSP	713.2370
39	PSP	233.0530
40	CBS	582.0360
41	CBS	367.1500
42	CBS	264.5000
43	CBS	190.9850
44	CBS	343.5230
45	PSP	176.8050
46	CBS	319.3500

```

47 CBS 218.8500
48 CBS 253.5370
49 CBS 652.9000
50 CBS 344.9500
51 PSP 545.3210
52 CBS 685.2000
53 CBS 618.3500
54 CBS 507.9095
55 CBS 246.4260
56 CBS 546.4000
57 CBS 456.5250
59 CBS 370.9500
60 PSP 570.9500
61 PSP 306.2360
62 CBS 428.6500
63 CBS 298.0500
64 CBS 125.0000
65 CBS 350.7500
66 PSP 509.7530
67 CBS 309.7500
68 PSP 577.3770
69 PSP 414.4840

```

The following outliers were removed from the CBS: 1174.82 from the PSP: .

Shapiro-Wilk normality test

```

data: dfabeta[(dfabeta$DX_APD == "CBS"), ]$logabeta
W = 0.96823, p-value = 0.3462

```

Shapiro-Wilk normality test

```

data: dfabeta[(dfabeta$DX_APD == "PSP"), ]$logabeta
W = 0.94239, p-value = 0.1272

```

Levene's Test for Homogeneity of Variance (center = median)

```

      Df F value Pr(>F)
group 1  1.2898 0.2603
      64

```

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

```

count format(round(mean(abeta_2, na.rm = T), 2), 2) sd
1 66 466.17 217.8691

```

A tibble: 2 × 4

```

DX_APD count `format(round(mean(abeta_2, na.rm = T), 2), 2)` sd
<chr> <int> <chr> <dbl>
1 CBS 38 408.61 159.
2 PSP 28 544.29 262.

```

```
[1] 159.4879
```

```
[1] 261.5791
```

Two Sample t-test

65

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

```
count format(round(mean(ptau_2, na.rm = T), 2), 2)      sd
1      66                                52.07 27.29162
```

A tibble: 2 × 4

```
DX_APD count `format(round(mean(ptau_2, na.rm = T), 2), 2)`      sd
<chr>   <int> <chr>                                           <dbl>
1 CBS      38 59.05                                           30.0
2 PSP      28 42.59                                           20.0
[1] 29.9647
[1] 20.02399
```

Two Sample t-test

data: dfptau\$logptau by dfptau\$DX_APD

t = 2.4251, df = 64, p-value = 0.01813

alternative hypothesis: true difference in means between group CBS and group PSP
is not equal to 0

95 percent confidence interval:

0.05505646 0.56973159

sample estimates:

mean in group CBS mean in group PSP
3.950560 3.638165

Anova Table (Type II tests)

Response: logptau

	Sum Sq	Df	F value	Pr(>F)
Age	0.0300	1	0.1106	0.74054
DX_APD	1.5289	1	5.6360	0.02066 *
Residuals	17.0903	63		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

OK: residuals appear as normally distributed (p = 0.294).

	eta.sq	eta.sq.part
Age	0.001605352	0.001752876
DX_APD	0.081787677	0.082114395

#####

4.1.7. BIOMARKERS: TTAU

#####

#####

----- GOES IN TABLE 1: DEMOGRAPHICS -----

[1] 1352.4

[1] 837.1

The following outliers were removed from the CBS: 1352.4 from the PSP: 837.1

.

Shapiro-Wilk normality test

```
data:  dfttau[(dfttau$DX_APD == "CBS"), ]$logttau
W = 0.96996, p-value = 0.4073
```

Shapiro-Wilk normality test

```
data:  dfttau[(dfttau$DX_APD == "PSP"), ]$logttau
W = 0.92868, p-value = 0.06416
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1  0.6627 0.4186
      64
```

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

```
count format(round(mean(ttau_2, na.rm = T), 2), 2)      sd
1      65                                377.64 277.9726
# A tibble: 2 × 4
  DX_APD count `format(round(mean(ttau_2, na.rm = T), 2), 2)`      sd
  <chr>   <int> <chr>                                                              <dbl>
1 CBS      38 444.45                                                    326.
2 PSP      27 286.1                                                       158.
```

```
[1] 326.1839
```

```
[1] 157.6613
```

Two Sample t-test

```
data:  df$logttau by df$DX_APD
```

```
t = 1.9107, df = 64, p-value = 0.06052
```

```
alternative hypothesis: true difference in means between group CBS and group PSP
is not equal to 0
```

```
95 percent confidence interval:
```

```
-0.0158643  0.7128103
```

```
sample estimates:
```

```
mean in group CBS mean in group PSP
      5.874890      5.526417
```

Anova Table (Type II tests)

```
Response: logttau
```

```
      Sum Sq Df F value  Pr(>F)
Age      0.501  1  0.9327 0.33785
DX_APD    2.438  1  4.5416 0.03699 *
Residuals 33.817 63
```

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
OK: residuals appear as normally distributed (p = 0.400).
```

```
      eta.sq eta.sq.part
```

```
Age      0.01380163  0.01458896
```

DX_APD 0.06720334 0.06724137

```
#####
#####
##### 4.1.8. BIOMARKERS: ATI #
#####
#####
#####
```

```
----- GOES IN TABLE 1: DEMOGRAPHICS -----
-----
```

```
numeric(0)
numeric(0)
No outliers were removed for ATI comparisons
```

Shapiro-Wilk normality test

```
data: CBSdf$ATI_2
W = 0.91357, p-value = 0.006299
```

Shapiro-Wilk normality test

```
data: PSPdf$ATI_2
W = 0.9203, p-value = 0.03529
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1  1.4151 0.2386
      64
```

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

```
count format(round(mean(ATI_2, na.rm = T), 2), 2) sd
1      67                                0.79 0.43534
```

A tibble: 2 × 4

```
DX_APD count `format(round(mean(ATI_2, na.rm = T), 2), 2)` sd
<chr>  <int> <chr>                                     <dbl>
1 CBS      39 0.66                                       0.383
2 PSP      28 0.98                                       0.440
```

```
[1] 0.3831545
```

```
[1] 0.4399536
```

Wilcoxon rank sum test with continuity correction

```
data: df$ATI_2 by df$DX_APD
```

```
W = 296, p-value = 0.002247
```

alternative hypothesis: true location shift is not equal to 0

Warning message:

In wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...) :

cannot compute exact p-value with ties

Anova Table (Type II tests)

```
Response: ATI_2
      Sum Sq Df F value    Pr(>F)
Age      0.4005  1   2.4600 0.12179
DX_APD    0.9323  1   5.7262 0.01971 *
Residuals 10.2574 63
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
OK: residuals appear as normally distributed (p = 0.426).
      eta.sq eta.sq.part
Age      0.03251295  0.03757962
DX_APD 0.07568228  0.08331893
```

```
#####
#####
#####                                4.1.9. BIOMARKERS: NFL                                #
#####
#####
#####
```

```
----- GOES IN TABLE 1: DEMOGRAPHICS -----
-----
```

```
[1] 12101.20  6153.82  9997.64
[1] 5780.13 5748.61 7858.61
Outliers are values above 6775.568 in CBS subset.
Outliers are values above 7858.61 in PSP subset.
Following values were removed for the descriptive stats on Nfl: 12101.2 NA NA 9
997.64
```

Shapiro-Wilk normality test

```
data: dfnfl[dfnfl$DX_APD == "CBS", ]$logNFL
W = 0.96261, p-value = 0.2584
```

Shapiro-Wilk normality test

```
data: dfnfl[dfnfl$DX_APD == "PSP", ]$logNFL
W = 0.97556, p-value = 0.7516
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1  0.2413  0.625
      61
```

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

```
count format(round(mean(NFL_2, na.rm = T), 2), 2)      sd
1      63                                2344.74 1418.081
```

A tibble: 2 × 4

```
DX_APD count `format(round(mean(NFL_2, na.rm = T), 2), 2)`      sd
<chr>  <int> <chr>                                     <dbl>
1 CBS      36 2017.59                                1106.
```

```
2 PSP          27 2780.95          1674.
[1] 1106.203
[1] 1674.006
```

Two Sample t-test

```
data: dfnfl$logNFL by dfnfl$DX_APD
t = -2.2729, df = 61, p-value = 0.02657
alternative hypothesis: true difference in means between group CBS and group PSP
is not equal to 0
95 percent confidence interval:
 -0.54668377 -0.03496251
sample estimates:
mean in group CBS mean in group PSP
      7.492641      7.783464
```

Anova Table (Type II tests)

Response: logNFL

	Sum Sq	Df	F value	Pr(>F)
Age	0.0394	1	0.1537	0.6965
DX_APD	0.9835	1	3.8396	0.0547
Residuals	15.3693	60		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

OK: residuals appear as normally distributed (p = 0.296).

	eta.sq	eta.sq.part
Age	0.002354985	0.002554422
DX_APD	0.058847046	0.060145167

```
#####
#####
```

4.2. COHORT CHARACTERISTICS: CATEGORICAL VA RIABLES

```
#####
#####
```

```
#####
#####
```

4.2.1. SEX

#####

```
#####
#####
```

----- GOES IN TABLE 1: DEMOGRAPHICS -----

----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----

----- GOES IN eTABLE 2: CBS-AD+ vs CBS-AD- -----

----- GOES IN TEXT - RESULTS - COHORT CHARACTERISTICS -

Sex distribution in the dataset is:

A tibble: 4 × 3
Groups: DX_APD [2]

	DX_APD	Sex	n
	<chr>	<chr>	<int>
1	CBS	F	19
2	CBS	M	20
3	PSP	F	13
4	PSP	M	15

Proportion of females in total is:

[1] 0.4776119

Proportion of females in CBS is:[1] 0.4871795

Proportion of females in PSP is:[1] 0.4642857

	CBS	PSP
F	19	13
M	20	15

Pearson's Chi-squared test

data: table(df\$Sex, df\$DX_APD)

X-squared = 0.034238, df = 1, p-value = 0.8532

4.2.2. APOE #####

#####

----- GOES IN TABLE 1: DEMOGRAPHICS -----

----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----

----- GOES IN eTABLE 2: CBS-AD+ vs CBS-AD- -----

----- GOES IN TEXT - RESULTS - COHORT CHARACTERISTICS -

A tibble: 6 × 3
Groups: DX_APD [2]

	DX_APD	APOEe4	n
	<chr>	<fct>	<int>
1	CBS	Negative	30
2	CBS	Positive	7
3	CBS	NA	2
4	PSP	Negative	17
5	PSP	Positive	7
6	PSP	NA	4

CBS PSP

```
Negative 30 17
Positive  7  7
```

Pearson's Chi-squared test

```
data: table(df$APOEe4, df$DX_APD)
X-squared = 0.86452, df = 1, p-value = 0.3525
```

```
#####
#####
##### 4.2.3. AD #####
#####
#####
```

```
----- GOES IN TABLE 1: DEMOGRAPHICS -----
-----
----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----
-----
----- GOES IN eTABLE 2: CBS-AD+ vs CBS-AD- -----
-----
----- GOES IN TEXT - RESULTS - COHORT CHARACTERISTICS -
-----
```

```
# A tibble: 4 × 3
# Groups:   DX_APD [2]
  DX_APD AD      n
  <chr>   <chr> <int>
1 CBS    AD Negative 27
2 CBS    AD Positive 12
3 PSP    AD Negative 25
4 PSP    AD Positive  3
```

	AD Negative	AD Positive
CBS	27	12
PSP	25	3

Pearson's Chi-squared test

```
data: table(df$AD, df$DX_APD)
X-squared = 3.7726, df = 1, p-value = 0.0521
```

```
#####
#####
5. ASYN-SAA+ & COHORT CHARACTERISTICS
#####
#####
```



```

----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----
-----
----- GOES IN TEXT - RESULTS - ASYN-SAA+ & DEMOGRAPHICS -
-----

```

```

# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      DX_APD      n
  <fct>      <chr> <int>
1 aSyn-SAA negative CBS      25
2 aSyn-SAA negative PSP      20
3 aSyn-SAA positive CBS      14
4 aSyn-SAA positive PSP       8
[1] 9
[1] 3

```

```

#####
#####

```

5.1. ASYN-SAA+ COHORT CHARACTERISTICS: CATEGORICAL VARIABLES

```

#####
#####

```

```

----- GOES IN eTABLE 1: ASYN-SAA- vs ASYN-SAA+ -----
-----
----- GOES IN TEXT - RESULTS - ASYN-SAA+ & DEMOGRAPHICS -
-----

```

	aSyn-SAA negative	aSyn-SAA positive
F	20	12
M	25	10

Pearson's Chi-squared test

```

data: table(df$Sex, df$RTQUIC)
X-squared = 0.60426, df = 1, p-value = 0.437

```

	aSyn-SAA negative	aSyn-SAA positive
Negative	31	16
Positive	11	3

Fisher's Exact Test for Count Data

```

data: table(df$APOEe4, df$RTQUIC)
p-value = 0.5164
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.08370541 2.43483909
sample estimates:
odds ratio
 0.5335897

```

	aSyn-SAA negative	aSyn-SAA positive
No	23	12
Yes	22	10

Pearson's Chi-squared test

```
data: table(df$Parkinsonian_onset, df$RTQUIC)
X-squared = 0.069852, df = 1, p-value = 0.7916
```

```
#####
#####
```

5.2. ASYN-SAA+ COHORT CHARACTERISTICS: NUMERICAL VARIA

BLES

```
#####
#####
[1] 0.01666667
```

```
#####
#####
```

```
##### 5.2.1. ASYN-SAA*AGE #####
#####
#####
```

```
----- GOES IN eTABLE 1: ASYN-SAA- vs ASYN-SAA+ -----
-----
----- GOES IN TEXT - RESULTS - ASYN-SAA+ & DEMOGRAPHICS -
-----
```

Shapiro-Wilk normality test

```
data: RTposdf$Age
W = 0.96192, p-value = 0.5291
```

Shapiro-Wilk normality test

```
data: RTnegdf$Age
W = 0.98166, p-value = 0.6873
```

F test to compare two variances

```
data: Age by RTQUIC
F = 1.5408, num df = 44, denom df = 21, p-value = 0.286
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.6912078 3.1070414
sample estimates:
```

ratio of variances
1.540823

```
# A tibble: 2 × 4
  RTQUIC      count  mean    sd
  <fct>      <int> <dbl> <dbl>
1 aSyn-SAA negative    45  67.9  9.75
2 aSyn-SAA positive    22  70.2  7.85
```

Two Sample t-test

data: df\$Age by df\$RTQUIC
t = -0.93886, df = 65, p-value = 0.3513
alternative hypothesis: true difference in means between group aSyn-SAA negative
and group aSyn-SAA positive is not equal to 0
95 percent confidence interval:
-7.011610 2.527332
sample estimates:
mean in group aSyn-SAA negative mean in group aSyn-SAA positive
67.93632 70.17846

Anova Table (Type III tests)

Response: Age

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	104781	1	1397.4393	< 2.2e-16 ***
DX_APD	575	1	7.6656	0.007383 **
RTQUIC	97	1	1.2889	0.260547
DX_APD:RTQUIC	6	1	0.0739	0.786559
Residuals	4724	63		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Warning messages:

```
1: In printHypothesis(L, rhs, names(b)) :
  one or more coefficients in the hypothesis include
  arithmetic operators in their names;
  the printed representation of the hypothesis will be omitted
2: In printHypothesis(L, rhs, names(b)) :
  one or more coefficients in the hypothesis include
  arithmetic operators in their names;
  the printed representation of the hypothesis will be omitted
```

	eta.sq	eta.sq.part
DX_APD	0.1347944842	0.136760851
RTQUIC	0.0206138434	0.023654887
DX_APD:RTQUIC	0.0009987086	0.001172432

```
#####
#####
##### 5.2.2. ASYN-SAA*ONSET #####
#####
#####
```

#####

----- GOES IN eTABLE 1: ASYN-SAA- vs ASYN-SAA+ -----

----- GOES IN TEXT - RESULTS - ASYN-SAA+ & DEMOGRAPHICS -

Shapiro-Wilk normality test

data: RTposdf\$Onset_age
W = 0.96189, p-value = 0.5285

Shapiro-Wilk normality test

data: RTnegdf\$Onset_age
W = 0.96942, p-value = 0.2758

F test to compare two variances

data: Onset_age by RTQUIC
F = 1.5861, num df = 44, denom df = 21, p-value = 0.2547
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
0.7115405 3.1984383
sample estimates:
ratio of variances
1.586148

A tibble: 2 × 4

	RTQUIC <fct>	count <int>	mean <dbl>	sd <dbl>
1	aSyn-SAA negative	45	62.2	9.07
2	aSyn-SAA positive	22	65.9	7.20

Two Sample t-test

data: df\$Onset_age by df\$RTQUIC
t = -1.645, df = 65, p-value = 0.1048
alternative hypothesis: true difference in means between group aSyn-SAA negative
and group aSyn-SAA positive is not equal to 0
95 percent confidence interval:
-8.0623494 0.7795211
sample estimates:
mean in group aSyn-SAA negative mean in group aSyn-SAA positive
62.22222 65.86364

Anova Table (Type III tests)

Response: Onset_age

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	90360	1	1337.7303	<2e-16 ***

DX_APD	249	1	3.6802	0.0596	.
RTQUIC	107	1	1.5827	0.2130	
DX_APD:RTQUIC	9	1	0.1280	0.7217	
Residuals	4255	63			

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Warning messages:

- 1: In printHypothesis(L, rhs, names(b)) :
one or more coefficients in the hypothesis include
arithmetic operators in their names;
the printed representation of the hypothesis will be omitted
- 2: In printHypothesis(L, rhs, names(b)) :
one or more coefficients in the hypothesis include
arithmetic operators in their names;
the printed representation of the hypothesis will be omitted

	eta.sq	eta.sq.part
DX_APD	0.090208763	0.094137139
RTQUIC	0.049476840	0.053923494
DX_APD:RTQUIC	0.001763424	0.002027334

```
#####
#####
##### 5.2.3. ASYN-SAA*PARK_ONSET
#####
#####
#####
#####
----- GOES IN eTABLE 1: ASYN-SAA- vs ASYN-SAA+ -----
-----
----- GOES IN TEXT - RESULTS - ASYN-SAA+ & DEMOGRAPHICS -
-----
```

Shapiro-Wilk normality test

data: RTposdf\$Park_onset
W = 0.93718, p-value = 0.1731

Shapiro-Wilk normality test

data: RTnegdf\$Park_onset
W = 0.96579, p-value = 0.2133

F test to compare two variances

data: Park_onset by RTQUIC
F = 1.7798, num df = 43, denom df = 21, p-value = 0.1559
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
0.7969689 3.6030251
sample estimates:

ratio of variances
1.779805

A tibble: 2 × 4

	RTQUIC <fct>	count <int>	mean <dbl>	sd <dbl>
1	aSyn-SAA negative	45	63.6	8.97
2	aSyn-SAA positive	22	67.3	6.72

Two Sample t-test

data: df\$Park_onset by df\$RTQUIC
t = -1.6787, df = 64, p-value = 0.09809
alternative hypothesis: true difference in means between group aSyn-SAA negative
and group aSyn-SAA positive is not equal to 0
95 percent confidence interval:
-7.9638087 0.6910815
sample estimates:
mean in group aSyn-SAA negative mean in group aSyn-SAA positive
63.63636 67.27273

Anova Table (Type III tests)

Response: Park_onset

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	91513	1	1382.1001	< 2e-16 ***
DX_APD	188	1	2.8375	0.09711 .
RTQUIC	129	1	1.9501	0.16755
DX_APD:RTQUIC	1	1	0.0146	0.90407
Residuals	4105	62		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Warning messages:

1: In printHypothesis(L, rhs, names(b)) :
one or more coefficients in the hypothesis include
arithmetic operators in their names;
the printed representation of the hypothesis will be omitted
2: In printHypothesis(L, rhs, names(b)) :
one or more coefficients in the hypothesis include
arithmetic operators in their names;
the printed representation of the hypothesis will be omitted

	eta.sq	eta.sq.part
DX_APD	0.0648794369	0.0677511026
RTQUIC	0.0513827627	0.0544241009
DX_APD:RTQUIC	0.0002108903	0.0002361736

#####

6. AD+ & COHORT CHARACTERISTICS

```
#####
#####
```

```
----- GOES IN TEXT - RESULTS - ASYN-SAA+ & DEMOGRAPHICS -
-----
```

```
# A tibble: 4 × 3
# Groups:   DX_APD [2]
  DX_APD AD      n
  <chr>   <chr>  <int>
1 CBS    AD Negative  27
2 CBS    AD Positive  12
3 PSP    AD Negative  25
4 PSP    AD Positive   3
```

```
#####
#####
```

```
6.1. AD+ WHOLE COHORT CHARACTERISTICS: CATEGORICAL VA
RIABLES
```

```
#####
#####
```

```
----- FOR REFERENCE ONLY -----
-----
```

```
      F  M
AD Negative 22 30
AD Positive 10  5
```

Pearson's Chi-squared test

```
data: table(df$AD, df$Sex)
X-squared = 2.7687, df = 1, p-value = 0.09613
```

```
      No Yes
AD Negative 44  8
AD Positive  8  7
```

Fisher's Exact Test for Count Data

```
data: table(df$AD, df$anyPPA)
p-value = 0.02977
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 1.112209 20.203811
sample estimates:
odds ratio
 4.671131
```

```
      No Yes
AD Negative 26 26
```

AD Positive 9 6

Pearson's Chi-squared test

```
data: table(df$AD, df$Parkinsonian_onset)
X-squared = 0.46661, df = 1, p-value = 0.4946
```

	Negative	Positive
AD Negative	36	11
AD Positive	11	3

Fisher's Exact Test for Count Data

```
data: table(df$AD, df$APOEe4)
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.1360715 4.3027210
sample estimates:
odds ratio
 0.8941862
```


#####

6.2. AD+ WHOLE COHORT CHARACTERISTICS: NUMERICAL VARIABLES

#####

----- FOR REFERENCE ONLY -----

Shapiro-Wilk normality test

```
data: ADposdf$Age
W = 0.97209, p-value = 0.8877
```

Shapiro-Wilk normality test

```
data: ADnegdf$Age
W = 0.97163, p-value = 0.2474
```

Levene's Test for Homogeneity of Variance (center = median)

	Df	F value	Pr(>F)
group 1	0.6562	0.4209	
65			

Warning message:

```
In leveneTest.default(y = y, group = group, ...) : group coerced to factor.
# A tibble: 2 × 4
```


	AD	count	`format(round(mean(Age, na.rm = T), 2), 2)`	sd
	<chr>	<int>	<chr>	<dbl>
1	AD Negative	52	69.13	9.54
2	AD Positive	15	67.09	7.86

Two Sample t-test

```
data: df$Onset_age by df$AD
t = 0.44848, df = 65, p-value = 0.6553
alternative hypothesis: true difference in means between group AD Negative and g
roup AD Positive is not equal to 0
95 percent confidence interval:
-3.935658  6.215146
sample estimates:
mean in group AD Negative mean in group AD Positive
        63.67308             62.53333
```

Shapiro-Wilk normality test

```
data: ADposdf$Onset_age
W = 0.95877, p-value = 0.6711
```

Shapiro-Wilk normality test

```
data: ADnegdf$Onset_age
W = 0.95838, p-value = 0.06657
```

Levene's Test for Homogeneity of Variance (center = median)

	Df	F value	Pr(>F)
group 1	1	1.6381	0.2051
	65		

Warning message:

```
In leveneTest.default(y = y, group = group, ...) : group coerced to factor.
# A tibble: 2 × 4
```

	AD	count	`format(round(mean(Onset_age, na.rm = T), 2), 2)`	sd
	<chr>	<int>	<chr>	<dbl>
1	AD Negative	52	63.67	9.10
2	AD Positive	15	62.53	6.88

Two Sample t-test

```
data: df$Onset_age by df$AD
t = 0.44848, df = 65, p-value = 0.6553
alternative hypothesis: true difference in means between group AD Negative and g
roup AD Positive is not equal to 0
95 percent confidence interval:
-3.935658  6.215146
sample estimates:
mean in group AD Negative mean in group AD Positive
        63.67308             62.53333
```

Shapiro-Wilk normality test

```
data: ADposdf$Park_onset
W = 0.95173, p-value = 0.5879
```

Shapiro-Wilk normality test

```
data: ADnegdf$Park_onset
W = 0.95174, p-value = 0.03451
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1  1.1953 0.2784
      64
```

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

A tibble: 2 × 4

	AD	count	format(round(mean(Park_onset, na.rm = T), 2), 2)	sd
	<chr>	<int>	<chr>	<dbl>
1	AD Negative	52	65.02	8.87
2	AD Positive	15	64.21	6.65

Wilcoxon rank sum test with continuity correction

```
data: df$Park_onset by df$AD
W = 401, p-value = 0.5666
alternative hypothesis: true location shift is not equal to 0
```

Shapiro-Wilk normality test

```
data: ADposdf$LP2_Disease_Duration
W = 0.8728, p-value = 0.0371
```

Shapiro-Wilk normality test

```
data: ADnegdf$LP2_Disease_Duration
W = 0.75445, p-value = 5.928e-08
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1  0.0223 0.8818
      65
```

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

A tibble: 2 × 6

	AD	count	format(round(median(LP2_Disease_Duration... ¹	IQR	min	max
	<chr>	<int>	<chr>	<dbl>	<dbl>	<dbl>

```

1 AD Negative      52 4.35                                2.63  1.65  17.3
2 AD Positive      15 3.12                                3.03  1.03  10.7
# i abbreviated name:
# 1 `format(round(median(LP2_Disease_Duration, na.rm = T), 2), 2)`

```

Wilcoxon rank sum test with continuity correction

data: df\$LP2_Disease_Duration by df\$AD

W = 469.5, p-value = 0.2347

alternative hypothesis: true location shift is not equal to 0

```

#####
#####

```

6.3. AD+ CBS COHORT CHARACTERISTICS: CATEGORICAL VARIABLES

ABLES

```

#####
#####

```

```

----- GOES IN eTABLE 2: CBS-AD+ vs CBS-AD- -----
-----

```

	F	M
AD Negative	11	16
AD Positive	8	4

Pearson's Chi-squared test

data: table(CBSdf\$AD, CBSdf\$Sex)

X-squared = 2.2351, df = 1, p-value = 0.1349

	AD Negative	AD Positive
Negative	21	9
Positive	5	2

Fisher's Exact Test for Count Data

data: table(CBSdf\$APOEe4, CBSdf\$AD)

p-value = 1

alternative hypothesis: true odds ratio is not equal to 1

95 percent confidence interval:

0.07563492 7.17281592

sample estimates:

odds ratio

0.935053

	AD Negative	AD Positive
No	23	5
Yes	4	7

Fisher's Exact Test for Count Data

```
data: table(CBSdf$Language_onset, CBSdf$AD)
p-value = 0.01698
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 1.332041 51.349652
sample estimates:
odds ratio
 7.513935
```

	AD Negative	AD Positive
No	19	5
Yes	8	7

Fisher's Exact Test for Count Data

```
data: table(CBSdf$anyPPA, CBSdf$AD)
p-value = 0.1532
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.6534606 17.3822576
sample estimates:
odds ratio
 3.215136
```


#####

6.4. AD+ CBS COHORT CHARACTERISTICS: NUMERICAL VARIAB

LES

#####

#####

6.4.1. AGE, ONSET, PARK ONSET #
#####

#####

----- GOES IN eTABLE 2: CBS-AD+ vs CBS-AD- -----

[1] 0.01666667

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$AD == "AD Positive", ]$Age
W = 0.98409, p-value = 0.9951
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$AD == "AD Negative", ]$Age
W = 0.9459, p-value = 0.1703
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1  2.5781 0.1169
      37
```

Warning message:

```
In leveneTest.default(y = y, group = group, ...) : group coerced to factor.
```

```
count mean sd
1    39 65.918 8.584
```

```
# A tibble: 2 × 4
```

	AD	count	mean	sd
	<chr>	<int>	<chr>	<chr>
1	AD Negative	27	66.456	9.328
2	AD Positive	12	64.707	6.825

Two Sample t-test

```
data: CBSdf$Age by CBSdf$AD
```

```
t = 0.58228, df = 37, p-value = 0.5639
```

```
alternative hypothesis: true difference in means between group AD Negative and group AD Positive is not equal to 0
```

```
95 percent confidence interval:
```

```
-4.338025  7.836807
```

```
sample estimates:
```

mean in group AD Negative	mean in group AD Positive
66.45601	64.70662

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$AD == "AD Positive", ]$Onset_age
W = 0.95193, p-value = 0.6654
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$AD == "AD Negative", ]$Onset_age
W = 0.94304, p-value = 0.1448
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1  1.516  0.226
      37
```

Warning message:

```
In leveneTest.default(y = y, group = group, ...) : group coerced to factor.
```

```
count mean sd
1    39 61.359 8.327
```

```
# A tibble: 2 × 4
  AD          count mean  sd
<chr>      <int> <chr> <chr>
1 AD Negative    27 61.63 9.17
2 AD Positive    12 60.75 6.341
```

Two Sample t-test

```
data: CBSdf$Onset_age by CBSdf$AD
t = 0.3008, df = 37, p-value = 0.7652
alternative hypothesis: true difference in means between group AD Negative and g
roup AD Positive is not equal to 0
95 percent confidence interval:
 -5.045494  6.804754
sample estimates:
mean in group AD Negative mean in group AD Positive
      61.62963              60.75000
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$AD == "AD Positive", ]$Park_onset
W = 0.94659, p-value = 0.6008
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$AD == "AD Negative", ]$Park_onset
W = 0.93793, p-value = 0.1083
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1  1.8368 0.1838
      36
```

Warning message:

```
In leveneTest.default(y = y, group = group, ...) : group coerced to factor.
```

```
      count mean  sd
1      39 63.158 8.228
```

```
# A tibble: 2 × 4
  AD          count mean  sd
<chr>      <int> <chr> <chr>
1 AD Negative    27 63.37 8.945
2 AD Positive    12 62.636 6.485
```

Two Sample t-test

```
data: CBSdf$Park_onset by CBSdf$AD
t = 0.2462, df = 36, p-value = 0.8069
alternative hypothesis: true difference in means between group AD Negative and g
roup AD Positive is not equal to 0
95 percent confidence interval:
 -5.312346  6.780360
```

```
sample estimates:
mean in group AD Negative mean in group AD Positive
      63.37037             62.63636
```

```
#####
#####
#####                                6.4.2. NFL                                #
#####
#####
#####
```

```
----- GOES IN eTABLE 2: CBS-AD+ vs CBS-AD- -----
-----
```

```
[1] 12101.2
[1] 6153.82 9997.64
Outliers are values above 3030.122 in CBS-AD+ subset.
Outliers are values above 7545.9 in CBS-AD- subset.
Following values were removed for the descriptive stats on NFL: 12101.2 NA 9997
.64
```

Shapiro-Wilk normality test

```
data: CBSdfnfl[CBSdfnfl$AD == "AD Positive", ]$logNFL
W = 0.82416, p-value = 0.01956
```

Shapiro-Wilk normality test

```
data: CBSdfnfl[CBSdfnfl$AD == "AD Negative", ]$logNFL
W = 0.91206, p-value = 0.03389
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1  4.8885 0.03386 *
      34
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Warning message:

In leveneTest.default(y = y, group = group, ...) : group coerced to factor.

```
count format(round(median(NFL_2, na.rm = T), 2), 2)      IQR min      max
1      36                                1705.76 1247.092 738 6153.82
```

A tibble: 2 × 6

```
AD      count format(round(median(NFL_2, na.rm = T), 2...1      IQR      min      max
<chr>      <int> <chr>                                <dbl> <dbl> <dbl>
1 AD Negative      25 1456.97                                1520.  858. 6154.
2 AD Positive      11 1708.68                                350.  738 2149.
```

i abbreviated name: ¹ `format(round(median(NFL_2, na.rm = T), 2), 2)`

```
[1] 349.545
```

```
[1] 1520.12
```

Welch Two Sample t-test

```

data: CBSdfnfl$logNFL by CBSdfnfl$AD
t = 1.3167, df = 31.416, p-value = 0.1975
alternative hypothesis: true difference in means between group AD Negative and g
roup AD Positive is not equal to 0
95 percent confidence interval:
 -0.1003594  0.4665510
sample estimates:
mean in group AD Negative mean in group AD Positive
          7.548587              7.365491

```

```

      df      AIC
gls1  6 74.75601
gls2  5 66.77470
Warning message:
In AIC.default(gls1, gls2) :
  models are not all fitted to the same number of observations
Generalized least squares fit by REML
Model: logNFL ~ Age + AD
Data: CBSdfnfl
      AIC      BIC    logLik
66.7747 74.25724 -28.38735

```

```

Variance function:
Structure: Power of variance covariate
Formula: ~fitted(.)
Parameter estimates:
  power
10.5513

```

```

Coefficients:
              Value Std.Error   t-value p-value
(Intercept)  7.032552 0.5817078 12.089492  0.0000
Age           0.007731 0.0089026  0.868421  0.3914
ADAD Positive -0.158978 0.1538188 -1.033543  0.3089

```

```

Correlation:
      (Intr) Age
Age      -0.985
ADAD Positive -0.176  0.067

```

```

Standardized residuals:
      Min      Q1      Med      Q3      Max
-1.9632510 -0.7229886  0.2280254  0.4943355  2.7695795

```

```

Residual standard error: 2.74902e-10
Degrees of freedom: 36 total; 33 residual

```

```

#####
#####
#####
6.4.3. MOCA Z-SCORES
#

```



```
#####
#####
#####
----- GOES IN eTABLE 2: CBS-AD+ vs CBS-AD- -----
-----
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$AD == "AD Positive", ]$LP2_MOCA_Z.score
W = 0.97774, p-value = 0.973
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$AD == "AD Negative", ]$LP2_MOCA_Z.score
W = 0.92192, p-value = 0.08331
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1  0.0232  0.88
      32
```

Warning message:

```
In leveneTest.default(y = y, group = group, ...) : group coerced to factor.
```

```
      count format(round(median(LP2_MOCA_Z.score, na.rm = T), 2), 2)      IQR      min
1       39                                                    -6.32 7.9875 -18.35
      max
1 -0.16
```

```
# A tibble: 2 × 6
```

```
      AD      count format(round(median(LP2_MOCA_Z.score, na.rm = T), 2), 2)      IQR      min      max
<chr>      <int> <chr>                                                    <dbl> <dbl> <dbl>
1 AD Negative    27 -5.03                                                    6.33 -15.7 -0.16
2 AD Positive    12 -10.73                                                   5.11 -18.4 -1.84
```

```
# i abbreviated name:
```

```
# 1 `format(round(median(LP2_MOCA_Z.score, na.rm = T), 2), 2)`
```

Wilcoxon rank sum exact test

```
data: CBSdf$LP2_MOCA_Z.score by CBSdf$AD
```

```
W = 200, p-value = 0.0134
```

```
alternative hypothesis: true location shift is not equal to 0
```

```
#####
#####
7. ASYN-SAA+ & AD
#####
#####
```


#####

7.1. ASYN-SAA+ & AD: CATEGORICAL VARIABLES

#####

----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----

----- GOES IN TEXT - RESULTS - ASYN-SAA+ & DEMOGRAPHICS -

[1] 2
[1] 5
[1] 8
[1] 7

#####

7.1.1.FIGURE 1A #
#####

#####

----- GOES IN FIGURE 1A: ONSET * AD QUADRANTS -----

Below are the values for the creation of Fig 1.A:

Lower left quadrant: AD+ and young-onset

CBS subjects who are RTQUIC+ and young-onset and AD+: 5
PSP subjects who are RTQUIC+ and young-onset and AD+: 0
CBS subjects who are RTQUIC- and young-onset and AD+: 4
PSP subjects who are RTQUIC+ and young-onset and AD+: 0

Upper left quadrant: AD- and young-onset

CBS subjects who are RTQUIC+ and young-onset and AD-: 2
PSP subjects who are RTQUIC+ and young-onset and AD-: 1
CBS subjects who are RTQUIC- and young-onset and AD-: 14
PSP subjects who are RTQUIC+ and young-onset and AD-: 9

Lower right quadrant:

CBS subjects who are RTQUIC+ and late-onset and AD+: 2
PSP subjects who are RTQUIC+ and late-onset and AD+: 0
CBS subjects who are RTQUIC- and late-onset and AD+: 1
PSP subjects who are RTQUIC- and late-onset and AD+: 3

Upper right quadrant:

CBS subjects who are RTQUIC+ and late-onset and AD-: 5
PSP subjects who are RTQUIC+ and late-onset and AD-: 7
CBS subjects who are RTQUIC- and late-onset and AD-: 6
PSP subjects who are RTQUIC- and late-onset and AD-: 8

#####

```
#####
##### 7.1.2. FREQUENCY DATA #
#####
#####
#####
----- GOES IN TEXT - RESULTS - ASYN-SAA+ & AD+ -----
-----
----- GOES IN FIGURE 1A: ONSET * AD QUADRANTS -----
-----
[1] 0.01666667
```

	AD Negative	AD Positive
aSyn-SAA negative	37	8
aSyn-SAA positive	15	7

```
[1] 5
[1] 8
[1] 2
[1] 14
```

Fisher's Exact Test for Count Data

```
data: table(df$AD, df$RTQUIC)
p-value = 0.223
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.5516084 8.1666232
sample estimates:
odds ratio
 2.131801
```

```
Cramer V
 0.1582
  phi
0.158179
```

	aSyn-SAA negative	aSyn-SAA positive
AD Negative	23	3
AD Positive	4	5

Fisher's Exact Test for Count Data

```
data: table(YODdf$AD, YODdf$RTQUIC)
p-value = 0.01512
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 1.187507 82.550067
sample estimates:
odds ratio
 8.754574
```

```
Cramer V
 0.4581
```

phi
0.458144

	aSyn-SAA negative	aSyn-SAA positive
AD Negative	14	12
AD Positive	4	2

Fisher's Exact Test for Count Data

data: table(LODdf\$AD, LODdf\$RTQUIC)
p-value = 0.6722
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
0.0459508 5.0206949
sample estimates:
odds ratio
0.5929948

Cramer V
0.1009
phi
-0.100871

7.1.3. FREQUENCY DATA WITHIN DX #

----- GOES IN SUPP TEXT - ASYN-SAA+ & AD+ WITHIN DX -----

	AD Negative	AD Positive
aSyn-SAA negative	20	5
aSyn-SAA positive	7	7

Fisher's Exact Test for Count Data

data: table(CBSdf\$AD, CBSdf\$RTQUIC)
p-value = 0.07488
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
0.7664236 21.3857232
sample estimates:
odds ratio
3.843273

Cramer V
0.3118
phi
0.311805

```
[1] 25
```

	AD Negative	AD Positive
aSyn-SAA negative	14	4
aSyn-SAA positive	2	5

Fisher's Exact Test for Count Data

```
data: table(CBSdf[CBSdf$Early_onset == "Young-onset", ]$RTQUIC, CBSdf[CBSdf$Early_onset == "Young-onset", ]$AD)
p-value = 0.05812
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.8865897 113.3329588
sample estimates:
odds ratio
 7.85303
```

```
[1] 14
```

	AD Negative	AD Positive
aSyn-SAA negative	6	1
aSyn-SAA positive	5	2

Fisher's Exact Test for Count Data

```
data: table(CBSdf[CBSdf$Early_onset == "Late-onset", ]$RTQUIC, CBSdf[CBSdf$Early_onset == "Late-onset", ]$AD)
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.09086265 164.58062230
sample estimates:
odds ratio
 2.2554
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$RTQUIC == "aSyn-SAA positive", ]$Onset_age
W = 0.93077, p-value = 0.3128
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$RTQUIC == "aSyn-SAA negative", ]$Onset_age
W = 0.94595, p-value = 0.2028
```

F test to compare two variances

```
data: Onset_age by RTQUIC
```

F = 1.8716, num df = 24, denom df = 13, p-value = 0.2403
 alternative hypothesis: true ratio of variances is not equal to 1
 95 percent confidence interval:
 0.6469066 4.6826837
 sample estimates:
 ratio of variances
 1.871625

Two Sample t-test

data: CBSdf\$Onset_age by CBSdf\$RTQUIC
 t = -1.2509, df = 37, p-value = 0.2188
 alternative hypothesis: true difference in means between group aSyn-SAA negative
 and group aSyn-SAA positive is not equal to 0
 95 percent confidence interval:
 -9.042210 2.139353
 sample estimates:
 mean in group aSyn-SAA negative mean in group aSyn-SAA positive
 60.12000 63.57143

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
RTQUIC	1	106.9	106.91	1.545	0.222
AD	1	36.7	36.74	0.531	0.471
Residuals	36	2491.3	69.20		
		eta.sq	eta.sq.part		
RTQUIC		0.05207605	0.05220340		
AD		0.01394372	0.01453336		

Two Sample t-test

data: CBSdf\$Age by CBSdf\$RTQUIC
 t = -1.1501, df = 37, p-value = 0.2575
 alternative hypothesis: true difference in means between group aSyn-SAA negative
 and group aSyn-SAA positive is not equal to 0
 95 percent confidence interval:
 -9.062894 2.499684
 sample estimates:
 mean in group aSyn-SAA negative mean in group aSyn-SAA positive
 64.73973 68.02133

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
AD	1	25.4	25.42	0.348	0.559
RTQUIC	1	144.0	144.03	1.971	0.169
Residuals	36	2630.5	73.07		
		eta.sq	eta.sq.part		
AD		0.02600470	0.02693438		
RTQUIC		0.05144085	0.05191224		

	Late-onset	Young-onset
aSyn-SAA negative	11	9
aSyn-SAA positive	7	1

Fisher's Exact Test for Count Data

```
data: table(PSPdf$RTQUIC, PSPdf$Early_onset)
p-value = 0.1937
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.003499204 1.901090103
sample estimates:
odds ratio
 0.1844736
```

Shapiro-Wilk normality test

```
data: PSPdf[PSPdf$RTQUIC == "aSyn-SAA positive", ]$Onset_age
W = 0.90133, p-value = 0.297
```

Shapiro-Wilk normality test

```
data: PSPdf[PSPdf$RTQUIC == "aSyn-SAA negative", ]$Onset_age
W = 0.96336, p-value = 0.613
```

F test to compare two variances

```
data: Onset_age by RTQUIC
F = 1.6274, num df = 19, denom df = 7, p-value = 0.5252
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.3630251 4.9650044
sample estimates:
ratio of variances
 1.627407
```

Two Sample t-test

```
data: PSPdf$Onset_age by PSPdf$RTQUIC
t = -1.4737, df = 26, p-value = 0.1526
alternative hypothesis: true difference in means between group aSyn-SAA negative
and group aSyn-SAA positive is not equal to 0
95 percent confidence interval:
 -12.033993  1.983993
sample estimates:
mean in group aSyn-SAA negative mean in group aSyn-SAA positive
          64.850                  69.875
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
RTQUIC	1	144.3	144.29	2.172	0.153
Residuals	26	1727.4	66.44		

```
eta.sq eta.sq.part
RTQUIC 0.07708938 0.07708938
```

Two Sample t-test

```
data: PSPdf$Age by PSPdf$RTQUIC
t = -0.54813, df = 26, p-value = 0.5883
alternative hypothesis: true difference in means between group aSyn-SAA negative
and group aSyn-SAA positive is not equal to 0
95 percent confidence interval:
-9.601622 5.558882
sample estimates:
mean in group aSyn-SAA negative mean in group aSyn-SAA positive
71.93205 73.95342
```

```
eta.sq eta.sq.part
AD 0.02600470 0.02693438
RTQUIC 0.05144085 0.05191224
```

```
#####
#####
```

7.2. ASYN-SAA+ & AD: NUMERICAL VARIABLES

```
#####
#####
```

```
#####
#####
```

```
##### 7.2.1. ASYN-SAA+ & ABETA42 #
#####
```

```
#####
#####
```

```
----- GOES IN TABLE 2: MLR MODEL OUTPUT -----
-----
----- GOES IN TEXT - RESULTS - ASYN-SAA+ & AD+ -----
-----
```

```
[1] 1133.521 1174.820
numeric(0)
```

Shapiro-Wilk normality test

```
data: RTposdf$logabeta
W = 0.9362, p-value = 0.1651
```

Shapiro-Wilk normality test

```
data: RTnegdf$logabeta
W = 0.97854, p-value = 0.5616
```


Shapiro-Wilk normality test

data: CBSdf\$logabeta
W = 0.98765, p-value = 0.9391

Shapiro-Wilk normality test

data: PSPdf\$logabeta
W = 0.94239, p-value = 0.1272

Levene's Test for Homogeneity of Variance (center = median)

	Df	F	value	Pr(>F)
group	3	0.4888	0.6913	
	63			

Analysis of Variance Table

Model 1: logabeta ~ RTQUIC

Model 2: logabeta ~ RTQUIC + DX_APD

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	65	16.443				
2	64	15.658	1	0.78431	3.2057	0.07811

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Analysis of Variance Table

Model 1: logabeta ~ RTQUIC

Model 2: logabeta ~ RTQUIC + Sex

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	65	16.443				
2	64	16.432	1	0.01032	0.0402	0.8417

Pearson's product-moment correlation

data: df\$logabeta and df\$Onset_age
t = 2.9784, df = 65, p-value = 0.004069
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
0.1159849 0.5416588
sample estimates:
cor
0.3465388

Spearman's rank correlation rho

data: df\$logabeta and df\$Onset_age
S = 30561, p-value = 0.001097
alternative hypothesis: true rho is not equal to 0
sample estimates:
rho
0.3902022

Warning message:

```
In cor.test.default(df$logabeta, df$Onset_age, method = "spearman") :  
  Cannot compute exact p-value with ties
```

Call:

```
lm(formula = df$logabeta ~ df$Onset_age)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-1.20118	-0.27489	0.03238	0.29163	0.95346

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	4.758811	0.436583	10.900	2.59e-16 ***
df\$Onset_age	0.020320	0.006822	2.978	0.00407 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4777 on 65 degrees of freedom

Multiple R-squared: 0.1201, Adjusted R-squared: 0.1066

F-statistic: 8.871 on 1 and 65 DF, p-value: 0.004069

Warning messages:

1: Removed 2 rows containing non-finite outside the scale range (`stat_smooth()`).

2: Removed 2 rows containing non-finite outside the scale range (`stat_regline_equation()`).

3: Removed 2 rows containing missing values or values outside the scale range (`geom_point()`).

Warning messages:

1: Removed 2 rows containing non-finite outside the scale range (`stat_smooth()`).

2: Removed 2 rows containing non-finite outside the scale range (`stat_regline_equation()`).

3: Removed 2 rows containing missing values or values outside the scale range (`geom_point()`).

Warning messages:

1: Removed 2 rows containing non-finite outside the scale range (`stat_smooth()`).

2: Removed 2 rows containing non-finite outside the scale range (`stat_regline_equation()`).

3: Removed 2 rows containing missing values or values outside the scale range (`geom_point()`).

Pearson's product-moment correlation

data: df\$logabeta and df\$NFL_2

t = 2.3309, df = 63, p-value = 0.02297

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.04065892 0.49186131

sample estimates:

cor
0.2817639

Spearman's rank correlation rho

data: df\$logabeta and df\$NFL_2

S = 32704, p-value = 0.02155

alternative hypothesis: true rho is not equal to 0

sample estimates:

rho
0.2853147

Call:

lm(formula = df\$logabeta ~ df\$NFL_2)

Residuals:

Min	1Q	Median	3Q	Max
-1.2359	-0.3291	0.0206	0.3616	0.8730

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.865e+00	9.915e-02	59.157	<2e-16 ***
df\$NFL_2	6.956e-05	2.984e-05	2.331	0.023 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4938 on 63 degrees of freedom

(2 observations deleted due to missingness)

Multiple R-squared: 0.07939, Adjusted R-squared: 0.06478

F-statistic: 5.433 on 1 and 63 DF, p-value: 0.02297

Call:

lm(formula = df\$logabeta ~ df\$LP2_Disease_Duration)

Residuals:

Min	1Q	Median	3Q	Max
-1.15064	-0.33198	0.04481	0.34365	1.06798

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.94199	0.11434	51.969	<2e-16 ***
df\$LP2_Disease_Duration	0.02008	0.01833	1.095	0.277

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5046 on 65 degrees of freedom

Multiple R-squared: 0.01813, Adjusted R-squared: 0.003022

F-statistic: 1.2 on 1 and 65 DF, p-value: 0.2774

```
Call:
lm(formula = df$logabeta ~ df$ttau_2)

Residuals:
    Min       1Q   Median       3Q      Max
-1.12024 -0.31782  0.04374  0.30155  1.09479

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  6.0839558   0.1038904   58.561  <2e-16 ***
df$ttau_2    -0.0001096   0.0002076   -0.528    0.599
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5085 on 64 degrees of freedom
(1 observation deleted due to missingness)
Multiple R-squared:  0.004338, Adjusted R-squared:  -0.01122
F-statistic: 0.2788 on 1 and 64 DF, p-value: 0.5993
```

```
Call:
lm(formula = df$logabeta ~ df$ptau_2)

Residuals:
    Min       1Q   Median       3Q      Max
-1.20862 -0.31758  0.03157  0.34593  1.02863

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  6.0566369   0.1276037   47.464  <2e-16 ***
df$ptau_2    -0.0001706   0.00020746  -0.082    0.935
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5092 on 65 degrees of freedom
Multiple R-squared:  0.000104, Adjusted R-squared:  -0.01528
F-statistic: 0.006759 on 1 and 65 DF, p-value: 0.9347
```

```
Call:
lm(formula = logabeta ~ scale(Onset_age) * RTQUIC + DX_APD +
    scale(NFL_2), data = df)

Residuals:
    Min       1Q   Median       3Q      Max
-1.28752 -0.32248 -0.01025  0.34356  0.84231

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)      5.97571     0.09025   66.216  <2e-16
```

scale(Onset_age)	0.06085	0.06775	0.898	0.3728
RTQUICaSyn-SAA positive	0.03079	0.12848	0.240	0.8115
DX_APDPSP	0.07497	0.12250	0.612	0.5429
scale(NFL_2)	0.13973	0.05786	2.415	0.0189
scale(Onset_age):RTQUICaSyn-SAA positive	0.33499	0.13768	2.433	0.0180

```

(Intercept)                ***
scale(Onset_age)
RTQUICaSyn-SAA positive
DX_APDPSP
scale(NFL_2)                *
scale(Onset_age):RTQUICaSyn-SAA positive *
---

```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4554 on 59 degrees of freedom

(2 observations deleted due to missingness)

Multiple R-squared: 0.2668, Adjusted R-squared: 0.2047

F-statistic: 4.294 on 5 and 59 DF, p-value: 0.002131

[1] 89.90517

Call:

lm(formula = logabeta ~ scale(Onset_age) * RTQUIC + DX_APD, data = df)

Residuals:

Min	1Q	Median	3Q	Max
-1.13342	-0.28168	-0.05665	0.34966	0.85374

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.95824	0.09015	66.093	<2e-16
scale(Onset_age)	0.08251	0.06859	1.203	0.2336
RTQUICaSyn-SAA positive	0.05793	0.12826	0.452	0.6531
DX_APDPSP	0.10296	0.12256	0.840	0.4041
scale(Onset_age):RTQUICaSyn-SAA positive	0.29171	0.13990	2.085	0.0412

```

(Intercept)                ***
scale(Onset_age)
RTQUICaSyn-SAA positive
DX_APDPSP
scale(Onset_age):RTQUICaSyn-SAA positive *
---

```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4666 on 62 degrees of freedom

Multiple R-squared: 0.1993, Adjusted R-squared: 0.1477

F-statistic: 3.858 on 4 and 62 DF, p-value: 0.007301

[1] 94.78542

Call:

```
lm(formula = logabeta ~ scale(Onset_age) * RTQUIC, data = df)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.08935	-0.27009	-0.01783	0.35302	0.91339

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	6.0058	0.0700	85.793	<2e-16
scale(Onset_age)	0.0954	0.0667	1.430	0.1576
RTQUICaSyn-SAA positive	0.0404	0.1263	0.320	0.7500
scale(Onset_age):RTQUICaSyn-SAA positive	0.3050	0.1387	2.199	0.0315

(Intercept) ***
scale(Onset_age)
RTQUICaSyn-SAA positive
scale(Onset_age):RTQUICaSyn-SAA positive *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4655 on 63 degrees of freedom

Multiple R-squared: 0.1902, Adjusted R-squared: 0.1516

F-statistic: 4.932 on 3 and 63 DF, p-value: 0.003858

[1] 93.54383

Call:

```
lm(formula = logabeta ~ scale(Onset_age) + RTQUIC, data = df)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.16120	-0.25300	-0.00915	0.32704	0.92406

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	6.01558	0.07192	83.637	< 2e-16 ***
scale(Onset_age)	0.16594	0.06020	2.756	0.00761 **
RTQUICaSyn-SAA positive	0.09714	0.12724	0.763	0.44798

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4792 on 64 degrees of freedom

Multiple R-squared: 0.128, Adjusted R-squared: 0.1008

F-statistic: 4.699 on 2 and 64 DF, p-value: 0.01247

[1] 96.49943

Call:

```
lm(formula = logabeta ~ scale(Onset_age) * RTQUIC + scale(NFL_2),  
    data = df)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.2585	-0.3092	0.0265	0.3361	0.8854

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	6.01111	0.06890	87.243	<2e-16
scale(Onset_age)	0.06995	0.06576	1.064	0.2917
RTQUICaSyn-SAA positive	0.01484	0.12515	0.119	0.9060
scale(NFL_2)	0.14166	0.05747	2.465	0.0166
scale(Onset_age):RTQUICaSyn-SAA positive	0.34509	0.13598	2.538	0.0138

```

(Intercept)          ***
scale(Onset_age)
RTQUICaSyn-SAA positive
scale(NFL_2)          *
scale(Onset_age):RTQUICaSyn-SAA positive *
---

```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.453 on 60 degrees of freedom

(2 observations deleted due to missingness)

Multiple R-squared: 0.2622, Adjusted R-squared: 0.213

F-statistic: 5.329 on 4 and 60 DF, p-value: 0.0009697

[1] 88.3165

The model with the lowest AIC is the one including an interaction term of Onset age by aSyn-SAA status as NFL levels. Its AIC is almost identical to the one that incorporates Diagnosis. Diagnosis is an extremely important covariate that is relevant clinically. Therefore, we prefer to report the model with the lowest AIC that still includes diagnosis, model stdml r. Of note, all models have similar AIC and the interaction term was significant in every model that it was included in. Removing NFL did not affect the results, which is important since NFL outliers were not removed prior to running the analysis.

Call:

```
lm(formula = logabeta ~ scale(Onset_age) * RTQUIC + DX_APD +
    scale(NFL_2), data = df)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.28752	-0.32248	-0.01025	0.34356	0.84231

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.97571	0.09025	66.216	<2e-16
scale(Onset_age)	0.06085	0.06775	0.898	0.3728
RTQUICaSyn-SAA positive	0.03079	0.12848	0.240	0.8115
DX_APDPSP	0.07497	0.12250	0.612	0.5429
scale(NFL_2)	0.13973	0.05786	2.415	0.0189
scale(Onset_age):RTQUICaSyn-SAA positive	0.33499	0.13768	2.433	0.0180

```

(Intercept) ***
scale(Onset_age)
RTQUICaSyn-SAA positive
DX_APDPSP
scale(NFL_2) *
scale(Onset_age):RTQUICaSyn-SAA positive *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Residual standard error: 0.4554 on 59 degrees of freedom
 (2 observations deleted due to missingness)
 Multiple R-squared: 0.2668, Adjusted R-squared: 0.2047
 F-statistic: 4.294 on 5 and 59 DF, p-value: 0.002131

OK: residuals appear as normally distributed (p = 0.267).

	DX_APD	abeta_2	logabeta	Onset_age	RTQUIC	NFL_2
5	CBS	582.615	6.367527	35	aSyn-SAA negative	1070.23
22	CBS	557.7	6.323821	69	aSyn-SAA negative	1456.97
28	PSP	641.779	6.464244	58	aSyn-SAA negative	3005.4
38	PSP	713.237	6.569814	69	aSyn-SAA negative	2502.6
46	CBS	319.35	5.766288	63	aSyn-SAA negative	NA
67	CBS	309.75	5.735766	57	aSyn-SAA negative	1149.77

Call:
 lm(formula = logabeta ~ scale(Onset_age) * RTQUIC + DX_APD +
 scale(NFL_2), data = test)

Residuals:

	Min	1Q	Median	3Q	Max
	-1.33044	-0.31106	-0.00376	0.32119	0.87557

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.96938	0.08974	66.519	<2e-16
scale(Onset_age)	0.10900	0.06813	1.600	0.1150
RTQUICaSyn-SAA positive	0.05744	0.12501	0.460	0.6476
DX_APDPSP	0.07842	0.12035	0.652	0.5172
scale(NFL_2)	0.14222	0.05705	2.493	0.0155
scale(Onset_age):RTQUICaSyn-SAA positive	0.25439	0.12800	1.987	0.0516

```

(Intercept) ***
scale(Onset_age)
RTQUICaSyn-SAA positive
DX_APDPSP
scale(NFL_2) *
scale(Onset_age):RTQUICaSyn-SAA positive .
---

```


Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4473 on 58 degrees of freedom

(2 observations deleted due to missingness)

Multiple R-squared: 0.3001, Adjusted R-squared: 0.2398

F-statistic: 4.974 on 5 and 58 DF, p-value: 0.0007393

Call:

```
lm(formula = logabeta ~ scale(Onset_age) * RTQUIC + DX_APD +  
    scale(NFL_2), data = test)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.28271	-0.33144	0.00364	0.34214	0.84028

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.95855	0.09254	64.390	<2e-16
scale(Onset_age)	0.05162	0.06904	0.748	0.4577
RTQUICaSyn-SAA positive	0.04082	0.12993	0.314	0.7546
DX_APDPSP	0.09100	0.12409	0.733	0.4663
scale(NFL_2)	0.14460	0.05848	2.473	0.0164
scale(Onset_age):RTQUICaSyn-SAA positive	0.34232	0.13872	2.468	0.0166

```
(Intercept) ***  
scale(Onset_age)  
RTQUICaSyn-SAA positive  
DX_APDPSP  
scale(NFL_2) *  
scale(Onset_age):RTQUICaSyn-SAA positive *  
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4563 on 58 degrees of freedom

(2 observations deleted due to missingness)

Multiple R-squared: 0.273, Adjusted R-squared: 0.2103

F-statistic: 4.356 on 5 and 58 DF, p-value: 0.001962

Call:

```
lm(formula = logabeta ~ scale(Onset_age) * RTQUIC + DX_APD +  
    scale(NFL_2), data = test)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.27180	-0.31960	-0.00466	0.34186	0.86515

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.97557	0.09046	66.060	<2e-16
scale(Onset_age)	0.06845	0.06854	0.999	0.3221

RTQUICaSyn-SAA positive	0.03958	0.12841	0.308	0.7590
DX_APDPSP	0.05546	0.12425	0.446	0.6570
scale(NFL_2)	0.13908	0.05837	2.383	0.0205
scale(Onset_age):RTQUICaSyn-SAA positive	0.33400	0.13843	2.413	0.0190

(Intercept) ***

scale(Onset_age)

RTQUICaSyn-SAA positive

DX_APDPSP

scale(NFL_2) *

scale(Onset_age):RTQUICaSyn-SAA positive *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4557 on 58 degrees of freedom

(2 observations deleted due to missingness)

Multiple R-squared: 0.2706, Adjusted R-squared: 0.2077

F-statistic: 4.303 on 5 and 58 DF, p-value: 0.002136

Call:

lm(formula = logabeta ~ scale(Onset_age) * RTQUIC + DX_APD +
scale(NFL_2), data = test)

Residuals:

Min	1Q	Median	3Q	Max
-1.26254	-0.31886	0.00363	0.35433	0.86131

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.97036	0.09004	66.308	<2e-16
scale(Onset_age)	0.05456	0.06819	0.800	0.4270
RTQUICaSyn-SAA positive	0.03655	0.12882	0.284	0.7776
DX_APDPSP	0.05824	0.12322	0.473	0.6382
scale(NFL_2)	0.14270	0.05824	2.450	0.0173
scale(Onset_age):RTQUICaSyn-SAA positive	0.34748	0.13841	2.511	0.0149

(Intercept) ***

scale(Onset_age)

RTQUICaSyn-SAA positive

DX_APDPSP

scale(NFL_2) *

scale(Onset_age):RTQUICaSyn-SAA positive *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4546 on 58 degrees of freedom

(2 observations deleted due to missingness)

Multiple R-squared: 0.2696, Adjusted R-squared: 0.2067

F-statistic: 4.283 on 5 and 58 DF, p-value: 0.002205

Call:

```
lm(formula = logabeta ~ scale(Onset_age) * RTQUIC + DX_APD +  
    scale(NFL_2), data = test)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.28752	-0.32248	-0.01025	0.34356	0.84231

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.97575	0.09026	66.208	<2e-16
scale(Onset_age)	0.06132	0.06827	0.898	0.3728
RTQUICaSyn-SAA positive	0.03103	0.12846	0.242	0.8099
DX_APDPSP	0.07497	0.12250	0.612	0.5429
scale(NFL_2)	0.13973	0.05786	2.415	0.0189
scale(Onset_age):RTQUICaSyn-SAA positive	0.33755	0.13873	2.433	0.0180

(Intercept)	***
scale(Onset_age)	
RTQUICaSyn-SAA positive	
DX_APDPSP	
scale(NFL_2)	*
scale(Onset_age):RTQUICaSyn-SAA positive	*

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4554 on 59 degrees of freedom

(1 observation deleted due to missingness)

Multiple R-squared: 0.2668, Adjusted R-squared: 0.2047

F-statistic: 4.294 on 5 and 59 DF, p-value: 0.002131

Call:

```
lm(formula = logabeta ~ scale(Onset_age) * RTQUIC + DX_APD +  
    scale(NFL_2), data = test)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.28644	-0.32886	0.00183	0.34507	0.84133

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	5.98127	0.09252	64.647	<2e-16
scale(Onset_age)	0.06030	0.06863	0.879	0.3832
RTQUICaSyn-SAA positive	0.03199	0.12976	0.247	0.8061
DX_APDPSP	0.07233	0.12412	0.583	0.5623
scale(NFL_2)	0.13942	0.05870	2.375	0.0209
scale(Onset_age):RTQUICaSyn-SAA positive	0.33745	0.13942	2.420	0.0187

(Intercept)	***
scale(Onset_age)	
RTQUICaSyn-SAA positive	

```

DX_APDPSP
scale(NFL_2)
scale(Onset_age):RTQUICaSyn-SAA positive *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

Residual standard error: 0.4591 on 58 degrees of freedom
(2 observations deleted due to missingness)
Multiple R-squared:  0.263,    Adjusted R-squared:  0.1995
F-statistic:  4.14 on 5 and 58 DF,  p-value: 0.002771

```

studentized Breusch-Pagan test

```

data:  stdmlr
BP = 7.4909, df = 5, p-value = 0.1866

```

```

lag Autocorrelation D-W Statistic p-value
1      0.1083846      1.781022    0.372
Alternative hypothesis: rho != 0
there are higher-order terms (interactions) in this model
consider setting type = 'predictor'; see ?vif
      scale(Onset_age)      RTQUIC      DX_APD
      1.459046      1.131585      1.142161
      scale(NFL_2) scale(Onset_age):RTQUIC
      1.033238      1.443803

```

```

$emtrends
RTQUIC      Onset_age.trend      SE df lower.CL upper.CL
aSyn-SAA negative      0.00706 0.00786 59 -0.00867  0.0228
aSyn-SAA positive      0.04593 0.01429 59  0.01733  0.0745

```

```

Results are averaged over the levels of: DX_APD
Confidence level used: 0.95

```

```

$contrasts
contrast      estimate      SE df t.ratio p.value
(aSyn-SAA negative) - (aSyn-SAA positive) -0.0389 0.016 59 -2.433 0.0180

```

```

Results are averaged over the levels of: DX_APD

```

```

NOTE: Results may be misleading due to involvement in interactions
RTQUIC      emmean      SE df lower.CL upper.CL
aSyn-SAA negative  6.01 0.0693 59  5.87  6.15
aSyn-SAA positive  6.04 0.1093 59  5.82  6.26

```

```

Results are averaged over the levels of: DX_APD
Confidence level used: 0.95

```

```

DX_APD emmean      SE df lower.CL upper.CL
CBS      5.99 0.0772 59  5.84  6.14
PSP      6.07 0.1001 59  5.86  6.27

```

```

Results are averaged over the levels of: RTQUIC

```

Confidence level used: 0.95

```
#####
#####
#####                                7.2.2. FIGURE 1.B.                                #
#####
#####
#####
#####
----- GOES IN FIGURE 1B: ASYN-SAA+ vs ASYN-SAA- -----
-----
```

Warning messages:

```
1: In summary.lm(res.lm) :
  essentially perfect fit: summary may be unreliable
2: In summary.lm(res.lm) :
  essentially perfect fit: summary may be unreliable
3: In summary.lm(res.lm) :
  essentially perfect fit: summary may be unreliable
4: In summary.lm(res.lm) :
  essentially perfect fit: summary may be unreliable
```

Warning messages:

```
1: In summary.lm(res.lm) :
  essentially perfect fit: summary may be unreliable
2: In summary.lm(res.lm) :
  essentially perfect fit: summary may be unreliable
3: In summary.lm(res.lm) :
  essentially perfect fit: summary may be unreliable
4: In summary.lm(res.lm) :
  essentially perfect fit: summary may be unreliable
```

```
#####
#####
8. ASYN-SAA+ & ALL VARIABLES
#####
#####
```

```
#####
#####
8.1. ASYN-SAA+ & NFL
#####
#####
```

```
#####
#####
#####                                8.1.1. NFL MLR                                #####
#####
```

```
#####  
#####
```

```
----- GOES IN TEXT - RESULTS - ASYN-SAA+ & NFL -----  
-----
```

```
[1] 12101.20 6153.82 9997.64
```

```
[1] 5780.13 5748.61 7858.61
```

```
Outliers are values above 6775.568 in CBS subset.
```

```
Outliers are values above 7858.61 in PSP subset.
```

```
Following values were removed for the descriptive stats on NFL: 12101.2 NA NA 9  
997.64
```

Shapiro-Wilk normality test

```
data: dfNFL[dfNFL$DX_APD == "CBS", ]$logNFL
```

```
W = 0.96261, p-value = 0.2584
```

Shapiro-Wilk normality test

```
data: dfNFL[dfNFL$DX_APD == "PSP", ]$logNFL
```

```
W = 0.97556, p-value = 0.7516
```

Shapiro-Wilk normality test

```
data: dfNFL[dfNFL$RTQUIC == "aSyn-SAA positive", ]$logNFL
```

```
W = 0.91836, p-value = 0.09216
```

Shapiro-Wilk normality test

```
data: dfNFL[dfNFL$RTQUIC == "aSyn-SAA negative", ]$logNFL
```

```
W = 0.97249, p-value = 0.3839
```

Shapiro-Wilk normality test

```
data: dfNFL[dfNFL$AD == "AD Positive", ]$logNFL
```

```
W = 0.90972, p-value = 0.1561
```

Shapiro-Wilk normality test

```
data: dfNFL[dfNFL$AD == "AD Negative", ]$logNFL
```

```
W = 0.96128, p-value = 0.107
```

Levene's Test for Homogeneity of Variance (center = median)

```
Df F value Pr(>F)
```

```
group 6 1.1766 0.332
```

```
56
```

Analysis of Variance Table

```

Model 1: logNFL ~ RTQUIC
Model 2: logNFL ~ RTQUIC + DX_APD
  Res.Df    RSS Df Sum of Sq    F Pr(>F)
1      61 16.623
2      60 15.377  1      1.246 4.8619 0.0313 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Analysis of Variance Table

```

```

Model 1: logNFL ~ RTQUIC
Model 2: logNFL ~ RTQUIC + AD
  Res.Df    RSS Df Sum of Sq    F Pr(>F)
1      61 16.623
2      60 15.945  1      0.67755 2.5496 0.1156

```

```

Call:
lm(formula = dfnfl$logNFL ~ dfnfl$Age)

```

```

Residuals:
      Min       1Q   Median       3Q      Max
-0.96048 -0.42486 -0.04107  0.31145  1.23321

```

```

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  7.063196   0.482090   14.65  <2e-16 ***
dfnfl$Age     0.008069   0.006956    1.16   0.251
---

```

```

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

Residual standard error: 0.5178 on 61 degrees of freedom
Multiple R-squared:  0.02158, Adjusted R-squared:  0.005544
F-statistic: 1.346 on 1 and 61 DF, p-value: 0.2506

```

```

Call:
lm(formula = dfnfl$logNFL ~ dfnfl$LP2_Disease_Duration)

```

```

Residuals:
      Min       1Q   Median       3Q      Max
-1.00926 -0.41465 -0.05653  0.28669  1.35379

```

```

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    7.60744    0.12119  62.776  <2e-16 ***
dfnfl$LP2_Disease_Duration 0.00185    0.01912   0.097   0.923
---

```

```

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

Residual standard error: 0.5234 on 61 degrees of freedom
Multiple R-squared:  0.0001535, Adjusted R-squared:  -0.01624
F-statistic: 0.009365 on 1 and 61 DF, p-value: 0.9232

```

```
Call:
lm(formula = dfnfl$logNFL ~ dfnfl$abeta_2)

Residuals:
    Min       1Q   Median       3Q      Max
-0.89492 -0.34549 -0.01374  0.21666  1.20997

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  7.2573600   0.1468411  49.423  <2e-16 ***
dfnfl$abeta_2  0.0007680   0.0002837   2.707   0.0088 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4946 on 61 degrees of freedom
Multiple R-squared:  0.1072,    Adjusted R-squared:  0.0926
F-statistic: 7.327 on 1 and 61 DF,  p-value: 0.008797
```

```
Call:
lm(formula = dfnfl$logNFL ~ dfnfl$ptau_2)

Residuals:
    Min       1Q   Median       3Q      Max
-0.97886 -0.41905 -0.03975  0.29057  1.34893

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  7.713347   0.132485  58.220  <2e-16 ***
dfnfl$ptau_2 -0.001804   0.002162  -0.835   0.407
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5205 on 61 degrees of freedom
Multiple R-squared:  0.01129,    Adjusted R-squared:  -0.004921
F-statistic: 0.6964 on 1 and 61 DF,  p-value: 0.4073
```

```
Call:
lm(formula = dfnfl$logNFL ~ dfnfl$ttau_2)

Residuals:
    Min       1Q   Median       3Q      Max
-1.01292 -0.40270 -0.02267  0.29122  1.34669

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  7.6657704   0.1084848  70.662  <2e-16 ***
dfnfl$ttau_2 -0.0001497   0.0002192  -0.683   0.497
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Residual standard error: 0.5191 on 60 degrees of freedom
(1 observation deleted due to missingness)
Multiple R-squared: 0.007718, Adjusted R-squared: -0.00882
F-statistic: 0.4667 on 1 and 60 DF, p-value: 0.4972

Call:

```
lm(formula = logNFL ~ RTQUIC * DX_APD + scale(abeta_2), data = dfNFL)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.91541	-0.27896	-0.06221	0.27836	1.14385

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	7.50151	0.10223	73.380	<2e-16 ***
RTQUICaSyn-SAA positive	0.08831	0.16702	0.529	0.5990
DX_APDPSP	0.33528	0.15024	2.232	0.0295 *
scale(abeta_2)	0.16122	0.06517	2.474	0.0163 *
RTQUICaSyn-SAA positive:DX_APDPSP	-0.50362	0.27044	-1.862	0.0676 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4802 on 58 degrees of freedom
Multiple R-squared: 0.1997, Adjusted R-squared: 0.1445
F-statistic: 3.618 on 4 and 58 DF, p-value: 0.01063

[1] 93.15681

Call:

```
lm(formula = logNFL ~ RTQUIC + DX_APD + scale(abeta_2), data = dfNFL)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.90290	-0.33584	-0.09789	0.23158	1.26717

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	7.56632	0.09811	77.120	<2e-16 ***
RTQUICaSyn-SAA positive	-0.10055	0.13545	-0.742	0.4608
DX_APDPSP	0.19339	0.13217	1.463	0.1487
scale(abeta_2)	0.14780	0.06611	2.236	0.0292 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4902 on 59 degrees of freedom
Multiple R-squared: 0.1518, Adjusted R-squared: 0.1087
F-statistic: 3.521 on 3 and 59 DF, p-value: 0.02037

[1] 94.81533

OK: residuals appear as normally distributed (p = 0.315).

```

  abeta_2 logabeta          RTQUIC DX_APD   NFL_2
9 990.464 6.898174 aSyn-SAA positive    PSP 2296.71
  abeta_2 logabeta          RTQUIC DX_APD   NFL_2
39 233.053 5.451266 aSyn-SAA negative    PSP 2638.08
  abeta_2 logabeta          RTQUIC DX_APD   NFL_2
59 370.95 5.916067 aSyn-SAA negative    CBS 1137.16
  abeta_2 logabeta          RTQUIC DX_APD   NFL_2
62 428.65 6.060641 aSyn-SAA negative    CBS 1708.68

```

Call:

```
lm(formula = logNFL ~ RTQUIC * DX_APD + scale(abeta_2), data = test)
```

Residuals:

```

      Min       1Q   Median       3Q      Max
-0.91565 -0.28194 -0.06793  0.27820  1.14366

```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	7.49599	0.10272	72.977	<2e-16 ***
RTQUICaSyn-SAA positive	0.08793	0.16847	0.522	0.6037
DX_APDPSP	0.33421	0.15171	2.203	0.0317 *
scale(abeta_2)	0.15706	0.06487	2.421	0.0187 *
RTQUICaSyn-SAA positive:DX_APDPSP	-0.49369	0.28152	-1.754	0.0849 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4843 on 57 degrees of freedom

Multiple R-squared: 0.1993, Adjusted R-squared: 0.1431

F-statistic: 3.546 on 4 and 57 DF, p-value: 0.01186

Call:

```
lm(formula = logNFL ~ RTQUIC * DX_APD + scale(abeta_2), data = test)
```

Residuals:

```

      Min       1Q   Median       3Q      Max
-0.90445 -0.28094 -0.07794  0.27607  1.14340

```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	7.50603	0.10323	72.708	<2e-16 ***
RTQUICaSyn-SAA positive	0.08740	0.16818	0.520	0.6053
DX_APDPSP	0.32118	0.15438	2.081	0.0420 *
scale(abeta_2)	0.16627	0.06653	2.499	0.0154 *
RTQUICaSyn-SAA positive:DX_APDPSP	-0.49450	0.27303	-1.811	0.0754 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4835 on 57 degrees of freedom

Multiple R-squared: 0.1993, Adjusted R-squared: 0.1431

F-statistic: 3.547 on 4 and 57 DF, p-value: 0.01184

```
Call:
lm(formula = logNFL ~ RTQUIC * DX_APD + scale(abeta_2), data = test)

Residuals:
    Min       1Q   Median       3Q      Max
-0.9153 -0.2837 -0.0564  0.2625  1.1439

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      7.52027    0.10472  71.811  <2e-16 ***
RTQUICaSyn-SAA positive  0.07056    0.16879   0.418   0.6775
DX_APDPSP        0.31783    0.15207   2.090   0.0411 *
scale(abeta_2)    0.16131    0.06578   2.452   0.0173 *
RTQUICaSyn-SAA positive:DX_APDPSP -0.48526    0.27202  -1.784   0.0798 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4815 on 57 degrees of freedom
Multiple R-squared:  0.1928,    Adjusted R-squared:  0.1362
F-statistic: 3.405 on 4 and 57 DF,  p-value: 0.01448
```

```
Call:
lm(formula = logNFL ~ RTQUIC * DX_APD + scale(abeta_2), data = test)

Residuals:
    Min       1Q   Median       3Q      Max
-0.91542 -0.28162 -0.07366  0.27835  1.14385

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)      7.50332    0.10546  71.147  <2e-16 ***
RTQUICaSyn-SAA positive  0.08699    0.16987   0.512   0.6106
DX_APDPSP        0.33393    0.15316   2.180   0.0334 *
scale(abeta_2)    0.16257    0.06627   2.453   0.0172 *
RTQUICaSyn-SAA positive:DX_APDPSP -0.50234    0.27360  -1.836   0.0716 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4844 on 57 degrees of freedom
Multiple R-squared:  0.1983,    Adjusted R-squared:  0.142
F-statistic: 3.524 on 4 and 57 DF,  p-value: 0.01223
```

studentized Breusch-Pagan test

```
data: stdmlr
BP = 1.5504, df = 4, p-value = 0.8177
```

```
lag Autocorrelation D-W Statistic p-value
 1      0.02629406      1.933946  0.708
```

Alternative hypothesis: rho != 0
there are higher-order terms (interactions) in this model
consider setting type = 'predictor'; see ?vif

RTQUIC	DX_APD	scale(abeta_2)	RTQUIC:DX_APD
1.651222	1.510114	1.141793	1.973264
RTQUIC	DX_APD	emmean	SE df lower.CL upper.CL
aSyn-SAA negative CBS		7.50	0.102 58 7.30 7.71
aSyn-SAA positive CBS		7.59	0.134 58 7.32 7.86
aSyn-SAA negative PSP		7.84	0.108 58 7.62 8.05
aSyn-SAA positive PSP		7.42	0.189 58 7.04 7.80

Confidence level used: 0.95

contrast	estimate	SE	df	t.ratio
(aSyn-SAA negative CBS) - (aSyn-SAA positive CBS)	-0.0883	0.167	58	-0.529
(aSyn-SAA negative CBS) - (aSyn-SAA negative PSP)	-0.3353	0.150	58	-2.232
(aSyn-SAA negative CBS) - (aSyn-SAA positive PSP)	0.0800	0.220	58	0.364
(aSyn-SAA positive CBS) - (aSyn-SAA negative PSP)	-0.2470	0.172	58	-1.433
(aSyn-SAA positive CBS) - (aSyn-SAA positive PSP)	0.1683	0.233	58	0.721
(aSyn-SAA negative PSP) - (aSyn-SAA positive PSP)	0.4153	0.215	58	1.933
p.value				
0.9518				
0.1268				
0.9833				
0.4841				
0.8883				
0.2259				

P value adjustment: tukey method for comparing a family of 4 estimates

```
#####
#####
##### 8.1.2. FIG 1.D. #####
#####
#####
#####
----- FOR REFERENCE ONLY -----
--
```

Call:

lm(formula = logNFL ~ RTQUIC * DX_APD + abeta_2, data = dfnfl)

Residuals:

Min	1Q	Median	3Q	Max
-0.91541	-0.27896	-0.06221	0.27836	1.14385

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	7.1602333	0.1542851	46.409	<2e-16 ***
RTQUICaSyn-SAA positive	0.0883131	0.1670216	0.529	0.5990
DX_APDPSP	0.3352832	0.1502418	2.232	0.0295 *
abeta_2	0.0007282	0.0002944	2.474	0.0163 *

RTQUICaSyn-SAA positive:DX_APDPSP -0.5036172 0.2704387 -1.862 0.0676 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4802 on 58 degrees of freedom

Multiple R-squared: 0.1997, Adjusted R-squared: 0.1445

F-statistic: 3.618 on 4 and 58 DF, p-value: 0.01063

`geom_smooth()` using formula = 'y ~ x'

`geom_smooth()` using formula = 'y ~ x'

----- GOES IN FIGURE 1D: ASYN-SAA+ vs ASYN-SAA- -----

#####

8.2. ASYN-SAA+ & SYMPTOMS

#####

#####

8.2.1. CBS-ONLY NUMERICAL VARIABLES ###
#####

#####

----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----

Shapiro-Wilk normality test

data: CBSdf[CBSdf\$RTQUIC == "aSyn-SAA positive",]\$Age
W = 0.95004, p-value = 0.5613

Shapiro-Wilk normality test

data: CBSdf[CBSdf\$RTQUIC == "aSyn-SAA negative",]\$Age
W = 0.96496, p-value = 0.5217

F test to compare two variances

data: Age by RTQUIC
F = 1.3081, num df = 24, denom df = 13, p-value = 0.626
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
0.452126 3.272749
sample estimates:
ratio of variances
1.308087

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$RTQUIC == "aSyn-SAA positive", ]$Onset_age  
W = 0.93077, p-value = 0.3128
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$RTQUIC == "aSyn-SAA negative", ]$Onset_age  
W = 0.94595, p-value = 0.2028
```

F test to compare two variances

```
data: Onset_age by RTQUIC  
F = 1.8716, num df = 24, denom df = 13, p-value = 0.2403  
alternative hypothesis: true ratio of variances is not equal to 1  
95 percent confidence interval:  
 0.6469066 4.6826837  
sample estimates:  
ratio of variances  
 1.871625
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$RTQUIC == "aSyn-SAA positive", ]$Park_onset  
W = 0.93165, p-value = 0.3218
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$RTQUIC == "aSyn-SAA negative", ]$Park_onset  
W = 0.94546, p-value = 0.2156
```

F test to compare two variances

```
data: Park_onset by RTQUIC  
F = 1.9243, num df = 23, denom df = 13, p-value = 0.222  
alternative hypothesis: true ratio of variances is not equal to 1  
95 percent confidence interval:  
 0.6623739 4.8700231  
sample estimates:  
ratio of variances  
 1.924299
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$RTQUIC == "aSyn-SAA positive", ]$Age
W = 0.95004, p-value = 0.5613
```

Shapiro-Wilk normality test

```
data: CBSdf[CBSdf$RTQUIC == "aSyn-SAA negative", ]$Age
W = 0.96496, p-value = 0.5217
```

F test to compare two variances

```
data: Age by RTQUIC
F = 1.3081, num df = 24, denom df = 13, p-value = 0.626
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.452126 3.272749
sample estimates:
ratio of variances
      1.308087
```

```
# A tibble: 2 × 3
  RTQUIC      `format(round(mean(Age, na.rm = T), 2), 2)`      sd
  <fct>      <chr>                                     <dbl>
1 aSyn-SAA negative 64.74                                     8.92
2 aSyn-SAA positive 68.02                                     7.80
# A tibble: 2 × 3
  RTQUIC      `format(round(mean(Onset_age, na.rm = T), 2), 2)`      sd
  <fct>      <chr>                                     <dbl>
1 aSyn-SAA negative 60.12                                     9.04
2 aSyn-SAA positive 63.57                                     6.61
# A tibble: 2 × 3
  RTQUIC      `format(round(mean(Park_onset, na.rm = T), 2), 2)`      sd
  <fct>      <chr>                                     <dbl>
1 aSyn-SAA negative 61.75                                     8.94
2 aSyn-SAA positive 65.57                                     6.44
```

Two Sample t-test

```
data: CBSdf$Age by CBSdf$RTQUIC
t = -1.1501, df = 37, p-value = 0.2575
alternative hypothesis: true difference in means between group aSyn-SAA negative
and group aSyn-SAA positive is not equal to 0
95 percent confidence interval:
 -9.062894  2.499684
sample estimates:
mean in group aSyn-SAA negative mean in group aSyn-SAA positive
      64.73973                  68.02133
```

Two Sample t-test

```

data: CBSdf$Onset_age by CBSdf$RTQUIC
t = -1.2509, df = 37, p-value = 0.2188
alternative hypothesis: true difference in means between group aSyn-SAA negative
and group aSyn-SAA positive is not equal to 0
95 percent confidence interval:
-9.042210  2.139353
sample estimates:
mean in group aSyn-SAA negative mean in group aSyn-SAA positive
        60.12000                63.57143

```

Two Sample t-test

```

data: CBSdf$Park_onset by CBSdf$RTQUIC
t = -1.3987, df = 36, p-value = 0.1704
alternative hypothesis: true difference in means between group aSyn-SAA negative
and group aSyn-SAA positive is not equal to 0
95 percent confidence interval:
-9.362269  1.719412
sample estimates:
mean in group aSyn-SAA negative mean in group aSyn-SAA positive
        61.75000                65.57143

```

```

#####
#####
#####                                8.2.2. CBS-ONLY CATEGORICAL VARIABLES                                #
#####
#####
#####
#####

```

```

----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----
-----

```

```

# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Sex      n
  <fct>      <chr> <int>
1 aSyn-SAA negative F      10
2 aSyn-SAA negative M      15
3 aSyn-SAA positive F       9
4 aSyn-SAA positive M       5
# A tibble: 6 × 3
# Groups:   RTQUIC [2]
  RTQUIC      APOEe4      n
  <fct>      <fct> <int>
1 aSyn-SAA negative Negative    18
2 aSyn-SAA negative Positive     6
3 aSyn-SAA negative NA           1
4 aSyn-SAA positive Negative    12
5 aSyn-SAA positive Positive     1
6 aSyn-SAA positive NA           1
# A tibble: 4 × 3

```



```

# Groups:   RTQUIC [2]
  RTQUIC      Parkinsonian_onset      n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No      17
2 aSyn-SAA negative Yes      8
3 aSyn-SAA positive No     10
4 aSyn-SAA positive Yes      4
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Tremor_binary      n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No      15
2 aSyn-SAA negative Yes     10
3 aSyn-SAA positive No     10
4 aSyn-SAA positive Yes      4
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      RestTremor      n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No      24
2 aSyn-SAA negative Yes      1
3 aSyn-SAA positive No     13
4 aSyn-SAA positive Yes      1
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      LimbRigidity      n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No      8
2 aSyn-SAA negative Yes     17
3 aSyn-SAA positive No      7
4 aSyn-SAA positive Yes      7
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Slowness_binary      n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No      5
2 aSyn-SAA negative Yes     20
3 aSyn-SAA positive No      4
4 aSyn-SAA positive Yes     10
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      LP2_falls_PI      n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No      6
2 aSyn-SAA negative Yes     19
3 aSyn-SAA positive No      6
4 aSyn-SAA positive Yes      8
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      LP2_gait      n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No      8

```

```

2 aSyn-SAA negative Yes      17
3 aSyn-SAA positive No       9
4 aSyn-SAA positive Yes      5
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      RBD_binary      n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No      24
2 aSyn-SAA negative Yes      1
3 aSyn-SAA positive No     12
4 aSyn-SAA positive Yes      2
# A tibble: 5 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Lifetime_Dopa_responder_true      n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No      4
2 aSyn-SAA negative Yes      2
3 aSyn-SAA negative NA     19
4 aSyn-SAA positive No      4
5 aSyn-SAA positive NA     10
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Lifetime_VisualHallucinations_binary      n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No      24
2 aSyn-SAA negative Yes      1
3 aSyn-SAA positive No     11
4 aSyn-SAA positive Yes      3
# A tibble: 3 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Constipation_binary      n
  <fct>      <lgl>      <int>
1 aSyn-SAA negative FALSE      22
2 aSyn-SAA negative TRUE       3
3 aSyn-SAA positive FALSE     14
# A tibble: 3 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Sexual_binary      n
  <fct>      <lgl>      <int>
1 aSyn-SAA negative FALSE     24
2 aSyn-SAA negative TRUE      1
3 aSyn-SAA positive FALSE    14
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Urinary_binary      n
  <fct>      <lgl>      <int>
1 aSyn-SAA negative FALSE     19
2 aSyn-SAA negative TRUE      6
3 aSyn-SAA positive FALSE      9
4 aSyn-SAA positive TRUE      5
# A tibble: 4 × 3
# Groups:   RTQUIC [2]

```

```

RTQUIC          Bowel_binary      n
<fct>           <lgl>             <int>
1 aSyn-SAA negative FALSE          22
2 aSyn-SAA negative TRUE           3
3 aSyn-SAA positive FALSE         12
4 aSyn-SAA positive TRUE           2
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
RTQUIC          anyPPA            n
<fct>           <chr>             <int>
1 aSyn-SAA negative No             17
2 aSyn-SAA negative Yes            8
3 aSyn-SAA positive No             7
4 aSyn-SAA positive Yes            7

```

Pearson's Chi-squared test with Yates' continuity correction

```

data: table(CBSdf$Sex, CBSdf$RTQUIC)
X-squared = 1.258, df = 1, p-value = 0.262

```

Fisher's Exact Test for Count Data

```

data: CBSdf$APOEe4 and CBSdf$RTQUIC
p-value = 0.3828
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.005029025 2.566732716
sample estimates:
odds ratio
 0.2580524

```

Fisher's Exact Test for Count Data

```

data: CBSdf$Parkinsonian_onset and CBSdf$RTQUIC
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.1484647 4.2812730
sample estimates:
odds ratio
 0.8535194

```

Pearson's Chi-squared test with Yates' continuity correction

```

data: table(CBSdf$Tremor_binary, CBSdf$RTQUIC)
X-squared = 0.13379, df = 1, p-value = 0.7145

```

Pearson's Chi-squared test with Yates' continuity correction

```
data: table(CBSdf$LimbRigidity, CBSdf$RTQUIC)
X-squared = 0.5857, df = 1, p-value = 0.4441
```

Fisher's Exact Test for Count Data

```
data: CBSdf$Slowness_binary and CBSdf$RTQUIC
p-value = 0.6958
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.1074803 3.9350123
sample estimates:
odds ratio
 0.6328383
```

Fisher's Exact Test for Count Data

```
data: CBSdf$LP2_falls_PI and CBSdf$RTQUIC
p-value = 0.2869
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.08353211 2.15495833
sample estimates:
odds ratio
 0.4311153
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: table(CBSdf$LP2_gait, CBSdf$RTQUIC)
X-squared = 2.6046, df = 1, p-value = 0.1066
```

Fisher's Exact Test for Count Data

```
data: CBSdf$Lifetime_Dopa_responder_true and CBSdf$RTQUIC
p-value = 0.4667
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.000000 8.076414
sample estimates:
odds ratio
 0
```

Fisher's Exact Test for Count Data

```
data: CBSdf$Lifetime_VisualHallucinations_binary and CBSdf$RTQUIC
p-value = 0.1228
alternative hypothesis: true odds ratio is not equal to 1
```

```
95 percent confidence interval:
  0.442479 356.700748
sample estimates:
odds ratio
  6.21328
```

Fisher's Exact Test for Count Data

```
data: CBSdf$Constipation_binary and CBSdf$RTQUIC
p-value = 0.5404
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
  0.000000 4.314503
sample estimates:
odds ratio
  0
```

Fisher's Exact Test for Count Data

```
data: CBSdf$Urinary_binary and CBSdf$RTQUIC
p-value = 0.478
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
  0.324475 9.090888
sample estimates:
odds ratio
  1.732988
```

Fisher's Exact Test for Count Data

```
data: CBSdf$Bowel_binary and CBSdf$RTQUIC
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
  0.08986523 12.22872401
sample estimates:
odds ratio
  1.215804
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: table(CBSdf$anyPPA, CBSdf$RTQUIC)
X-squared = 0.5857, df = 1, p-value = 0.4441
```

```
#####
#####
```

```
##### 8.2.3. PSP-ONLY NUMERICAL VARIABLES ###
#####
#####
#####
----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----
-----
```

Shapiro-Wilk normality test

```
data: PSPdf[PSPdf$RTQUIC == "aSyn-SAA positive", ]$Age
W = 0.96, p-value = 0.8101
```

Shapiro-Wilk normality test

```
data: PSPdf[PSPdf$RTQUIC == "aSyn-SAA negative", ]$Age
W = 0.93967, p-value = 0.2363
```

F test to compare two variances

```
data: Age by RTQUIC
F = 1.9241, num df = 19, denom df = 7, p-value = 0.3827
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.4292154 5.8702728
sample estimates:
ratio of variances
      1.924132
```

Shapiro-Wilk normality test

```
data: PSPdf[PSPdf$RTQUIC == "aSyn-SAA positive", ]$Onset_age
W = 0.90133, p-value = 0.297
```

Shapiro-Wilk normality test

```
data: PSPdf[PSPdf$RTQUIC == "aSyn-SAA negative", ]$Onset_age
W = 0.96336, p-value = 0.613
```

F test to compare two variances

```
data: Onset_age by RTQUIC
F = 1.6274, num df = 19, denom df = 7, p-value = 0.5252
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.3630251 4.9650044
sample estimates:
ratio of variances
```

1.627407

Shapiro-Wilk normality test

data: PSPdf[PSPdf\$RTQUIC == "aSyn-SAA positive",]\$Park_onset
W = 0.89162, p-value = 0.2423

Shapiro-Wilk normality test

data: PSPdf[PSPdf\$RTQUIC == "aSyn-SAA negative",]\$Park_onset
W = 0.9484, p-value = 0.3434

F test to compare two variances

data: Park_onset by RTQUIC
F = 1.7731, num df = 19, denom df = 7, p-value = 0.4485
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
0.3955307 5.4095760
sample estimates:
ratio of variances
1.773127

Shapiro-Wilk normality test

data: PSPdf[PSPdf\$RTQUIC == "aSyn-SAA positive",]\$Age
W = 0.96, p-value = 0.8101

Shapiro-Wilk normality test

data: PSPdf[PSPdf\$RTQUIC == "aSyn-SAA negative",]\$Age
W = 0.93967, p-value = 0.2363

F test to compare two variances

data: Age by RTQUIC
F = 1.9241, num df = 19, denom df = 7, p-value = 0.3827
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
0.4292154 5.8702728
sample estimates:
ratio of variances
1.924132

```
# A tibble: 2 × 3  
  RTQUIC      mean(Age, na.rm = T)      sd
```

	<fct>	<chr>	<dbl>
1	aSyn-SAA negative	71.93	9.45
2	aSyn-SAA positive	73.95	6.81

A tibble: 2 × 3

	RTQUIC	`format(round(mean(Onset_age, na.rm = T), 2), 2)`	sd
	<fct>	<chr>	<dbl>
1	aSyn-SAA negative	64.85	8.61
2	aSyn-SAA positive	69.88	6.75

A tibble: 2 × 3

	RTQUIC	`format(round(mean(Park_onset, na.rm = T), 2), 2)`	sd
	<fct>	<chr>	<dbl>
1	aSyn-SAA negative	65.9	8.68
2	aSyn-SAA positive	70.25	6.52

Two Sample t-test

data: PSPdf\$Age by PSPdf\$RTQUIC
t = -0.54813, df = 26, p-value = 0.5883
alternative hypothesis: true difference in means between group aSyn-SAA negative and group aSyn-SAA positive is not equal to 0
95 percent confidence interval:
-9.601622 5.558882
sample estimates:
mean in group aSyn-SAA negative mean in group aSyn-SAA positive
71.93205 73.95342

Two Sample t-test

data: PSPdf\$Onset_age by PSPdf\$RTQUIC
t = -1.4737, df = 26, p-value = 0.1526
alternative hypothesis: true difference in means between group aSyn-SAA negative and group aSyn-SAA positive is not equal to 0
95 percent confidence interval:
-12.033993 1.983993
sample estimates:
mean in group aSyn-SAA negative mean in group aSyn-SAA positive
64.850 69.875

Two Sample t-test

data: PSPdf\$Park_onset by PSPdf\$RTQUIC
t = -1.275, df = 26, p-value = 0.2136
alternative hypothesis: true difference in means between group aSyn-SAA negative and group aSyn-SAA positive is not equal to 0
95 percent confidence interval:
-11.362796 2.662796
sample estimates:
mean in group aSyn-SAA negative mean in group aSyn-SAA positive
65.90 70.25


```
#####
#####
##### 8.2.4. PSP-ONLY CATEGORICAL VARIABLES #####
#####
#####
#####
----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----
-----
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Sex      n
  <fct>      <chr> <int>
1 aSyn-SAA negative F      10
2 aSyn-SAA negative M      10
3 aSyn-SAA positive F       3
4 aSyn-SAA positive M       5
# A tibble: 6 × 3
# Groups:   RTQUIC [2]
  RTQUIC      APOEε4      n
  <fct>      <fct> <int>
1 aSyn-SAA negative Negative  13
2 aSyn-SAA negative Positive   5
3 aSyn-SAA negative  NA       2
4 aSyn-SAA positive Negative   4
5 aSyn-SAA positive Positive   2
6 aSyn-SAA positive  NA       2
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Parkinsonian_onset      n
  <fct>      <chr> <int>
1 aSyn-SAA negative No           6
2 aSyn-SAA negative Yes        14
3 aSyn-SAA positive No           2
4 aSyn-SAA positive Yes          6
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Tremor_binary      n
  <fct>      <chr> <int>
1 aSyn-SAA negative No         11
2 aSyn-SAA negative Yes          9
3 aSyn-SAA positive No           3
4 aSyn-SAA positive Yes          5
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      RestTremor      n
  <fct>      <chr> <int>
1 aSyn-SAA negative No         18
2 aSyn-SAA negative Yes          2
3 aSyn-SAA positive No           7
4 aSyn-SAA positive Yes          1
```

```

# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      LimbRigidity    n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No          3
2 aSyn-SAA negative Yes        17
3 aSyn-SAA positive No          3
4 aSyn-SAA positive Yes         5
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Slowness_binary    n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No          1
2 aSyn-SAA negative Yes        19
3 aSyn-SAA positive No          1
4 aSyn-SAA positive Yes         7
# A tibble: 3 × 3
# Groups:   RTQUIC [2]
  RTQUIC      LP2_falls_PI    n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No          1
2 aSyn-SAA negative Yes        19
3 aSyn-SAA positive Yes         8
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      LP2_gait    n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No          2
2 aSyn-SAA negative Yes        18
3 aSyn-SAA positive No          1
4 aSyn-SAA positive Yes         7
# A tibble: 3 × 3
# Groups:   RTQUIC [2]
  RTQUIC      RBD_binary    n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No        20
2 aSyn-SAA positive No         4
3 aSyn-SAA positive Yes         4
# A tibble: 6 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Lifetime_Dopa_responder_true    n
  <fct>      <chr>      <int>
1 aSyn-SAA negative No        10
2 aSyn-SAA negative Yes         4
3 aSyn-SAA negative NA         6
4 aSyn-SAA positive No         2
5 aSyn-SAA positive Yes         3
6 aSyn-SAA positive NA         3
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Lifetime_VisualHallucinations_binary    n
  <fct>      <chr>      <int>

```

1	aSyn-SAA negative	No	17
2	aSyn-SAA negative	Yes	3
3	aSyn-SAA positive	No	6
4	aSyn-SAA positive	Yes	2

A tibble: 4 × 3

Groups: RTQUIC [2]

	RTQUIC	Constipation_binary	n
	<fct>	<lgl>	<int>
1	aSyn-SAA negative	FALSE	14
2	aSyn-SAA negative	TRUE	6
3	aSyn-SAA positive	FALSE	6
4	aSyn-SAA positive	TRUE	2

A tibble: 4 × 3

Groups: RTQUIC [2]

	RTQUIC	Sexual_binary	n
	<fct>	<lgl>	<int>
1	aSyn-SAA negative	FALSE	18
2	aSyn-SAA negative	TRUE	2
3	aSyn-SAA positive	FALSE	7
4	aSyn-SAA positive	TRUE	1

A tibble: 4 × 3

Groups: RTQUIC [2]

	RTQUIC	Urinary_binary	n
	<fct>	<lgl>	<int>
1	aSyn-SAA negative	FALSE	3
2	aSyn-SAA negative	TRUE	17
3	aSyn-SAA positive	FALSE	2
4	aSyn-SAA positive	TRUE	6

A tibble: 4 × 3

Groups: RTQUIC [2]

	RTQUIC	Bowel_binary	n
	<fct>	<lgl>	<int>
1	aSyn-SAA negative	FALSE	16
2	aSyn-SAA negative	TRUE	4
3	aSyn-SAA positive	FALSE	7
4	aSyn-SAA positive	TRUE	1

Fisher's Exact Test for Count Data

data: PSPdf\$Sex and PSPdf\$RTQUIC
p-value = 0.686
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
0.2384413 13.5110071
sample estimates:
odds ratio
1.636637

Fisher's Exact Test for Count Data

data: PSPdf\$APOEe4 and PSPdf\$RTQUIC

```
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
  0.08937451 12.95765657
sample estimates:
odds ratio
  1.285414
```

Fisher's Exact Test for Count Data

```
data: PSPdf$Parkinsonian_onset and PSPdf$RTQUIC
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
  0.157035 16.475021
sample estimates:
odds ratio
  1.274496
```

Fisher's Exact Test for Count Data

```
data: PSPdf$Tremor_binary and PSPdf$RTQUIC
p-value = 0.6776
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
  0.2897147 16.4540308
sample estimates:
odds ratio
  1.98554
```

Fisher's Exact Test for Count Data

```
data: PSPdf$LimbRigidity and PSPdf$RTQUIC
p-value = 0.3107
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
  0.03036191 3.04869702
sample estimates:
odds ratio
  0.3095039
```

Fisher's Exact Test for Count Data

```
data: PSPdf$Slowness_binary and PSPdf$RTQUIC
p-value = 0.4974
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
  0.00447247 33.01630326
```

sample estimates:
odds ratio
0.3838855

Fisher's Exact Test for Count Data

data: PSPdf\$LP2_falls_PI and PSPdf\$RTQUIC
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
0.01027188 Inf
sample estimates:
odds ratio
Inf

Fisher's Exact Test for Count Data

data: PSPdf\$LP2_gait and PSPdf\$RTQUIC
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
0.03528132 52.36689579
sample estimates:
odds ratio
0.7850664

Fisher's Exact Test for Count Data

data: PSPdf\$RBD_binary and PSPdf\$RTQUIC
p-value = 0.003419
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
2.179296 Inf
sample estimates:
odds ratio
Inf

Fisher's Exact Test for Count Data

data: PSPdf\$Lifetime_Dopa_responder_true and PSPdf\$RTQUIC
p-value = 0.3047
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
0.2826482 57.3397574
sample estimates:
odds ratio
3.470449

Fisher's Exact Test for Count Data

```
data: PSPdf$Lifetime_VisualHallucinations_binary and PSPdf$RTQUIC
p-value = 0.6056
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.1252442 20.7164164
sample estimates:
odds ratio
 1.8428
```

Fisher's Exact Test for Count Data

```
data: PSPdf$Constipation_binary and PSPdf$RTQUIC
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.06069795 6.36800803
sample estimates:
odds ratio
 0.7846237
```

Fisher's Exact Test for Count Data

```
data: PSPdf$Urinary_binary and PSPdf$RTQUIC
p-value = 0.6056
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.0482709 7.9844016
sample estimates:
odds ratio
 0.5426526
```

Fisher's Exact Test for Count Data

```
data: PSPdf$Bowel_binary and PSPdf$RTQUIC
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.01017649 7.47489134
sample estimates:
odds ratio
 0.5820007
```

```
#####
#####
```

```
##### 8.2.5. BOTH DX NUMERICAL VARIABLES #####
#####
#####
#####
----- GET FROM SECTIONS 5.2. -----
-----
```

```
#####
#####
##### 8.2.6. BOTH DX CATEGORICAL VARIABLES #####
#####
#####
----- GOES IN eTABLE 1: ASYN-SAA+ vs ASYN-SAA- -----
-----
```

```
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Sex      n
  <fct>      <chr> <int>
1 aSyn-SAA negative F      20
2 aSyn-SAA negative M      25
3 aSyn-SAA positive F      12
4 aSyn-SAA positive M      10
# A tibble: 6 × 3
# Groups:   RTQUIC [2]
  RTQUIC      APOEε4      n
  <fct>      <fct> <int>
1 aSyn-SAA negative Negative    31
2 aSyn-SAA negative Positive    11
3 aSyn-SAA negative NA          3
4 aSyn-SAA positive Negative    16
5 aSyn-SAA positive Positive     3
6 aSyn-SAA positive NA          3
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Parkinsonian_onset      n
  <fct>      <chr> <int>
1 aSyn-SAA negative No            23
2 aSyn-SAA negative Yes           22
3 aSyn-SAA positive No            12
4 aSyn-SAA positive Yes           10
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Tremor_binary      n
  <fct>      <chr> <int>
1 aSyn-SAA negative No            26
2 aSyn-SAA negative Yes           19
3 aSyn-SAA positive No            13
4 aSyn-SAA positive Yes            9
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
```

```

RTQUIC          RestTremor      n
<fct>           <chr>          <int>
1 aSyn-SAA negative No          42
2 aSyn-SAA negative Yes         3
3 aSyn-SAA positive No         20
4 aSyn-SAA positive Yes         2
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
RTQUIC          LimbRigidity     n
<fct>           <chr>          <int>
1 aSyn-SAA negative No          11
2 aSyn-SAA negative Yes        34
3 aSyn-SAA positive No         10
4 aSyn-SAA positive Yes        12
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
RTQUIC          Slowness_binary  n
<fct>           <chr>          <int>
1 aSyn-SAA negative No           6
2 aSyn-SAA negative Yes        39
3 aSyn-SAA positive No           5
4 aSyn-SAA positive Yes       17
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
RTQUIC          LP2_falls_PI     n
<fct>           <chr>          <int>
1 aSyn-SAA negative No           7
2 aSyn-SAA negative Yes        38
3 aSyn-SAA positive No           6
4 aSyn-SAA positive Yes       16
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
RTQUIC          LP2_gait         n
<fct>           <chr>          <int>
1 aSyn-SAA negative No          10
2 aSyn-SAA negative Yes         35
3 aSyn-SAA positive No          10
4 aSyn-SAA positive Yes         12
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
RTQUIC          RBD_binary         n
<fct>           <chr>          <int>
1 aSyn-SAA negative No          44
2 aSyn-SAA negative Yes           1
3 aSyn-SAA positive No          16
4 aSyn-SAA positive Yes           6
# A tibble: 6 × 3
# Groups:   RTQUIC [2]
RTQUIC          Lifetime_Dopa_responder_true  n
<fct>           <chr>          <int>
1 aSyn-SAA negative No          14
2 aSyn-SAA negative Yes           6

```



```

3 aSyn-SAA negative NA 25
4 aSyn-SAA positive No 6
5 aSyn-SAA positive Yes 3
6 aSyn-SAA positive NA 13
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Lifetime_VisualHallucinations_binary  n
  <fct>      <chr>                                <int>
1 aSyn-SAA negative No 41
2 aSyn-SAA negative Yes 4
3 aSyn-SAA positive No 17
4 aSyn-SAA positive Yes 5
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Constipation_binary  n
  <fct>      <lgl>                    <int>
1 aSyn-SAA negative FALSE 36
2 aSyn-SAA negative TRUE 9
3 aSyn-SAA positive FALSE 20
4 aSyn-SAA positive TRUE 2
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Sexual_binary  n
  <fct>      <lgl>            <int>
1 aSyn-SAA negative FALSE 42
2 aSyn-SAA negative TRUE 3
3 aSyn-SAA positive FALSE 21
4 aSyn-SAA positive TRUE 1
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Urinary_binary  n
  <fct>      <lgl>            <int>
1 aSyn-SAA negative FALSE 22
2 aSyn-SAA negative TRUE 23
3 aSyn-SAA positive FALSE 11
4 aSyn-SAA positive TRUE 11
# A tibble: 4 × 3
# Groups:   RTQUIC [2]
  RTQUIC      Bowel_binary  n
  <fct>      <lgl>            <int>
1 aSyn-SAA negative FALSE 38
2 aSyn-SAA negative TRUE 7
3 aSyn-SAA positive FALSE 19
4 aSyn-SAA positive TRUE 3

```

Pearson's Chi-squared test with Yates' continuity correction

```

data: table(df$Sex, df$RTQUIC)
X-squared = 0.26722, df = 1, p-value = 0.6052

```

Fisher's Exact Test for Count Data

```
data: df$APOEε4 and df$RTQUIC
p-value = 0.5164
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.08370541 2.43483909
sample estimates:
odds ratio
 0.5335897
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: table(df$Parkinsonian_onset, df$RTQUIC)
X-squared = 1.5106e-05, df = 1, p-value = 0.9969
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: table(df$Tremor_binary, df$RTQUIC)
X-squared = 0, df = 1, p-value = 1
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: table(df$LimbRigidity, df$RTQUIC)
X-squared = 2.1333, df = 1, p-value = 0.1441
```

Fisher's Exact Test for Count Data

```
data: df$Slowness_binary and df$RTQUIC
p-value = 0.4834
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.115735 2.509391
sample estimates:
odds ratio
 0.5285138
```

Fisher's Exact Test for Count Data

```
data: df$LP2_falls_PI and df$RTQUIC
p-value = 0.3271
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.1204831 2.0925592
sample estimates:
odds ratio
 0.4968569
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: table(df$LP2_gait, df$RTQUIC)
X-squared = 2.7799, df = 1, p-value = 0.09545
```

Fisher's Exact Test for Count Data

```
data: df$RBD_binary and df$RTQUIC
p-value = 0.004057
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 1.715434 772.058733
sample estimates:
odds ratio
15.75251
```

Fisher's Exact Test for Count Data

```
data: df$Lifetime_Dopa_responder_true and df$RTQUIC
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.1403631 8.0655487
sample estimates:
odds ratio
1.160399
```

Fisher's Exact Test for Count Data

```
data: df$Lifetime_VisualHallucinations_binary and df$RTQUIC
p-value = 0.1415
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.5616313 16.8749320
sample estimates:
odds ratio
2.959418
```

Fisher's Exact Test for Count Data

```
data: df$Constipation_binary and df$RTQUIC
p-value = 0.3165
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.03891295 2.24031974
sample estimates:
odds ratio
```

0.4048595

Fisher's Exact Test for Count Data

```
data: df$Sexual_binary and df$RTQUIC
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.01213466 8.94481037
sample estimates:
odds ratio
 0.6704391
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: table(df$Urinary_binary, df$RTQUIC)
X-squared = 0, df = 1, p-value = 1
```

Fisher's Exact Test for Count Data

```
data: df$Bowel_binary and df$RTQUIC
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.1289181 4.3125694
sample estimates:
odds ratio
 0.8590504
```


#####

8.2.7. RADAR PLOTS #####

#####

----- GOES IN FIGURE 1C: ASYN-SAA+ vs ASYN-SAA- -----

```
[1] "aSyn-SAA positive"
[1] "aSyn-SAA negative"
[1] 28.571429 7.142857 50.000000 71.428571 64.285714 35.714286 57.142857
[1] 40 4 68 80 64 68 76
```

	Tremor	Rest	Limb	Slowness	Apraxia	Gait
Max	100.00000	100.00000	100	100.00000	100.00000	100.00000
Min	0.00000	0.00000	0	0.00000	0.00000	0.00000
aSyn-SAA negative	28.57143	7.142857	50	71.42857	64.28571	35.71429
aSyn-SAA positive	40.00000	4.00000	68	80.00000	64.00000	68.00000
Falls						

```

Max          100.00000
Min           0.00000
aSyn-SAA negative  57.14286
aSyn-SAA positive  76.00000
[1] "aSyn-SAA positive"
[1] "aSyn-SAA negative"
[1] 62.5 12.5 62.5 87.5 87.5 87.5 87.5 100.0
[1] 45 10 85 90 95 95 90 95
      Tremor Rest Limb Axial Slowness OM Gait Falls
Max      100.0 100.0 100.0 100.0 100.0 100.0 100.0 100
Min         0.0  0.0  0.0  0.0  0.0  0.0  0.0  0
aSyn-SAA negative  62.5 12.5 62.5 87.5 87.5 87.5 87.5 100
aSyn-SAA positive  45.0 10.0 85.0 90.0 95.0 95.0 90.0 95
pdf
  2

```

```

#####
#####
9. BINARY LOGISTIC REGRESSION
#####
#####

```

```

----- GOES IN TEXT - RESULTS - LOGISTIC REGRESSION -----
-----

```

```

Call:
glm(formula = RTQUIC_BLR ~ DX_APD + scale(Onset_age) * scale(logabeta) +
     RBD_binary + LP2_gait + scale(logNFL), family = binomial(logit),
     data = dfblr)

```

```

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    0.2373     0.6490   0.366  0.71459
DX_APDPSP     -1.4575     0.9908  -1.471  0.14128
scale(Onset_age)  1.5575     0.6583   2.366  0.01799 *
scale(logabeta)  0.7127     0.5850   1.218  0.22304
RBD_binaryYes    5.1058     1.6350   3.123  0.00179 **
LP2_gaitYes     -2.7869     1.0824  -2.575  0.01003 *
scale(logNFL)   -0.7345     0.4956  -1.482  0.13831
scale(Onset_age):scale(logabeta)  1.0211     0.5067   2.015  0.04387 *
---

```

```

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

(Dispersion parameter for binomial family taken to be 1)

```

```

Null deviance: 81.792 on 64 degrees of freedom
Residual deviance: 49.759 on 57 degrees of freedom
AIC: 65.759

```

Number of Fisher Scoring iterations: 6

```
[1] 65.75874
[1] 68.55218
[1] 66.2534
[1] 66.5125
[1] 66.5125
[1] 72.87027
[1] 79.97648
```

fitting null model for pseudo-r2

McFadden

0.3916408

DX_APD	scale(Onset_age)	RBD_binary	LP2_gait
1.347620	2.441283	1.503927	2.124081

scale(logNFL)	DX_APD	scale(logabeta)	RBD_binary	LP2_gait	scale(logNFL)
1.068010	1.233808	1.569275	1.247782	1.164635	1.289880

DX_APD	scale(Onset_age)	scale(logabeta)	RBD_binary
1.309351	2.522389	1.749046	1.587635

LP2_gait	scale(logNFL)
2.057364	1.370489

there are higher-order terms (interactions) in this model

consider setting type = 'predictor'; see ?vif

DX_APD	scale(Onset_age)
1.627432	3.128605

scale(logabeta)	RBD_binary
2.676131	1.734627

LP2_gait	scale(logNFL)
2.290486	1.874543

scale(Onset_age):scale(logabeta)
1.568962

lag Autocorrelation D-W Statistic p-value

1 -0.0592418 2.116274 0.788

Alternative hypothesis: rho != 0

	Overall
DX_APDPSP	1.471025
scale(Onset_age)	2.365896
scale(logabeta)	1.218474
RBD_binaryYes	3.122778
LP2_gaitYes	2.574706
scale(logNFL)	1.482103
scale(Onset_age):scale(logabeta)	2.015318

```
`geom_smooth()` using formula = 'y ~ x'
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
`geom_smooth()` using formula = 'y ~ x'
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
`geom_smooth()` using formula = 'y ~ x'
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

Call:

glm(formula = RTQUIC_BLR ~ DX_APD + scale(Onset_age) * scale(logabeta) +

```
RBD_binary + LP2_gait + scale(logNFL), family = binomial(logit),
data = dfabetablrr)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.2304	0.7137	0.323	0.74679
DX_APDPSP	-0.8659	1.0131	-0.855	0.39273
scale(Onset_age)	2.0910	0.8201	2.550	0.01078 *
scale(logabeta)	0.9847	0.6890	1.429	0.15296
RBD_binaryYes	7.0648	2.3168	3.049	0.00229 **
LP2_gaitYes	-3.5014	1.3505	-2.593	0.00953 **
scale(logNFL)	-1.3361	0.6520	-2.049	0.04043 *
scale(Onset_age):scale(logabeta)	0.3437	0.6383	0.538	0.59029

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 77.138 on 62 degrees of freedom
Residual deviance: 41.885 on 55 degrees of freedom
AIC: 57.885

Number of Fisher Scoring iterations: 6

[1] 57.8853

```
`geom_smooth()` using formula = 'y ~ x'
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
`geom_smooth()` using formula = 'y ~ x'
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
`geom_smooth()` using formula = 'y ~ x'
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

RTQUIC AD Early_onset logabeta

1 aSyn-SAA positive AD Positive Late-onset 7.068870

2 aSyn-SAA positive AD Positive Young-onset 4.828314

The following IDs are removed based on Abeta42 values for the corrected logistic regression model with better diagnostics: 7.06887 4.828314

The issue is, both are aSyn-SAA+ (bringing down total number of aSyn-SAA+ to 20 instead of 22 (aSyn-SAA+ is the outcome measure for this model),

but 1 especially is one of the 8 aSyn-SAA+/young-onset, 7 aSyn-SAA+/AD+, and 5 aSyn-SAA+/AD+. We already know from Fig 1A that these combinations are rare

but they are of interest in our cohort due to 1. hypothesis 2. results of frequency analyses (categorical tests on AD+ vs Young-onset, so removing a subject that meets all these criteria would in itself be an issue.

Removing extreme Abeta42 values (even not identified by Tukey method) improves assumption testing output. It removes important information from the model though as it reduces significantly groups that were already underrepresented but of interest.

In this iteration, Onset age, Gait, RBD, and NfL are significantly predictors of aSyn-SAA+, but not Abeta 42.

Call:

```
glm(formula = RTQUIC_BLR ~ scale(Onset_age) * scale(logabeta) +
```

```
RBD_binary + LP2_gait, family = binomial(logit), data = dfblr)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.2561	0.5874	0.436	0.66288
scale(Onset_age)	1.5387	0.6084	2.529	0.01144 *
scale(logabeta)	0.1732	0.4037	0.429	0.66792
RBD_binaryYes	4.0981	1.4490	2.828	0.00468 **
LP2_gaitYes	-3.0127	1.0204	-2.952	0.00315 **
scale(Onset_age):scale(logabeta)	0.6276	0.3666	1.712	0.08690 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 81.792 on 64 degrees of freedom
Residual deviance: 54.768 on 59 degrees of freedom
AIC: 66.768

Number of Fisher Scoring iterations: 6

[1] 66.76798

```
`geom_smooth()` using formula = 'y ~ x'
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

```
`geom_smooth()` using formula = 'y ~ x'
```

```
`geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

Removing variables overall improves assumption testing output, except at very high age at onset(>80).

In this iteration, Onset age, Gait, and RBD are significantly predictors of aSyn-SAA+. Onset age by Abeta42 is significant at a 90% confidence level.

It is the best compromise between reducing violation of assumptions and representativity of the sample. It also reduces the issue of overfitting.

For the reasons above, no further efforts towards prediction are performed. OR will be given for scale. Visualization of the model is kept here for interpretation

but not included in the manuscript. Influence of outliers should be highlighted, but to remove them entirely would also be inappropriate.

Consistently significant effect of: Age at onset; Gait; and RBD.

(Intercept)	DX_APDPSP
0.2373303	-1.4575350
scale(Onset_age)	scale(logabeta)
1.5575150	0.7127483
RBD_binaryYes	LP2_gaitYes
5.1058142	-2.7869085
scale(logNFL)	scale(Onset_age):scale(logabeta)
-0.7344995	1.0210788
(Intercept)	DX_APDPSP
1.26785980	0.23280943
scale(Onset_age)	scale(logabeta)
4.74701012	2.03958891
RBD_binaryYes	LP2_gaitYes
164.97833640	0.06161139


```

                scale(logNFL) scale(Onset_age):scale(logabeta)
                0.47974549                2.77618822
Waiting for profiling to be done...

(odds_ratio      2.5 %
(Intercept)      0.2373303 1.26785980 0.352389256
DX_APDPSP        -1.4575350 0.23280943 0.025719856
scale(Onset_age) 1.5575150 4.74701012 1.505991556
scale(logabeta)   0.7127483 2.03958891 0.717141165
RBD_binaryYes     5.1058142 164.97833640 10.502297767
LP2_gaitYes       -2.7869085 0.06161139 0.005408024
scale(logNFL)     -0.7344995 0.47974549 0.153426284
scale(Onset_age):scale(logabeta) 1.0210788 2.77618822 1.109929368

```

```

                97.5 %
(Intercept)      4.8004636
DX_APDPSP        1.3915122
scale(Onset_age) 21.0904655
scale(logabeta)   7.4954446
RBD_binaryYes     8048.0626595
LP2_gaitYes       0.4092119
scale(logNFL)     1.1280402
scale(Onset_age):scale(logabeta) 8.8301725

```

```

                scale(Onset_age)
                0.2560521                1.5387101
                scale(logabeta)                RBD_binaryYes
                0.1732093                4.0981456
                LP2_gaitYes scale(Onset_age):scale(logabeta)
                -3.0126710                0.6276367
                (Intercept)                scale(Onset_age)
                1.2918200                4.6585773
                scale(logabeta)                RBD_binaryYes
                1.1891150                60.2284990
                LP2_gaitYes scale(Onset_age):scale(logabeta)
                0.0491602                1.8731784

```

```

Waiting for profiling to be done...

(odds_ratio      2.5 %      97.5 %
(Intercept)      0.2560521 1.2918200 0.411869833 4.3213617
scale(Onset_age) 1.5387101 4.6585773 1.602984464 18.1236359
scale(logabeta)   0.1732093 1.1891150 0.543441718 2.7253072
RBD_binaryYes     4.0981456 60.2284990 5.233289945 1965.7979098
LP2_gaitYes       -3.0126710 0.0491602 0.005025569 0.2946814
scale(Onset_age):scale(logabeta) 0.6276367 1.8731784 0.909549983 4.0258168

```

```

#####
#####
10. RTQUIC PARAMETERS SUPP ANALYSES
#####
#####

```

```
#####  
#####
```

10.1. RTQUIC PARAMETERS SUPP: LAG

```
#####  
#####
```

```
----- GOES IN REVIEW -----  
-----
```

Lag hours is the #hours required to reach max ThT. It makes the most sense to think about it as data suited for survival analysis.
For that purpose, we are censoring the subjects who never reached positivity (RT QUIC negative) as max ThT is not something that exists in this case
(they plateau early on in the analysis as their curve never rises – so comparign them to RT-QUIC+ subjects would not make sense.)

Shapiro-Wilk normality test

```
data: df[RTposdf$DX_APD == "CBS", ]$RTQUIC_survival_hours  
W = 0.73185, p-value = 2.072e-07
```

Shapiro-Wilk normality test

```
data: df[RTposdf$DX_APD == "PSP", ]$RTQUIC_survival_hours  
W = 0.52728, p-value = 7.026e-08
```

Shapiro-Wilk normality test

```
data: df[RTposdf$Early_onset == "Young-onset", ]$RTQUIC_survival_hours  
W = 0.80118, p-value = 0.000308
```

Shapiro-Wilk normality test

```
data: df[RTposdf$Early_onset == "Late-onset", ]$RTQUIC_survival_hours  
W = 0.56702, p-value = 4.661e-10
```

Shapiro-Wilk normality test

```
data: df[RTposdf$AD == "AD Positive", ]$RTQUIC_survival_hours  
W = 0.8159, p-value = 0.00116
```

Shapiro-Wilk normality test

```
data: df[RTposdf$AD == "AD Negative", ]$RTQUIC_survival_hours  
W = 0.57171, p-value = 2.279e-10
```

Levene's Test for Homogeneity of Variance (center = median)
Df F value Pr(>F)

```
group 1 0.6338 0.4353
      20
```

Warning message:

```
In leveneTest.default(y = y, group = group, ...) : group coerced to factor.
Levene's Test for Homogeneity of Variance (center = median)
```

```
      Df F value Pr(>F)
group 1 0.3208 0.5775
      20
```

Levene's Test for Homogeneity of Variance (center = median)

```
      Df F value Pr(>F)
group 1 0.2545 0.6194
      20
```

Warning message:

```
In leveneTest.default(y = y, group = group, ...) : group coerced to factor.
```

```
count format(round(median(RTQUIC_survival_hours, na.rm = T), 2), 2) IQR
1 22 27.88 6.625
min max
1 16.5 40
```

A tibble: 2 × 6

	DX_APD	count	format(round(median(RTQUIC_survival_hours, na.rm = T), 2), 2)	IQR	min	max
	<chr>	<int>	<chr>	<dbl>	<dbl>	<dbl>
1	CBS	14	31.5	8	26	40
2	PSP	8	24.75	3.12	16.5	31.5

i abbreviated name:

```
# 1 `format(round(median(RTQUIC_survival_hours, na.rm = T), 2), 2)`
count format(round(median(RTQUIC_survival_hours, na.rm = T), 2), 2) IQR
1 22 27.88 6.625
min max
1 16.5 40
```

A tibble: 2 × 6

	AD	count	format(round(median(RTQUIC_survival_hours, na.rm = T), 2), 2)	IQR	min	max
	<chr>	<int>	<chr>	<dbl>	<dbl>	<dbl>
1	AD Negative	15	26.25	6.75	16.5	40
2	AD Positive	7	32.25	5.25	26	39.8

i abbreviated name:

```
# 1 `format(round(median(RTQUIC_survival_hours, na.rm = T), 2), 2)`
count format(round(median(RTQUIC_survival_hours, na.rm = T), 2), 2) IQR
1 22 27.88 6.625
min max
1 16.5 40
```

A tibble: 2 × 6

	Early_onset	count	format(round(median(RTQUIC_survival_hours, na.rm = T), 2), 2)	IQR	min	max
	<fct>	<int>	<chr>	<dbl>	<dbl>	<dbl>
1	Late-onset	14	27.12	6.62	16.5	40
2	Young-onset	8	30.38	10.4	24.8	39.8

i abbreviated name:

```
# 1 `format(round(median(RTQUIC_survival_hours, na.rm = T), 2), 2)`
```

Spearman's rank correlation rho

data: RTposdf\$RTQUIC_survival_hours and RTposdf\$Onset_age

S = 2528.7, p-value = 0.047

```
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
-0.427841
```

```
Warning message:
In cor.test.default(RTposdf$RTQUIC_survival_hours, RTposdf$Onset_age, :
  Cannot compute exact p-value with ties
```

Spearman's rank correlation rho

```
data: RTposdf$RTQUIC_survival_hours and RTposdf$Age
S = 2351, p-value = 0.1368
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
-0.3274806
```

```
Warning message:
In cor.test.default(RTposdf$RTQUIC_survival_hours, RTposdf$Age, :
  Cannot compute exact p-value with ties
```

Spearman's rank correlation rho

```
data: RTposdf$RTQUIC_survival_hours and RTposdf$logabeta
S = 1925.5, p-value = 0.6994
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
-0.08725263
```

```
Warning message:
In cor.test.default(RTposdf$RTQUIC_survival_hours, RTposdf$logabeta, :
  Cannot compute exact p-value with ties
```

Spearman's rank correlation rho

```
data: RTposdf$RTQUIC_survival_hours and RTposdf$logNFL
S = 1620.3, p-value = 0.8224
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
-0.05215164
```

```
Warning message:
In cor.test.default(RTposdf$RTQUIC_survival_hours, RTposdf$logNFL, :
  Cannot compute exact p-value with ties
```

Spearman's rank correlation rho

```
data: RTposdf$RTQUIC_survival_hours and RTposdf$logptau
S = 856.9, p-value = 0.01393
```

```
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.5161503
```

Warning message:

```
In cor.test.default(RTposdf$RTQUIC_survival_hours, RTposdf$logptau, :
  Cannot compute exact p-value with ties
```

Spearman's rank correlation rho

```
data: RTposdf$RTQUIC_survival_hours and RTposdf$logttau
S = 1002, p-value = 0.1206
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.3493826
```

Warning message:

```
In cor.test.default(RTposdf$RTQUIC_survival_hours, RTposdf$logttau, :
  Cannot compute exact p-value with ties
```

Spearman's rank correlation rho

```
data: RTposdf$RTQUIC_survival_hours and RTposdf$ATI_2
S = 2052, p-value = 0.1409
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
-0.3324665
```

Warning message:

```
In cor.test.default(RTposdf$RTQUIC_survival_hours, RTposdf$ATI_2, :
  Cannot compute exact p-value with ties
```

Scale for **fill** is already present.

Adding another scale for **fill**, which will replace the existing scale.

Warning message:

```
No shared levels found between `names(values)` of the manual scale and the
data's colour values.
```

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Warning message:

```
No shared levels found between `names(values)` of the manual scale and the
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```

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Warning message:

```
No shared levels found between `names(values)` of the manual scale and the
data's colour values.
```

Scale for **fill** is already present.

Adding another scale for **fill**, which will replace the existing scale.

Warning messages:

```

1: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
.
2: Removed 1 row containing non-finite outside the scale range (`stat_cor()`).
3: No shared levels found between `names(values)` of the manual scale and the
data's colour values.
4: Removed 1 row containing missing values or values outside the scale range
(`geom_point()`).
Warning messages:
1: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
.
2: Removed 1 row containing non-finite outside the scale range (`stat_cor()`).
3: Removed 1 row containing missing values or values outside the scale range
(`geom_point()`).
Scale for fill is already present.
Adding another scale for fill, which will replace the existing scale.
Warning messages:
1: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
.
2: Removed 1 row containing non-finite outside the scale range (`stat_cor()`).
3: No shared levels found between `names(values)` of the manual scale and the
data's colour values.
4: Removed 1 row containing missing values or values outside the scale range
(`geom_point()`).
Warning messages:
1: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
.
2: Removed 1 row containing non-finite outside the scale range (`stat_cor()`).
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(`geom_point()`).
Scale for fill is already present.
Adding another scale for fill, which will replace the existing scale.
Warning messages:
1: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
.
2: Removed 1 row containing non-finite outside the scale range (`stat_cor()`).
3: No shared levels found between `names(values)` of the manual scale and the
data's colour values.
4: Removed 1 row containing missing values or values outside the scale range
(`geom_point()`).
Warning messages:
1: Removed 1 row containing non-finite outside the scale range (`stat_smooth()`).
.
2: Removed 1 row containing non-finite outside the scale range (`stat_cor()`).
3: Removed 1 row containing missing values or values outside the scale range
(`geom_point()`).
Call: survfit(formula = Surv(RTQUIC_survival_hours, RTQUIC_survived) ~
      Early_onset, data = df)

```

	Early_onset=Late-onset				
time	n.risk	n.event	survival	std.err	lower 95% CI
48.0000	18.0000	14.0000	0.5625	0.0877	0.4144
upper 95% CI					

0.7635

```
Early_onset=Young-onset
time      n.risk    n.event    survival    std.err lower 95% CI
48.000    27.000     8.000     0.771      0.071      0.644
upper 95% CI
0.924
```

Call:

```
survdiffformula = Surv(RTQUIC_survival_hours, RTQUIC_survived) ~
Early_onset, data = df)
```

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
Early_onset=Late-onset	32	14	9.54	2.08	3.73
Early_onset=Young-onset	35	8	12.46	1.59	3.73

Chisq= 3.7 on 1 degrees of freedom, p= 0.05

```
Call: survfit(formula = Surv(RTQUIC_survival_hours, RTQUIC_survived) ~
AD, data = df)
```

```
AD=AD Negative
time      n.risk    n.event    survival    std.err lower 95% CI
48.0000    37.0000    15.0000    0.7115      0.0628      0.5985
upper 95% CI
0.8460
```

```
AD=AD Positive
time      n.risk    n.event    survival    std.err lower 95% CI
48.000    8.000     7.000     0.533      0.129      0.332
upper 95% CI
0.856
```

Call:

```
survdiffformula = Surv(RTQUIC_survival_hours, RTQUIC_survived) ~
AD, data = df)
```

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
AD=AD Negative	52	15	17.02	0.239	1.07
AD=AD Positive	15	7	4.98	0.817	1.07

Chisq= 1.1 on 1 degrees of freedom, p= 0.3

```
Call: survfit(formula = Surv(RTQUIC_survival_hours, RTQUIC_survived) ~
DX_APD, data = df)
```

```
DX_APD=CBS
time      n.risk    n.event    survival    std.err lower 95% CI
48.0000    25.0000    14.0000    0.6410      0.0768      0.5068
upper 95% CI
0.8107
```

```
DX_APD=PSP
time      n.risk    n.event    survival    std.err lower 95% CI
```

48.0000	20.0000	8.0000	0.7143	0.0854	0.5651
---------	---------	--------	--------	--------	--------

upper 95% CI
0.9028

Call:

```
survdifff(formula = Surv(RTQUIC_survival_hours, RTQUIC_survived) ~  
DX_APD, data = df)
```

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
DX_APD=CBS	39	14	13.42	0.0254	0.066
DX_APD=PSP	28	8	8.58	0.0396	0.066

Chisq= 0.1 on 1 degrees of freedom, p= 0.8

#####

10.2. RTQUIC PARAMETERS SUPP: THT MAX

#####

THT max is the max fluorescent signal reached after 48 hours of monitoring of the assay.

Shapiro-Wilk normality test

```
data: df[RTposdf$DX_APD == "CBS", ]$ThTmax  
W = 0.97461, p-value = 0.8929
```

Shapiro-Wilk normality test

```
data: df[RTposdf$DX_APD == "PSP", ]$ThTmax  
W = 0.96251, p-value = 0.8254
```

Shapiro-Wilk normality test

```
data: df[RTposdf$Early_onset == "Young-onset", ]$ThTmax  
W = 0.98373, p-value = 0.9944
```

Shapiro-Wilk normality test

```
data: df[RTposdf$Early_onset == "Late-onset", ]$ThTmax  
W = 0.91162, p-value = 0.2923
```

Shapiro-Wilk normality test

```
data: df[RTposdf$AD == "AD Positive", ]$ThTmax  
W = 0.95514, p-value = 0.71
```