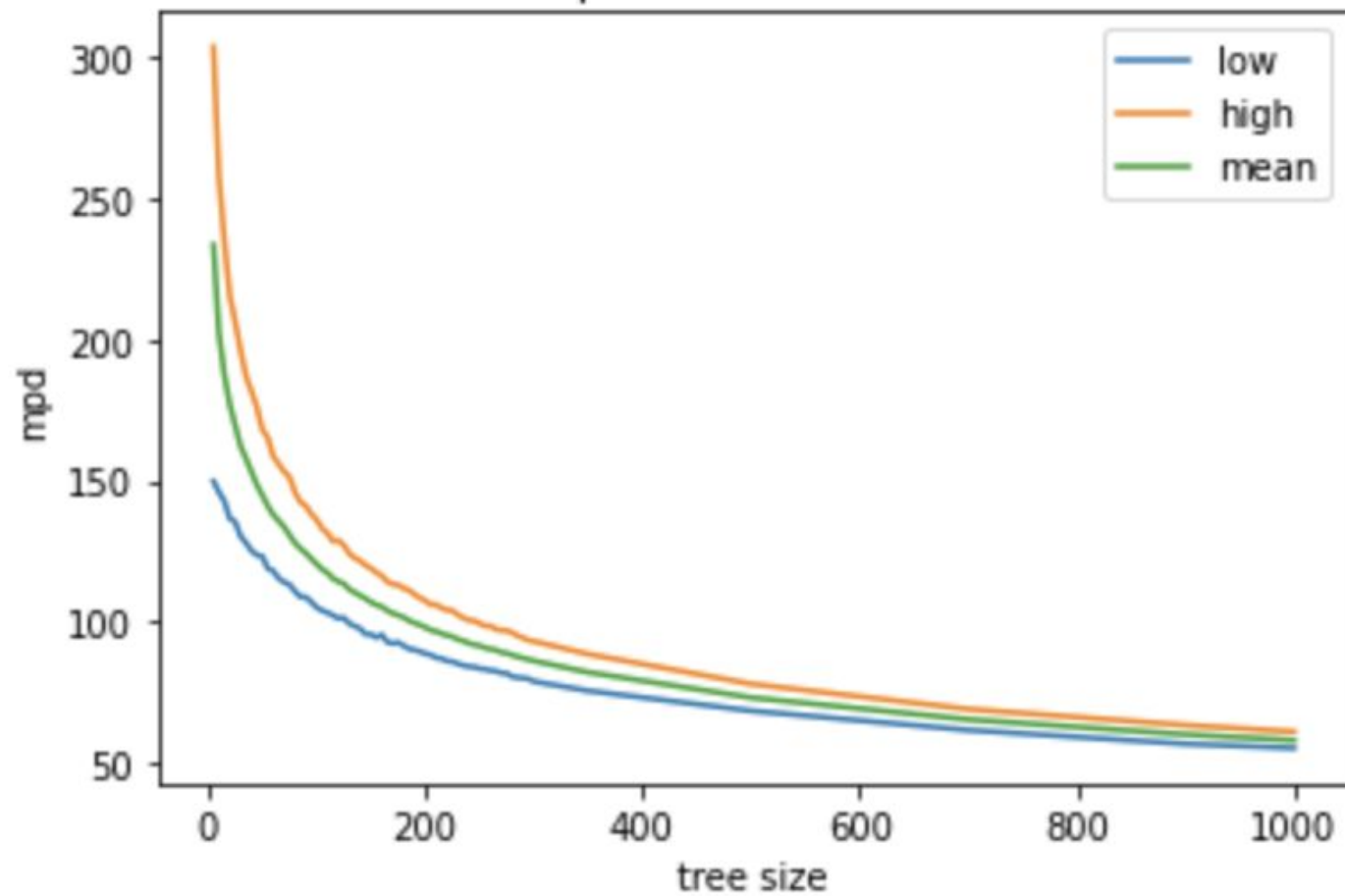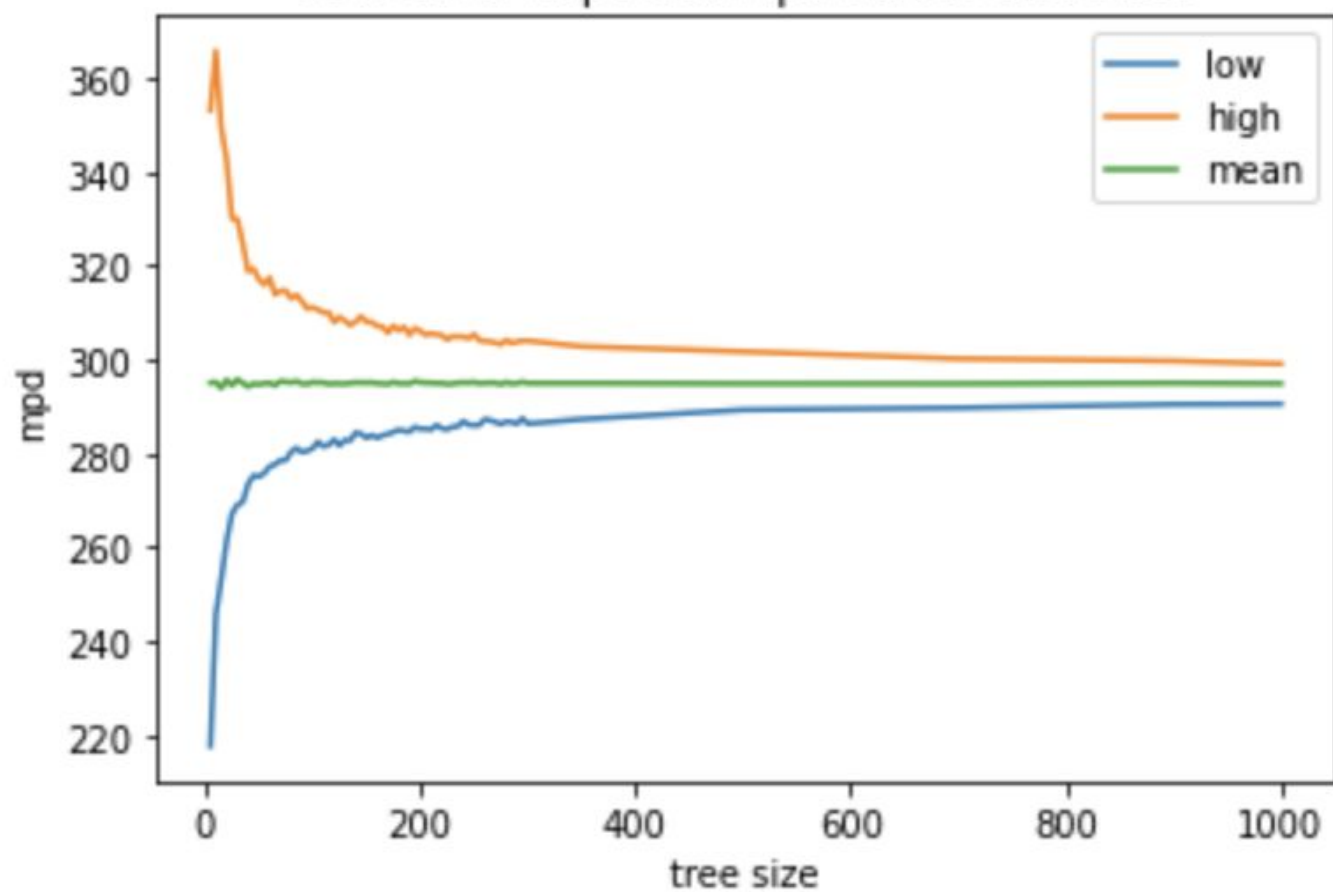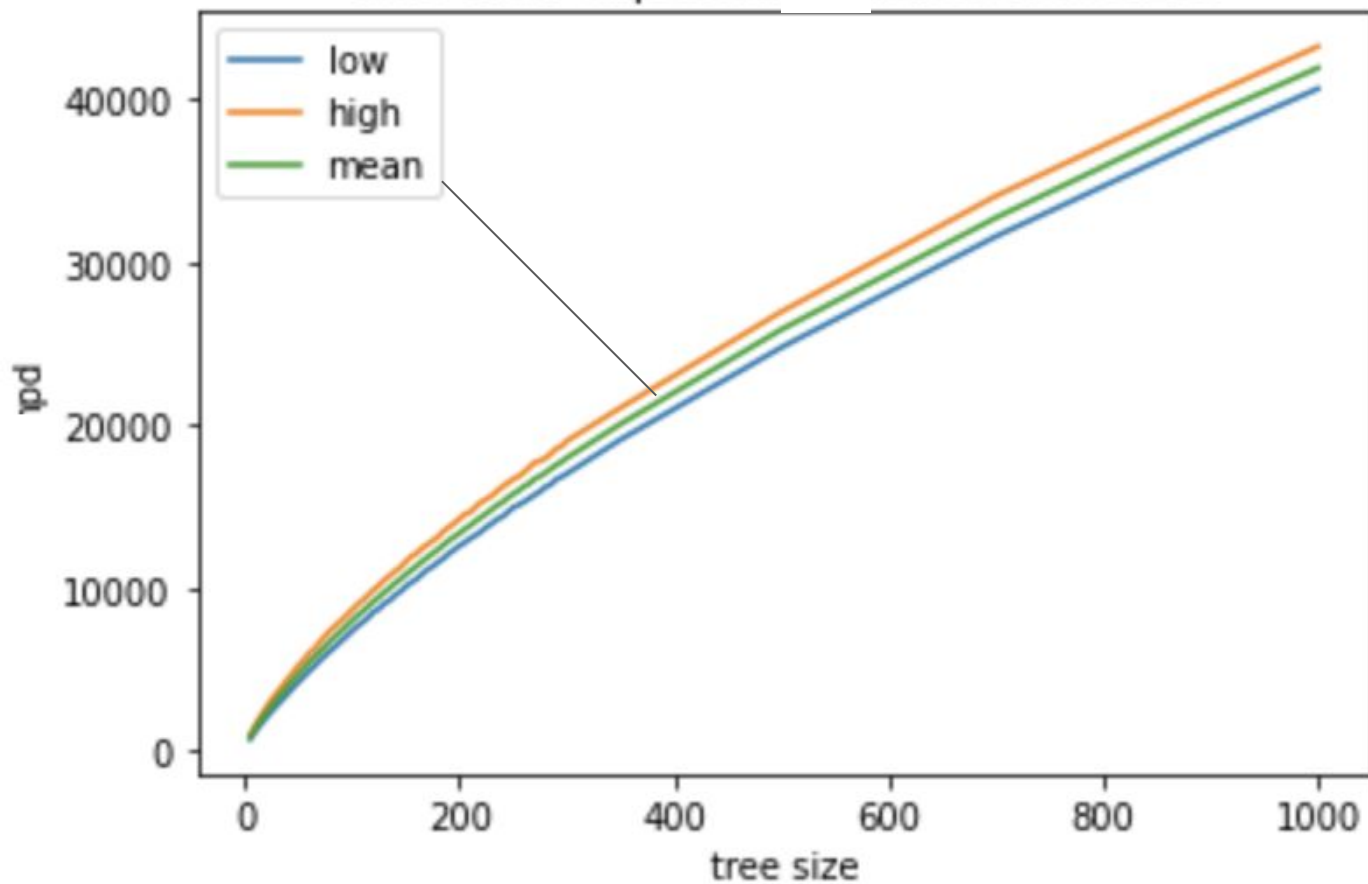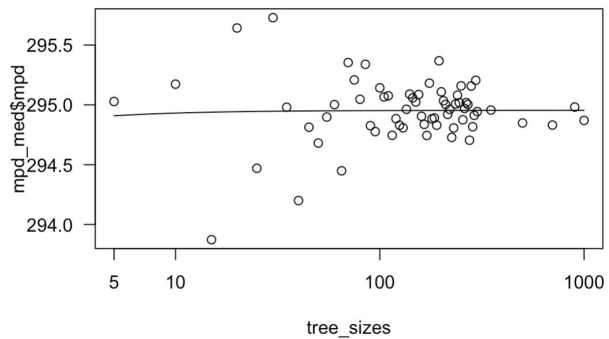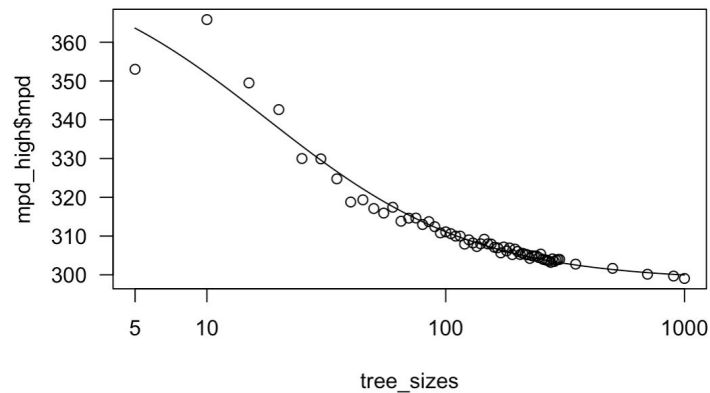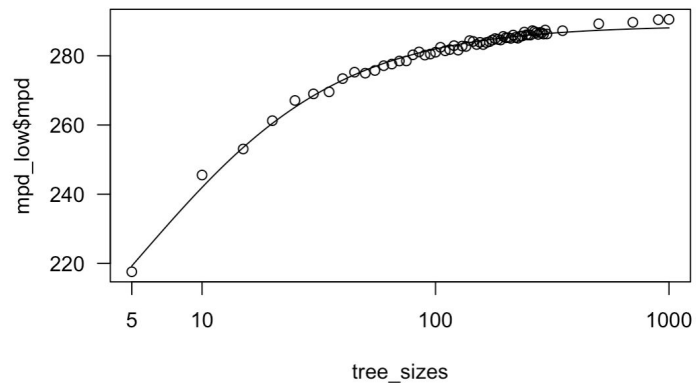95% CI for expected Mntd across tree sizes

95% CI for expected Mpd across tree sizes

95% CI for expected PD across tree sizes

MPD model fits (MM) (left = low, right = high, bottom = mean)

MM model fits (same order as last)

```
Model fitted: Shifted Michaelis-Menten (3 parms)

Parameter estimates:

                Estimate Std. Error   t-value     p-value
c:(Intercept) 153.80266     6.43215    23.912  < 2.2e-16 ***
d:(Intercept) 288.77776     0.22013 1311.824  < 2.2e-16 ***
e:(Intercept)   5.31036     0.40876    12.991  < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error:

  1.050495 (62 degrees of freedom)
```

```
Model fitted: Shifted Michaelis-Menten (3 parms)

Parameter estimates:

                Estimate Std. Error   t-value     p-value
c:(Intercept) 293.485815   51.918716    5.6528 4.262e-07 ***
d:(Intercept) 294.954658    0.040149 7346.4645 < 2.2e-16 ***
e:(Intercept)   0.161755    6.177303    0.0262    0.9792
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error:

 0.2781564 (62 degrees of freedom)
```

```
Model fitted: Shifted Michaelis-Menten (3 parms)

Parameter estimates:

                Estimate Std. Error   t-value     p-value
c:(Intercept) 381.89047     4.36858   87.4175  < 2.2e-16 ***
d:(Intercept) 298.49467     0.71264  418.8555  < 2.2e-16 ***
e:(Intercept)  17.82516     2.03952    8.7399  2.08e-12 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error:

 2.725612 (62 degrees of freedom)
```
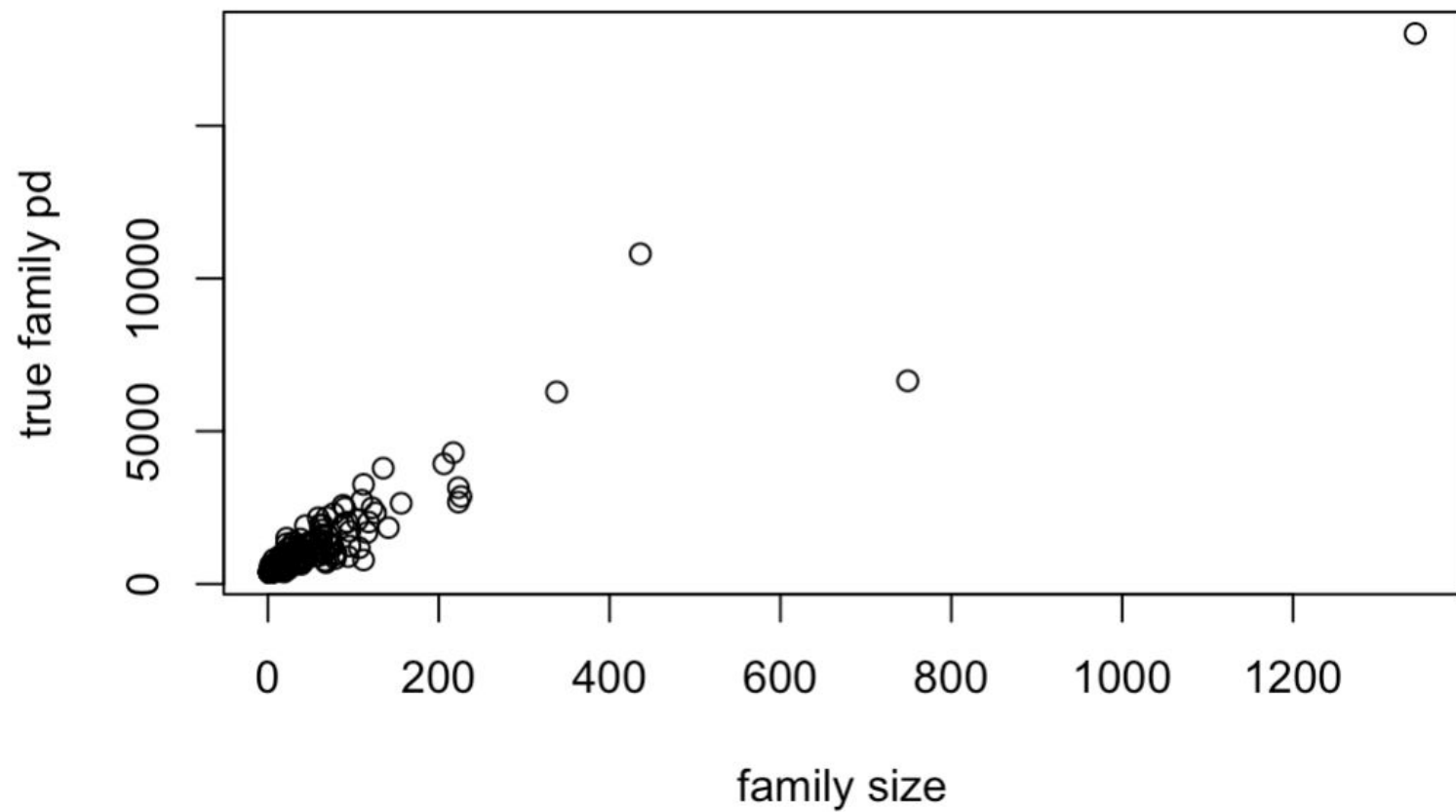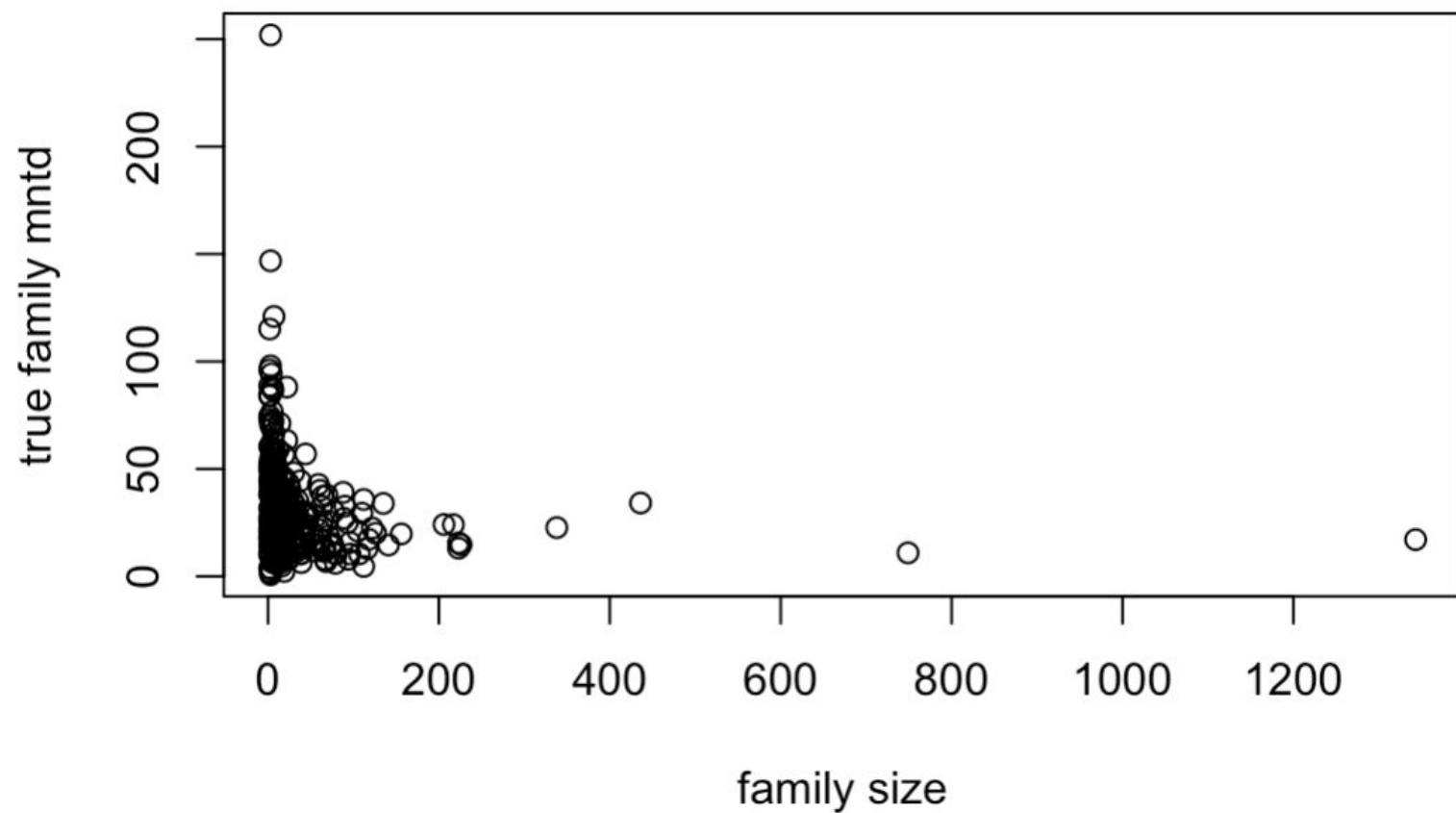
true pd of fish families

true mntd of fish families

95%CI of mpd compared with true fish fam values