Supplementary materials

"Accurate digital quantification of tau pathology in progressive supranuclear palsy" by Tanrada Pansuwan, Annelies Quaegebeur, Sanne S. Kaalund, Eric Hidari, Mayen Briggs, James B. Rowe, and Timothy Rittman

Extra examples of correct and incorrect classification

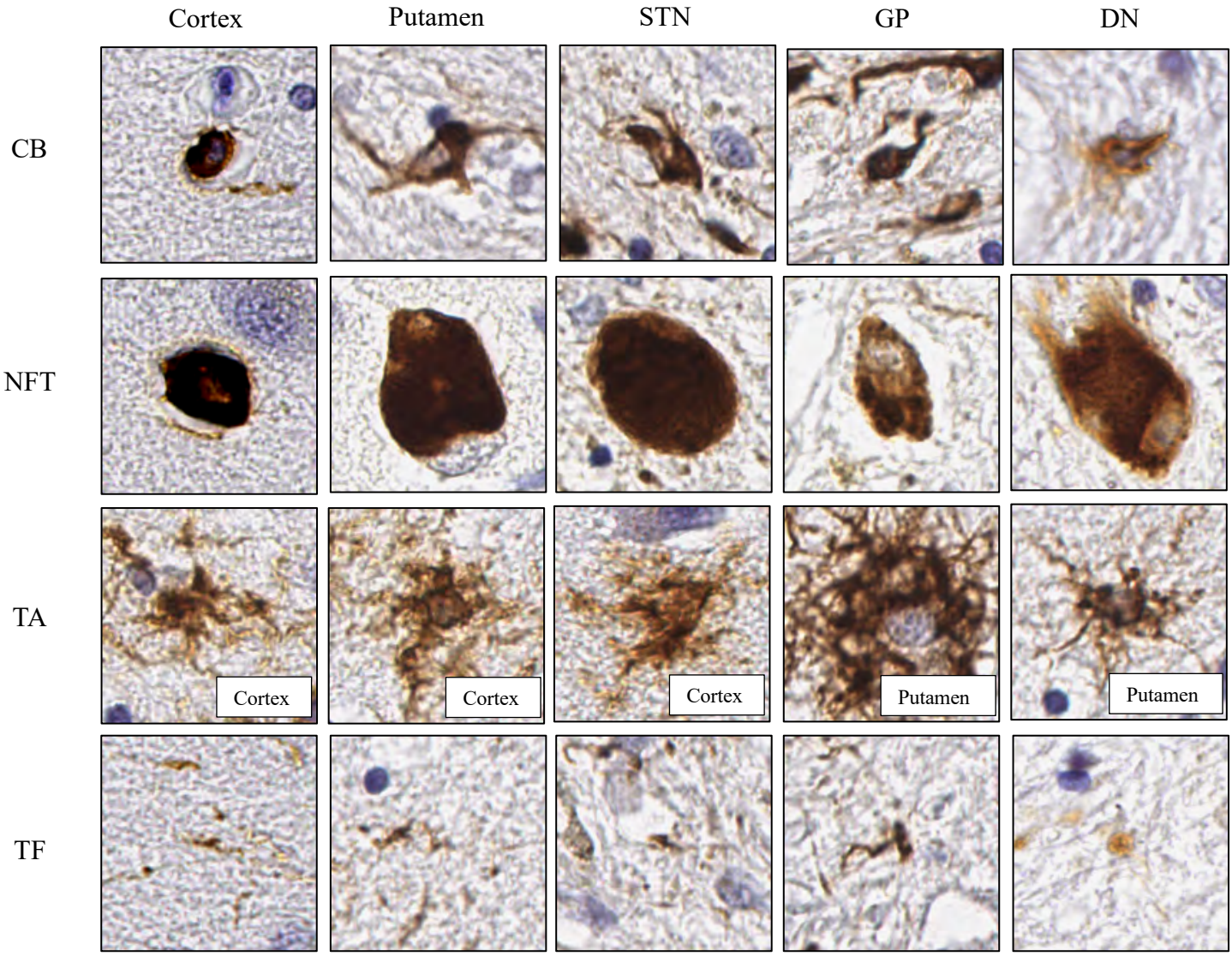


Figure 1: Examples of correct classification from the held-out test set for each tau aggregate type from the cortex, putamen, subthalamic nucleus (STN), globus pallidus (GP) and dentate nucleus (DN). All images were cropped 150 x 150 mm window size. TA examples are only drawn from the cortex and putamen. CB coiled body; NFT neurofibrillary tangle; TA tufted astrocyte; TF tau fragments.

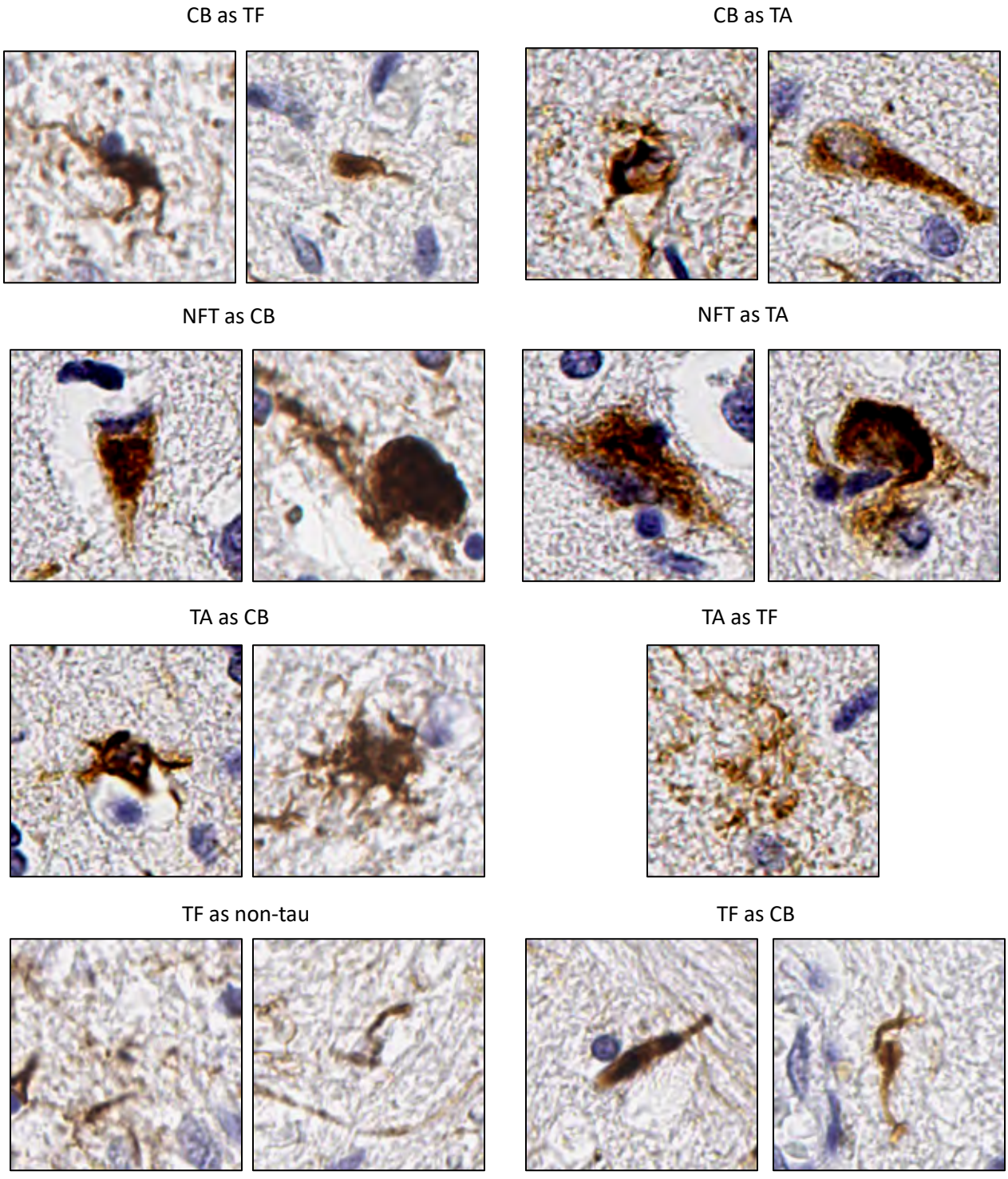
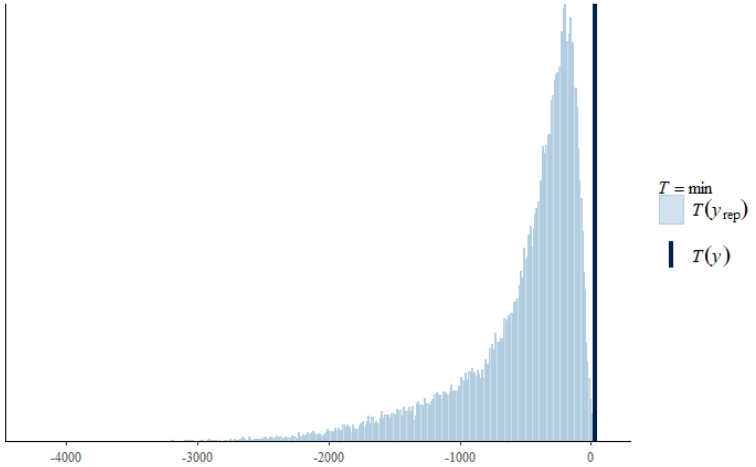


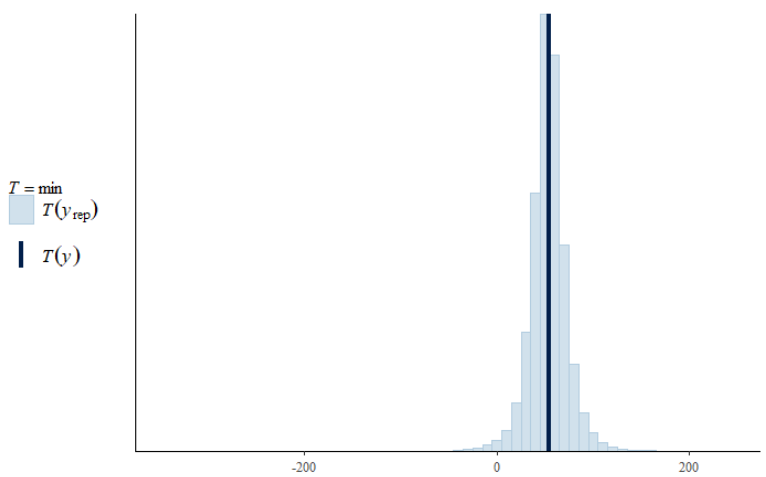
Figure 2: Example of possible misclassification observed between tau aggregate types from the held-out test set. Truth label as predicted label is presented. All images were cropped 150 x 150 mm window size. CB coiled body; NFT neurofibrillary tangle; TA tufted astrocyte; TF tau fragments.

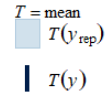
Bayesian regression results

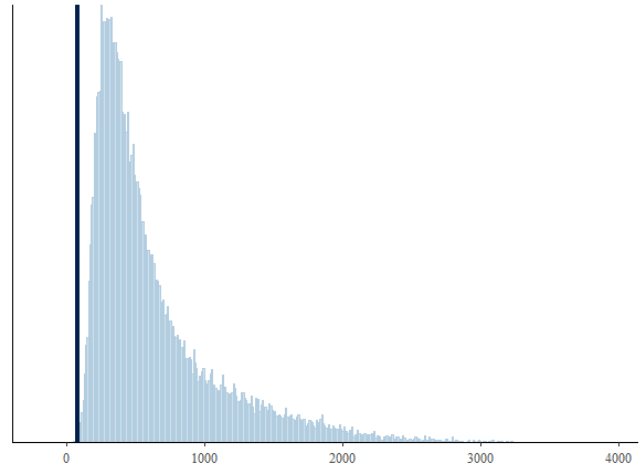
Final models only

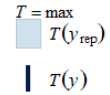
PSPRS score ~ PSP stage + disease duration + PSPRS-death interval

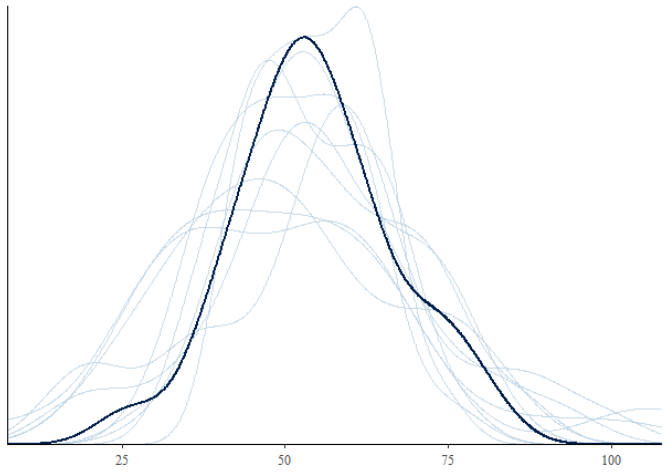













```
 Family: gaussian
  Links: mu = identity; sigma = identity
Formula: PSPRS.Total..last.assesment. ~ Stage + disease.duration..years. + years.PSPRS.and.death
   Data: data_PSPRS (Number of observations: 28)
  Draws: 4 chains, each with iter = 20000; warmup = 10000; thin = 1;
         total post-warmup draws = 40000

Population-Level Effects:
                      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                35.84      9.04    18.01    53.74 1.00    21713    25208
Stage3                    5.40     11.08   -16.44    27.20 1.00    22308    26378
Stage4                    7.68      8.68    -9.36    24.83 1.00    18989    23866
Stage5                    9.96      8.80    -7.29    27.40 1.00    18571    23418
Stage6                   29.59     11.15     7.75    51.57 1.00    22480    25702
disease.duration..years.  1.36      0.73    -0.08     2.80 1.00    33214    27678
years.PSPRS.and.death    -0.27      3.16    -6.56     6.01 1.00    31659    27764

Family Specific Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma    11.07      1.78     8.23    15.20 1.00    24687    26906

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
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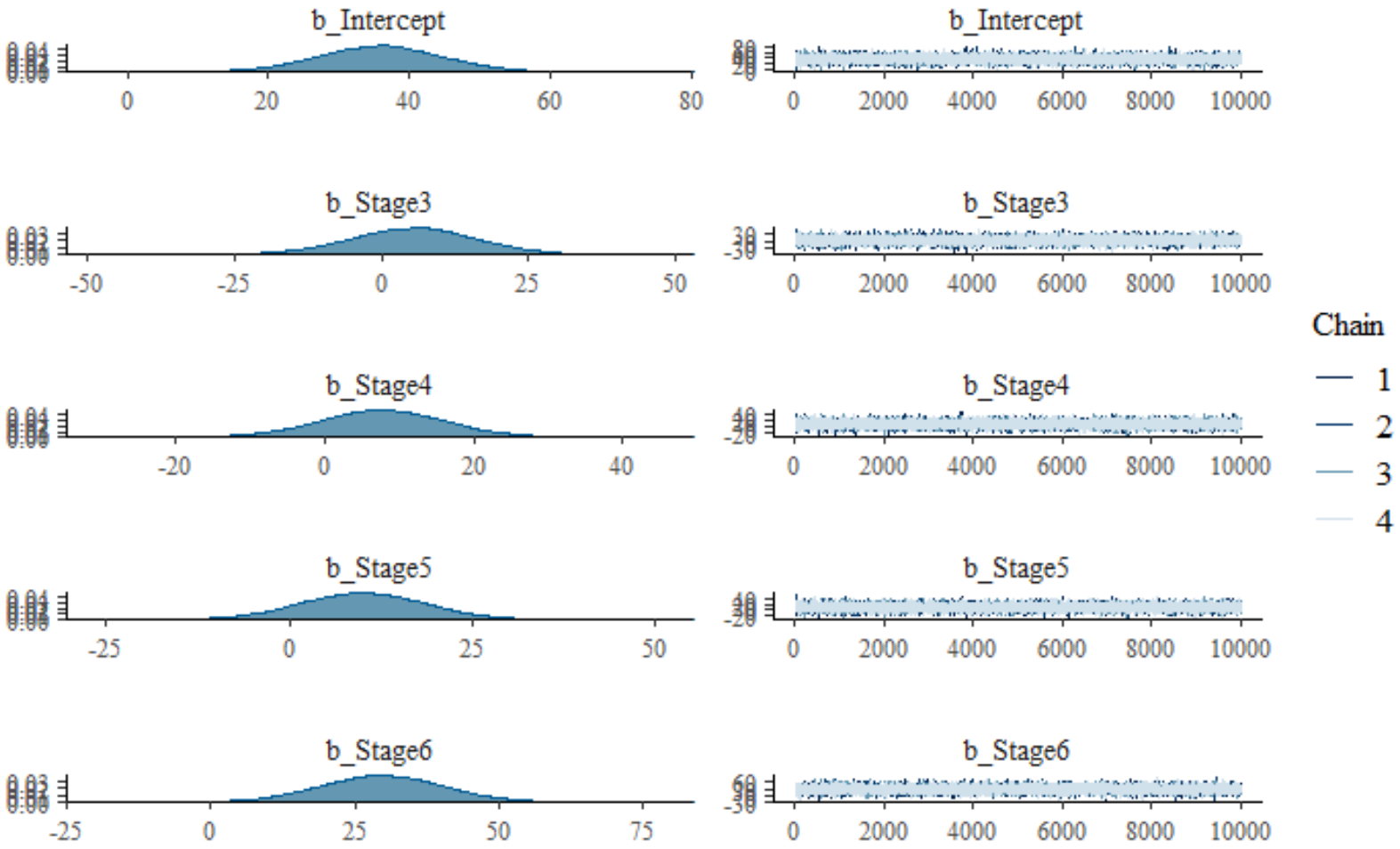
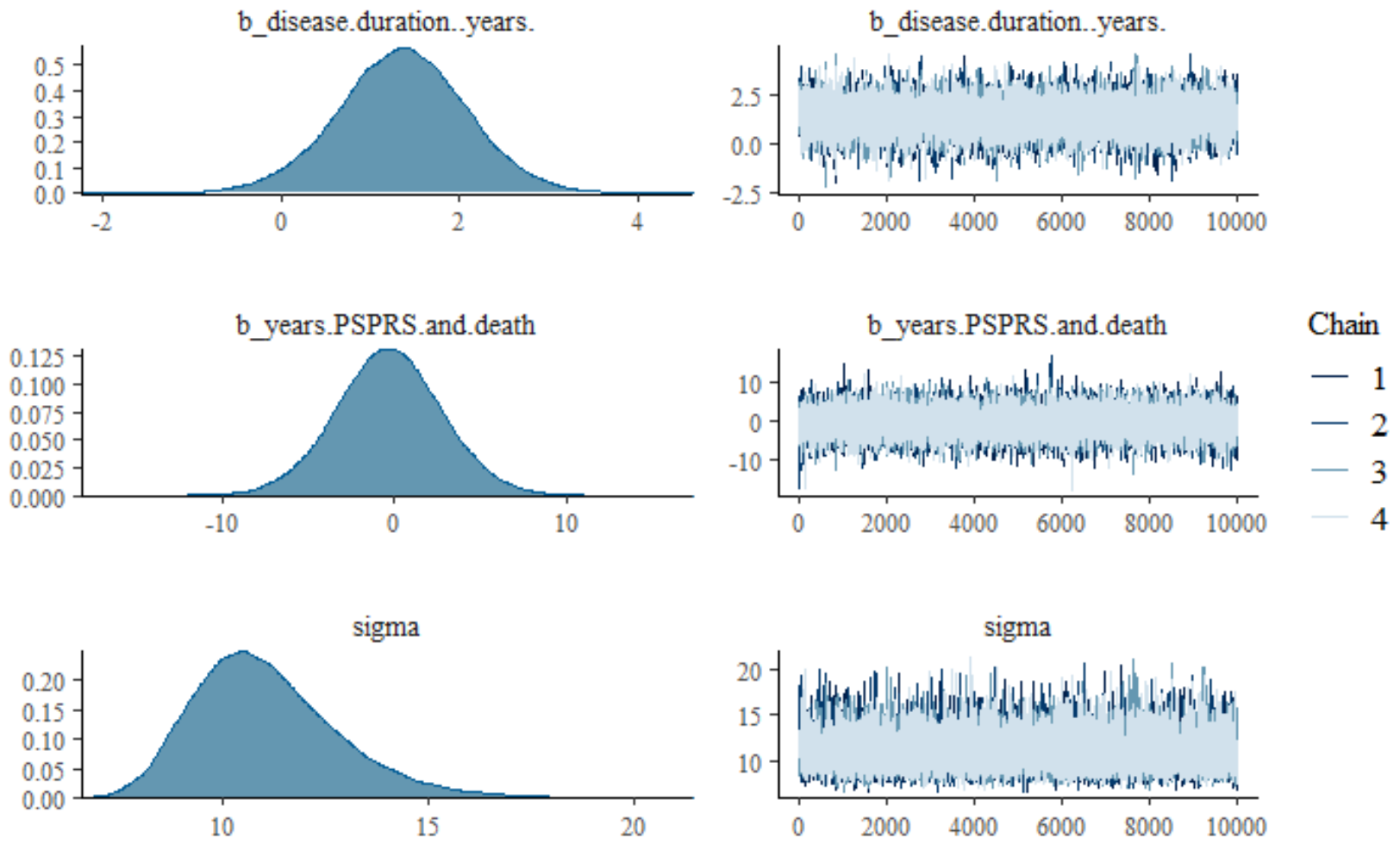
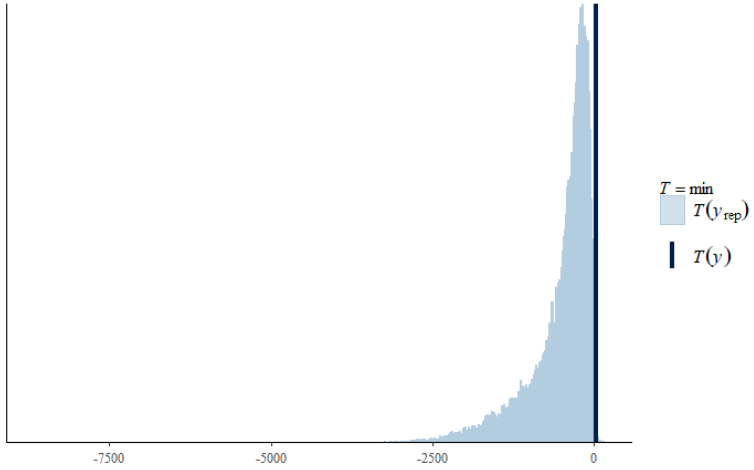
PSPRS score ~ PSP stage + disease duration + PSPRS-death interval

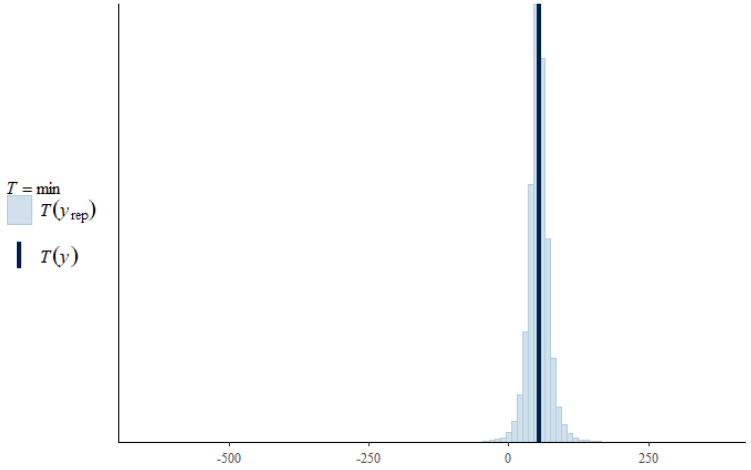


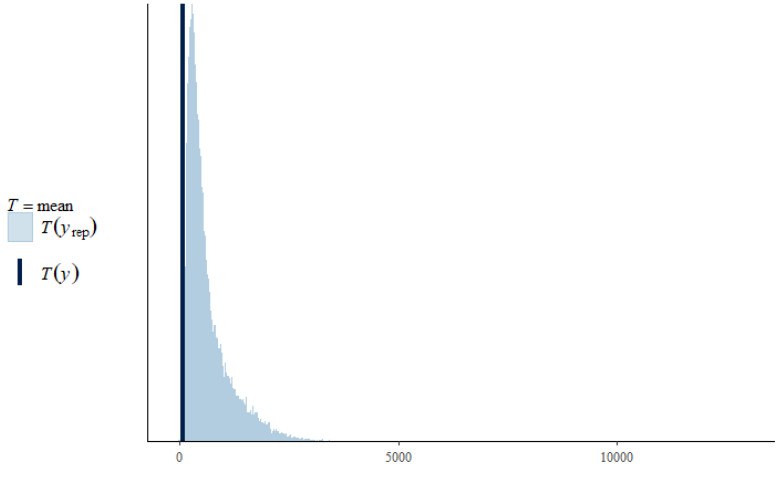
PSPRS score ~ PSP stage + disease duration + PSPRS-death interval

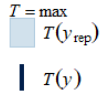


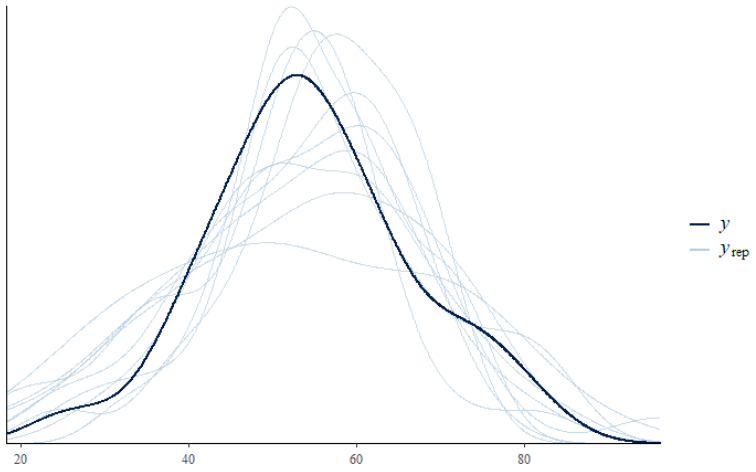
PSPRS score ~ total tau burden (all regions) + disease duration + PSPRS-death interval












```
 Family: gaussian
  Links: mu = identity; sigma = identity
Formula: PSPRS.Total..last.assesment. ~ mean_total_tau_density_log + disease.duration..years. +
years.PSPRS.and.death
   Data: selected_dat (Number of observations: 28)
  Draws: 4 chains, each with iter = 20000; warmup = 10000; thin = 1;
         total post-warmup draws = 40000

Population-Level Effects:
                          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                    91.32     24.75    42.01   140.14 1.00    44635    29960
mean_total_tau_density_log   10.93      5.52    -0.07    21.83 1.00    43093    29770
disease.duration..years.      1.95      0.76     0.46     3.45 1.00    43340    29822
years.PSPRS.and.death        -1.81      2.97    -7.64     4.13 1.00    42616    30011

Family Specific Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma    11.40      1.70     8.64    15.27 1.00    34280    28932

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
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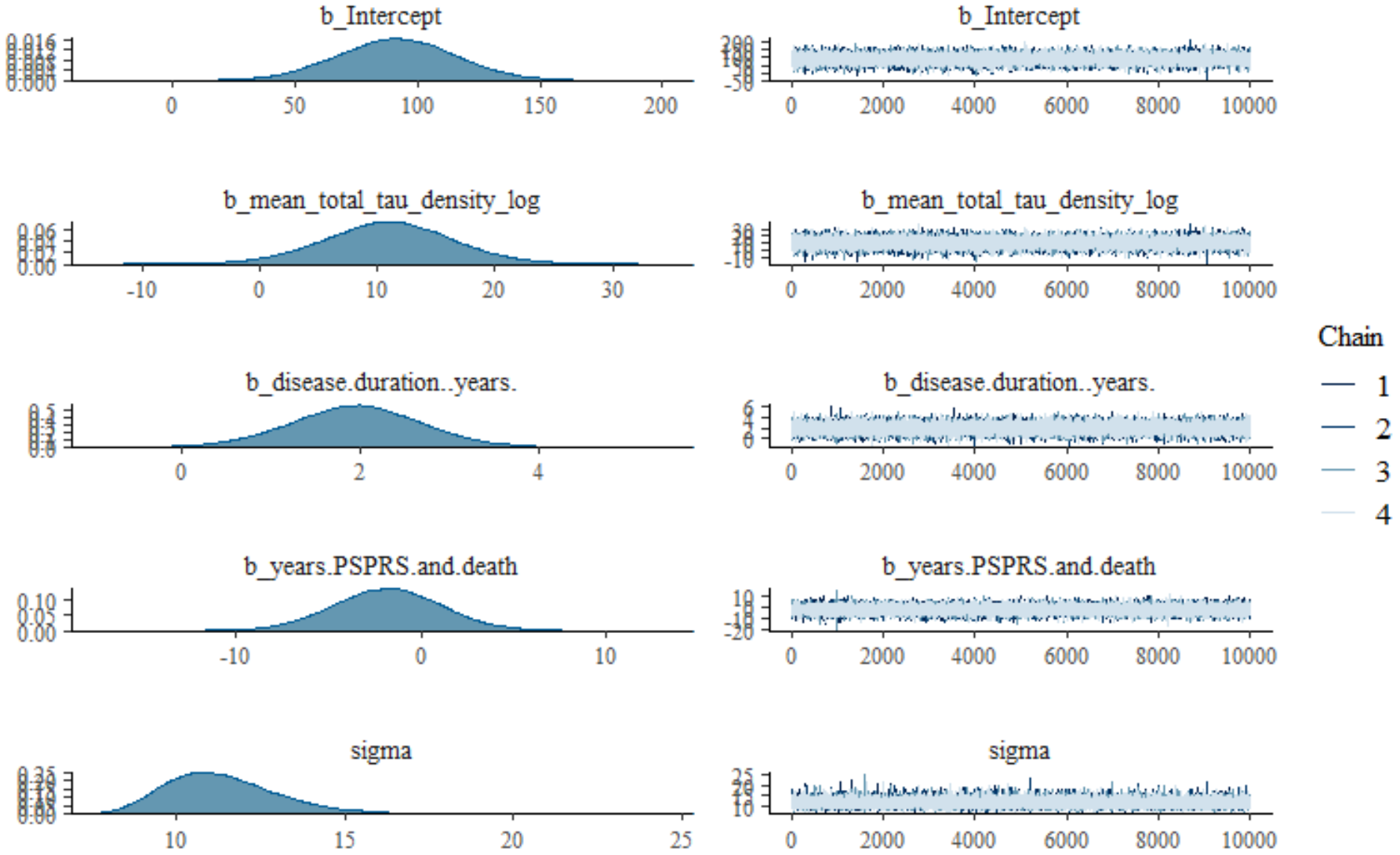
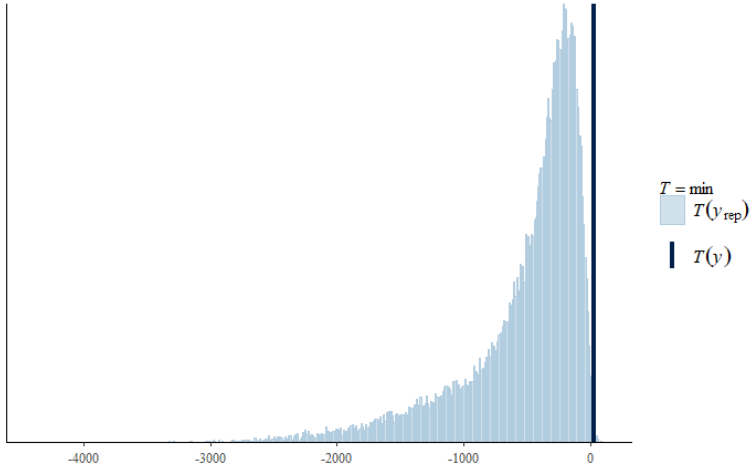
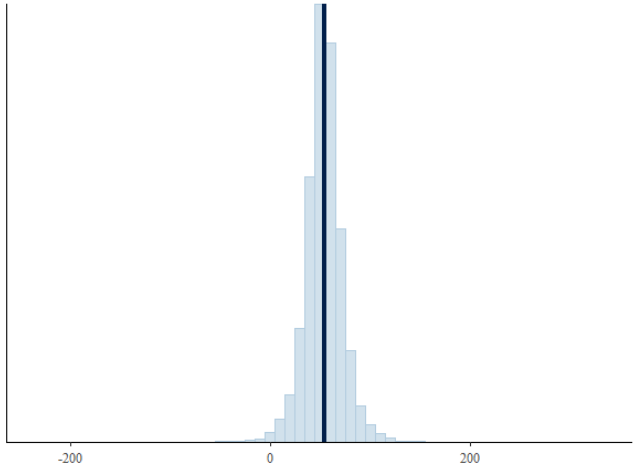
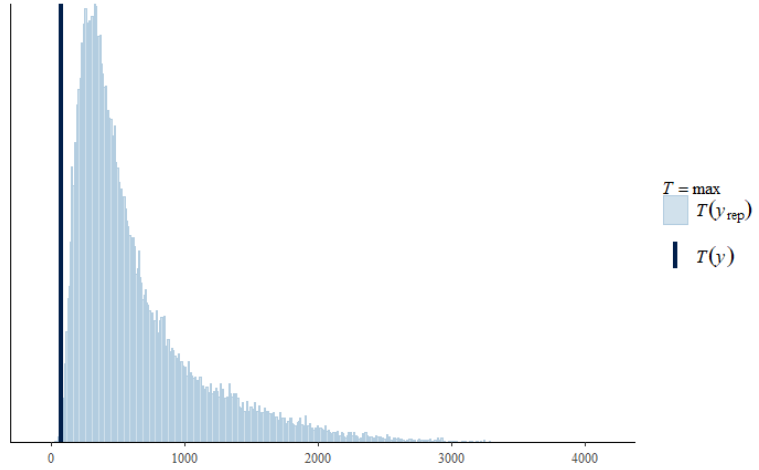
PSPRS score ~ total tau burden (all regions) + disease duration + PSPRS-death interval

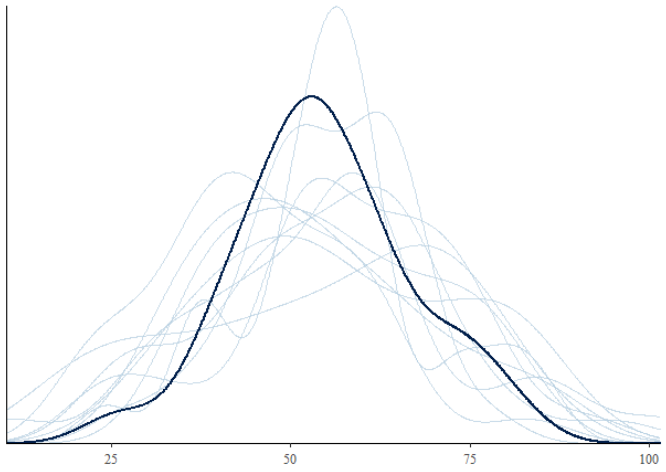


PSPRS score ~ total tau burden (cortical regions) + disease duration + PSPRS-death interval










```
 Family: gaussian
  Links: mu = identity; sigma = identity
Formula: PSPRS.Total..last.assesment. ~ mean_total_tau_density_log + disease.duration..years. +
years.PSPRS.and.death
   Data: selected_dat (Number of observations: 28)
  Draws: 4 chains, each with iter = 20000; warmup = 10000; thin = 1;
         total post-warmup draws = 40000

Population-Level Effects:
                          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                    94.11     20.32    54.24   133.95 1.00    47918    27332
mean_total_tau_density_log   10.69      4.13     2.54    18.81 1.00    47938    28093
disease.duration..years.      1.61      0.71     0.20     3.03 1.00    46485    29611
years.PSPRS.and.death        -1.12      2.75    -6.53     4.31 1.00    49023    29347

Family Specific Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma    10.86      1.62     8.21    14.56 1.00    37419    29950

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
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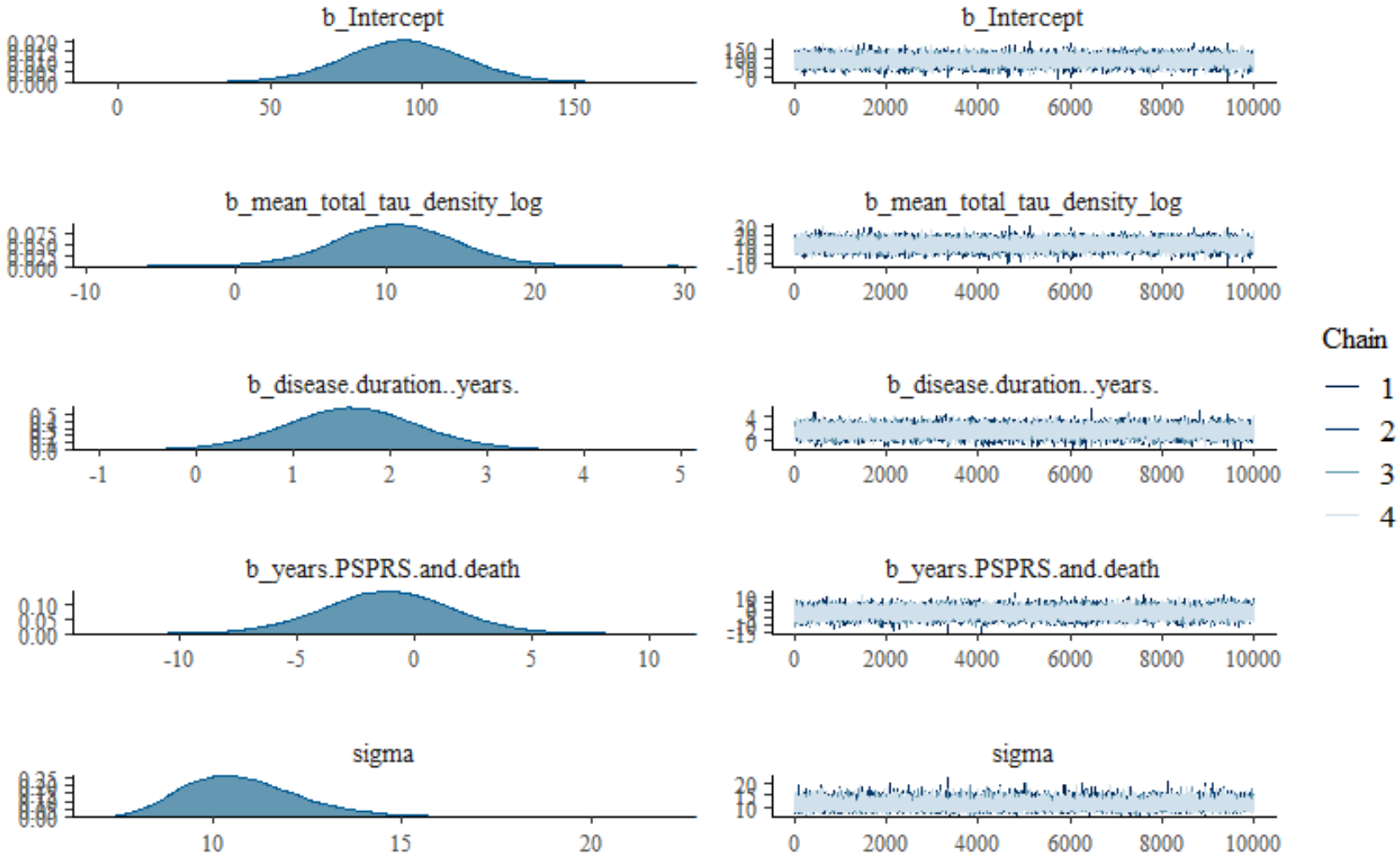
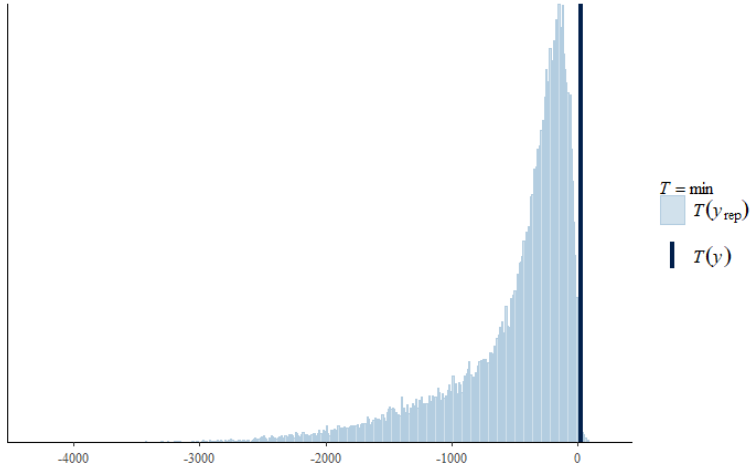
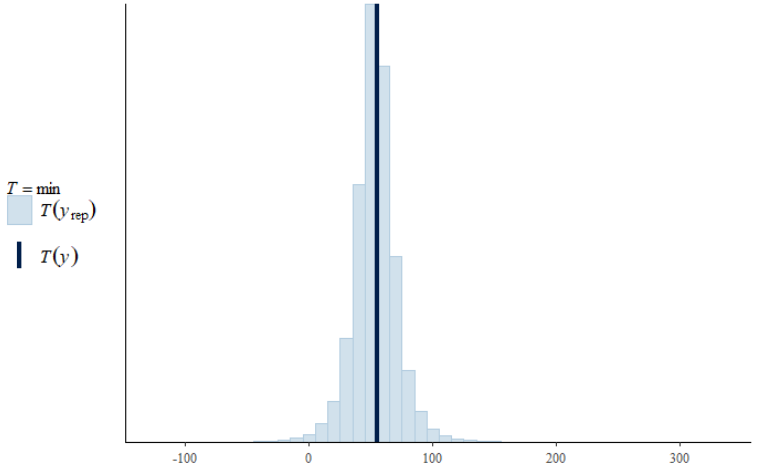
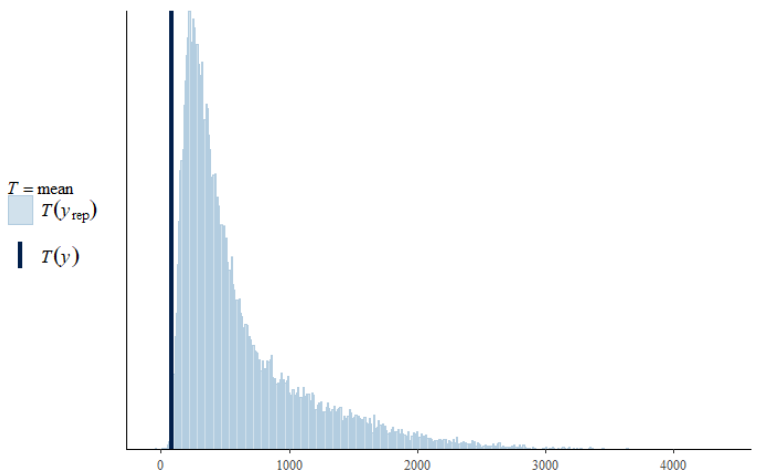
PSPRS score ~ total tau burden (cortical regions) + disease duration + PSPRS-death interval

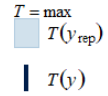


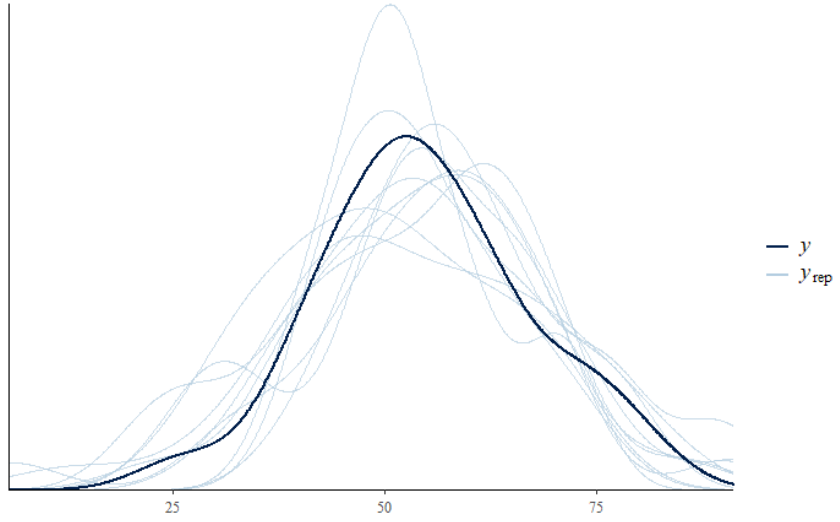
PSPRS score ~ NFT burden (subcortical regions) + disease duration + PSPRS-death interval












```
 Family: gaussian
  Links: mu = identity; sigma = identity
Formula: PSPRS.Total..last.assesment. ~ mean_NFT_density_log + disease.duration..years. + years.
PSPRS.and.death
   Data: selected_dat (Number of observations: 27)
  Draws: 4 chains, each with iter = 20000; warmup = 10000; thin = 1;
         total post-warmup draws = 40000

Population-Level Effects:
                        Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept                 129.06     40.55    48.86   208.81 1.00    42298    30783
mean_NFT_density_log       14.80      6.76     1.38    28.05 1.00    41054    30097
disease.duration..years.    2.74      0.85     1.05     4.43 1.00    41030    29428
years.PSPRS.and.death      -2.29      2.91    -8.07     3.46 1.00    41593    30086

Family Specific Parameters:
      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sigma    11.09      1.69     8.37    14.94 1.00    32610    28051

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
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PSPRS score ~ NFT burden (subcortical regions) + disease duration + PSPRS-death interval