Effort Titration

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Contents

1 WDNR Creel Titration

1.1 Purpose

The main question this analysis seeks to answer:

> **How much less creel data could be collected, on an individual survey basis while still maintaining the stratified random sampling design, and still produce exploitation rate (u) estimates that are NOT significantly different from exploitation rates obtained using the current creel survey design?**

The data informing these analyses has all been pulled from the Fisheries Management Information System (FMIS) using the `wdnr.fmdb` `R` package built to interface with this database. All analyses were conducted in `R` using R version 4.3.1 (2023-06-16 ucrt).

1.2 Current Creel Data as Baseline

DNR has amassed a large amount of inland creel information over many decades (1984, 2023) across many waterbodies (n=317). Using this data and functionality of `wdnr.fmdb` it is possible to calculate effort, catch, harvest, and harvest rate for multiple species for each unique creel survey conducted. This information can be further grouped by month, season, day type, etc. to provide insight into important temporal patterns in the fisheries metrics of interest. These calculations are accomplished fairly easily using the following code:

```
# reading in DNR creel data

cserv = get_creel_surveys()
cvis = get_creel_visits()
ccou = get_creel_counts()
```

```
cint = get_creel_int_party()
cfish = get_creel_fish_data()
```

```
ceff = calc_creel_effort(creel_count_data = ccou, creel_int_data = cint)

charv = calc_creel_harvest(creel_count_data = ccou, creel_int_data = cint,
    creel_fish_data = cfish)

charvR = calc_creel_harvest_rates(creel_fish_data = cfish)
```

1.3 Angler Effort

Here I'm using total angler effort estimates for ceded territory lakes only. I'm not working with directed effort hours for walleye because that is not what deroba does and it looks like all the calculations of harvest rate use total effort and not directed effort.

What I've done here is calculate effort based on the full data sets as well as for 5 scenarios:

1. all winter creel information removed
2. only creel information from 'summer' May to August is used
3. 25% of weekday creel visits per month are removed
4. 50% of weekday creel visits per month are removed
5. 50% of weekend creel visits per month are removed.

Creel visits are removed on a month by month basis by randomly removing creel visits to the lake that day

This random removal of days per month and day type should maintain the statistical integrity of the stratified random design that is a part of the creel survey. For context, this was not how data was removed in a similar analysis done by Deroba et al. (2007) where they removed entire weeks (randomly selected) per month instead of randomly selecting days. Their analysis also employed t-tests to analyze the resulting exploitation rates in each of their reduced data sets which relies on the assumption of normality and has been discussed above.

1.3.1 Bayesian Model Fitting

In order to estimate parameters for a model of the effort distribution that produced what is represented in the creel data a Bayesian modeling approach was used. This is because the effort data are not normally distributed and thus don't meet the assumptions of typical analyses based on normality. Here I've chosen to model the data with a lognormal distribution, other potential options for the type of data are the gamma distribution (see Appendix for more information). A Bayesian approach also allows for the inclusion of prior information about the system and does not rely on p-values (though some Bayesian p-values are presented later on, these work a bit differently) which are arbitrary in nature and can be manipulated via high sample sizes. The Bayesian approach can be adapted to accommodate any prior distribution we feel is necessary be it lognormal or gamma.

Individual likelihoods were constructed for each reduced data set and fit using the functions in the `BayesianTools` package in `R`. These model fits were checked for convergence using visual inspection of trace plots, posterior distributions, and Gelman-Rubin Diagnostic tests to ensure that models had converged. All models were fit using Differential Evolution Markov-Chain-Monte-Carlo algorithms run for 10,000 iterations with the first 5,000 discarded as burn-in.

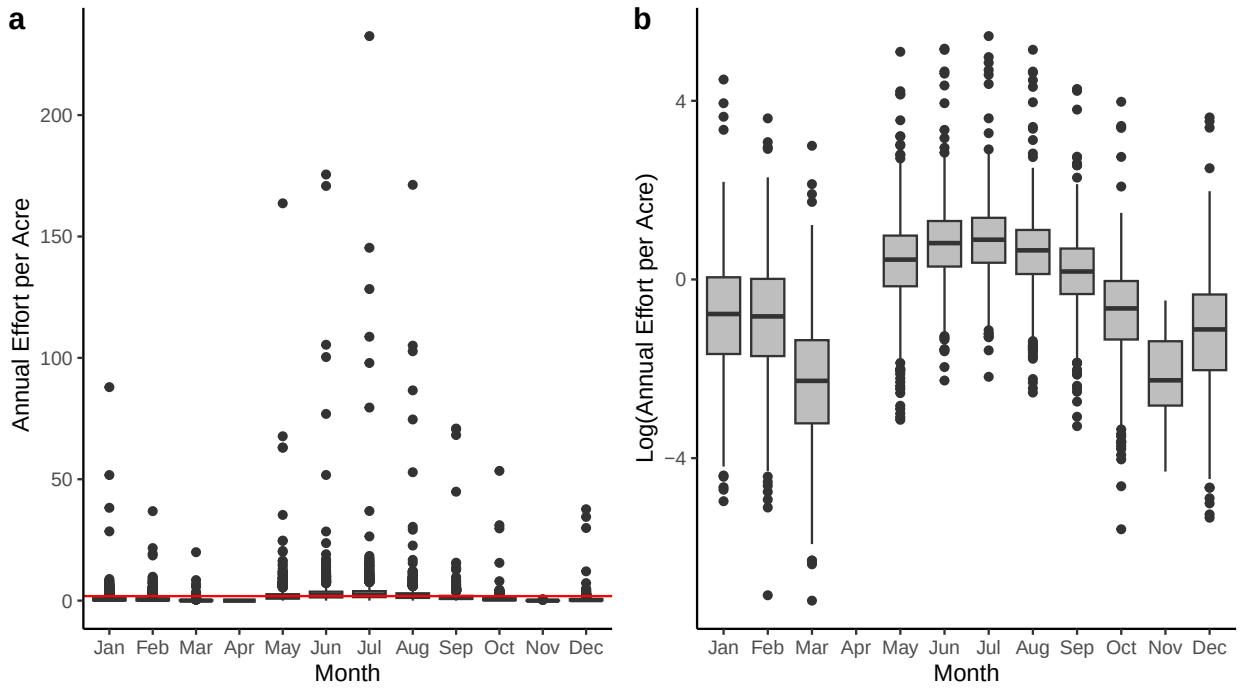


Figure 1: Distribution of effort estimates by month (panel a) for all years of CTWI creel data. Horizontal red line is overall mean effort. Black points are outliers. Panel B is the same information presented on a log-scale.

```
# one likelihood to estimate parms for using the 6
# different treatments creating data frame to model with
# effort estimates

# removing 0s since they can't be logged and if I were to
# make them a small number they would throw off the data
# and make it bimodal which would probably mean switching
# to a gamma distribution to model the data. There are 8
# 0's accounting for 1% of the data. I'm going to operate
# under the assumption that if a survey gives a 0 effort
# estimate with the full survey, then efs collecting less
# data isn't going to change that number.
zeros.actual = sum(ttrExp$total.eff[ttrExp$treat == "actual"] ==
    0)
zeros.nw = sum(ttrExp$total.eff[ttrExp$treat == "noWinter"] ==
    0)
zeros.ma = sum(ttrExp$total.eff[ttrExp$treat == "mayAug"] ==
    0)
zeros.wd25 = sum(ttrExp$total.eff[ttrExp$treat == "wd25"] ==
    0)
zeros.wd50 = sum(ttrExp$total.eff[ttrExp$treat == "wd50"] ==
    0)
zeros.we50 = sum(ttrExp$total.eff[ttrExp$treat == "we50"] ==
    0)

Ztab = data.frame(Scenario = c("Actual", "No Winter", "May-August",
```

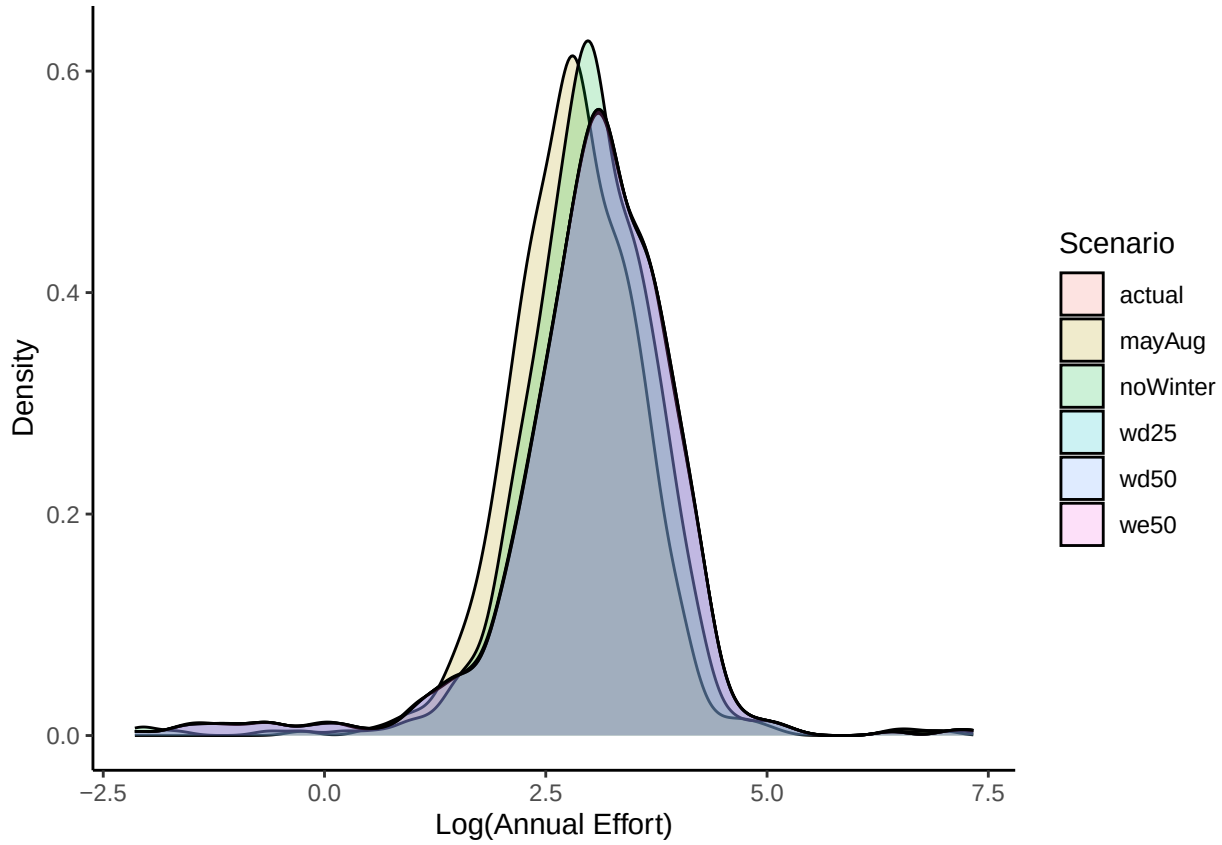


Figure 2: Distribution, on a log scale, of effort for the full data set plus 5 scenarios with reduced data. Actual = full data set, mayAug = May to August creel data only, noWinter = winter creel data removed, wd25 = 25% of weekday creel visits per month removed, wd50 = 50% of weekday creel visits per month removed, we50 = 50% of weekend creel visits per month removed.

Table 1: Table of the number of surveys with effort estimates equal to 0 for each data scenario.

Scenario	Zeros
Actual	86
No Winter	89
May-August	78
25% Weekday Reduction	86
50% Weekday Reduction	86
50% Weekend Reduction	86

```
    "25% Weekday Reduction", "50% Weekday Reduction", "50% Weekend Reduction"),
    Zeros = c(zeros.actual, zeros.nw, zeros.ma, zeros.wd25, zeros.wd50,
        zeros.we50))
kable(Ztab, format = "latex", caption = "Table of the number of surveys with effort estimates equal to
```

```
# removing 0s here as described in the text.
modDat = ttrExp[ttrExp$total.eff != 0, ]

#### ACTUAL ####
effLL.a = function(param) {
    alpha = param[1]
    beta = param[2]

    efs = rlnorm(nrow(modDat[modDat$treat == "actual", ]), meanlog = alpha,
        sdlog = beta)
    ll = dlnorm(modDat$total.eff[modDat$treat == "actual"], meanlog = mean(log(efs)),
        sdlog = sd(log(efs)), log = T)
    return(sum(ll))
}

prior = createTruncatedNormalPrior(mean = c(mean(log(modDat$total.eff[modDat$treat ==
    "actual"])), sd(log(modDat$total.eff[modDat$treat == "actual"]))),
    sd = c(1, 1), lower = c(-15, 0), upper = c(15, 5))

setup.actual = createBayesianSetup(effLL.a, prior = prior)

settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
eff.actual = runMCMC(bayesianSetup = setup.actual, sampler = "DEzs",
    settings = settings)  # takes about 10 seconds

#### NW ####
effLL.nw = function(param) {
    alpha = param[1]
    beta = param[2]

    efs = rlnorm(nrow(modDat[modDat$treat == "noWinter", ]),
        meanlog = alpha, sdlog = beta)
    ll = dlnorm(modDat$total.eff[modDat$treat == "noWinter"],
        meanlog = mean(log(efs)), sdlog = sd(log(efs)), log = T)
```

```
    return(sum(ll))
}

prior = createTruncatedNormalPrior(mean = c(mean(log(modDat$total.eff[modDat$treat ==
    "noWinter"])), sd(log(modDat$total.eff[modDat$treat == "noWinter"]))),
    sd = c(1, 1), lower = c(-15, 0), upper = c(15, 5))

setup.nw = createBayesianSetup(effLL.nw, prior = prior)

settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
eff.nw = runMCMC(bayesianSetup = setup.nw, sampler = "DEzs",
    settings = settings)

#### MA ####

effLL.ma = function(param) {
    alpha = param[1]
    beta = param[2]

    efs = rlnorm(nrow(modDat[modDat$treat == "mayAug", ]), meanlog = alpha,
        sdlog = beta)
    ll = dlnorm(modDat$total.eff[modDat$treat == "mayAug"], meanlog = mean(log(efs)),
        sdlog = sd(log(efs)), log = T)
    return(sum(ll))
}

prior = createTruncatedNormalPrior(mean = c(mean(log(modDat$total.eff[modDat$treat ==
    "mayAug"])), sd(log(modDat$total.eff[modDat$treat == "mayAug"]))),
    sd = c(1, 1), lower = c(-15, 0), upper = c(15, 5))

setup.ma = createBayesianSetup(effLL.ma, prior = prior)

settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
eff.ma = runMCMC(bayesianSetup = setup.ma, sampler = "DEzs",
    settings = settings)

#### WD25 ####

effLL.wd25 = function(param) {
    alpha = param[1]
    beta = param[2]

    efs = rlnorm(nrow(modDat[modDat$treat == "wd25", ]), meanlog = alpha,
        sdlog = beta)
    ll = dlnorm(modDat$total.eff[modDat$treat == "wd25"], meanlog = mean(log(efs)),
        sdlog = sd(log(efs)), log = T)
    return(sum(ll))
}
```

```r
prior = createTruncatedNormalPrior(mean = c(mean(log(modDat$total.eff[modDat$treat ==
    "wd25"])), sd(log(modDat$total.eff[modDat$treat == "wd25"]))),
    sd = c(1, 1), lower = c(-15, 0), upper = c(15, 5))

setup.wd25 = createBayesianSetup(effLL.wd25, prior = prior)

settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
eff.25wd = runMCMC(bayesianSetup = setup.wd25, sampler = "DEzs",
    settings = settings)

#### WD50 ####
effLL.wd50 = function(param) {
    alpha = param[1]
    beta = param[2]

    efs = rlnorm(nrow(modDat[modDat$treat == "wd50", ]), meanlog = alpha,
        sdlog = beta)
    ll = dlnorm(modDat$total.eff[modDat$treat == "wd50"], meanlog = mean(log(efs)),
        sdlog = sd(log(efs)), log = T)
    return(sum(ll))
}

prior = createTruncatedNormalPrior(mean = c(mean(log(modDat$total.eff[modDat$treat ==
    "wd50"])), sd(log(modDat$total.eff[modDat$treat == "wd50"]))),
    sd = c(1, 1), lower = c(-15, 0), upper = c(15, 5))

setup.wd50 = createBayesianSetup(effLL.wd50, prior = prior)

settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
eff.50wd = runMCMC(bayesianSetup = setup.wd50, sampler = "DEzs",
    settings = settings)

#### WE50 ####
effLL.we50 = function(param) {
    alpha = param[1]
    beta = param[2]

    efs = rlnorm(nrow(modDat[modDat$treat == "we50", ]), meanlog = alpha,
        sdlog = beta)
    ll = dlnorm(modDat$total.eff[modDat$treat == "we50"], meanlog = mean(log(efs)),
        sdlog = sd(log(efs)), log = T)
    return(sum(ll))
}

prior = createTruncatedNormalPrior(mean = c(mean(log(modDat$total.eff[modDat$treat ==
    "we50"])), sd(log(modDat$total.eff[modDat$treat == "we50"]))),
    sd = c(1, 1), lower = c(-15, 0), upper = c(15, 5))

setup.we50 = createBayesianSetup(effLL.we50, prior = prior)
```

```
settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
eff.50we = runMCMC(bayesianSetup = setup.we50, sampler = "DEzs",
    settings = settings)
```

1.3.2 Model Checking

Here model fit is being checked in several ways. Initially a visual inspection comparing data simulated using median parameter values from the posterior compared to the observed data for that scenario. A good model fit here is evident when the distribution of the observed and predicted data overlap nearly entirely (Figure 3).

Gelman-Rubin diagnostics were also used to assess convergence, while this doesn't assess model fit it does describe whether or not the MCMC algorithm converged on a solution or whether the parameter space has not been fully explored yet. For this test, values below 1.1 are considered 'converged' with a value of 1 being the lowest possible score. All models had Gelman-Rubin test values < 1.03.

Lastly, a Bayesian p-value was calculated for each model to further describe model fit to the data (Figure 2). Bayesian p-values are based on the same idea as a frequentist p-value : *What is the probability of observing a more extreme test statistic than the one calculated from the observed data*, but is calculated differently and easier to transparently critique. To calculate a Bayesian p-value each set of parameter values in the MCMC chain is used to parameterize a lognormal distribution from which a set of 'new' data are drawn. A test statistic is calculated for this new data and determined to either be more or less extreme than the test statistic that is for the observed data. The proportion of these test statistics that are more extreme than the observed is then calculated. If the model has done a good job of fitting the data then the parameter values should generally generate data that looks like the observed data and the test statistic should be equally likely to be more or less extreme than the observed value. Thus, with Bayesian p-values a value of 0.5 is ideal as it means the model can generate data that matches the distribution of the observed data really well (Table 2, 3. If this p-value was very low (<.10) or very high (>0.9) that would indicate that the model is not fitting the data well because it is unable to regularly reproduce the observed data.

In this analysis two test statistics have been chosen to provide alternate, but not unrelated, measures of model fit. These are the coefficient of variation and standard deviation. Any test statistic of choice could be chosen as long as it can be justified for the objectives of the analysis at hand (see the appendix for further exploration of alternative test statistics).

```
gelmanDiagnostics(eff.actual)  # 1.02 converged
gelmanDiagnostics(eff.nw)  # 1.02 converged
gelmanDiagnostics(eff.ma)  # 1.02 converged
gelmanDiagnostics(eff.25wd)  # 1.04 converged
gelmanDiagnostics(eff.50wd)  # 1.04 converged
gelmanDiagnostics(eff.50we)  # 1.02 converged
```

1.3.3 Inference

Having established that the models are fitting the data well, some inference can be gained as to whether or not the reductions in creel effort proposed here would result in a meaningful change in the total annual effort per acre estimated from the reduced data.

A Bayesian p-value can be employed here too. A test between the cv and sd of the actual data and the cv and sd of the reduced data can describe whether the model of the reduced data is able to approximate the actual data or not. Successful approximations are p-values close to 0.5 with reduced fit as values increase

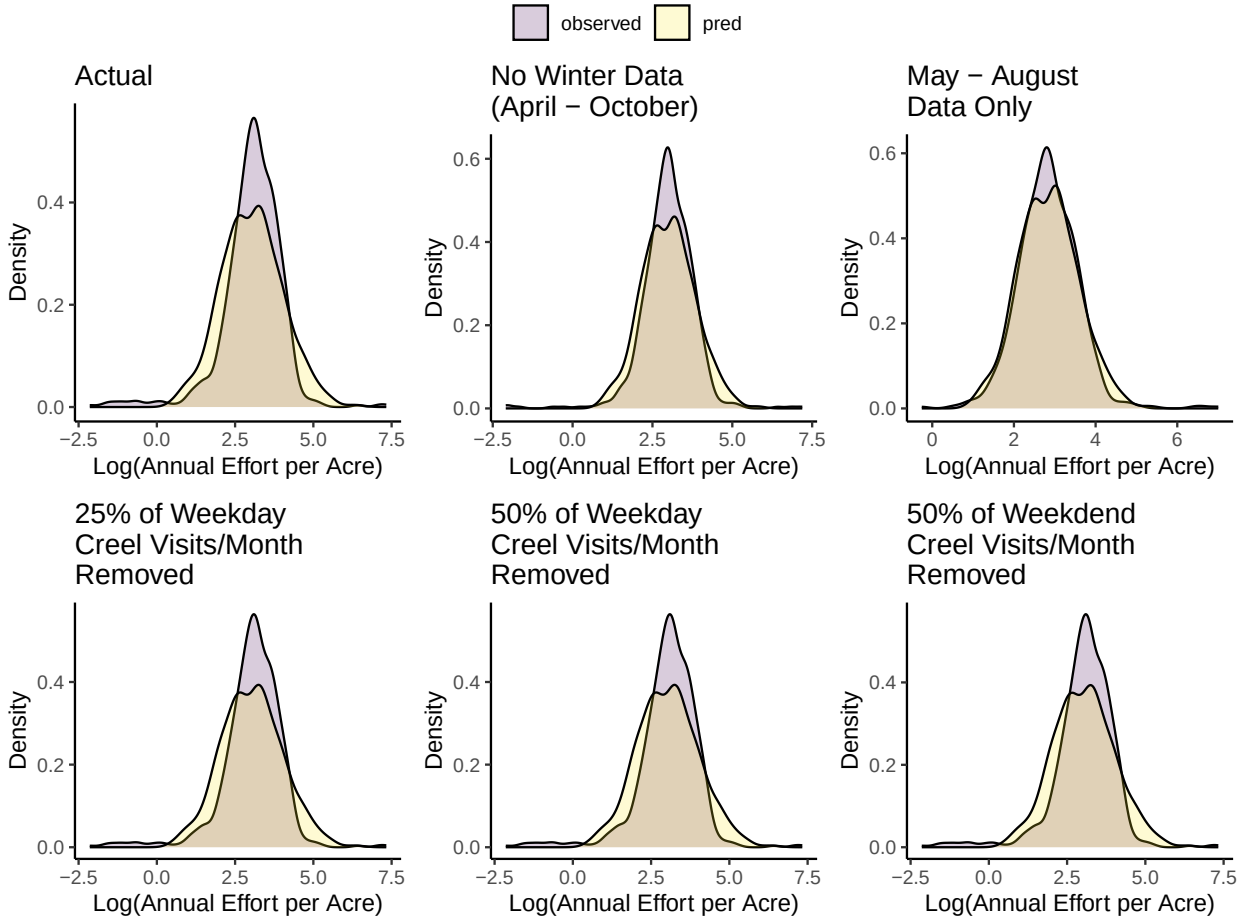


Figure 3: Distributions of the observed and model predicted data for each scenario. Model predicted data comes from lognormal distribution paramterized using the median parameter estimate of the model posterior.

Table 2: Bayesian p-values for a lognormal distributed model. Each p-value describes whether or not there is a significant difference between data generated by the fitted model and the actual data for that scenario. Two metrics are assessed here, coefficient of variation (CV) and standard devidation (SD).

Scenario	CV p-value	SD p-value
Actual	0.523	0.518
No Winter	0.525	0.529
May-August	0.504	0.502
25% weeday removal	0.509	0.517
50% weekday removal	0.533	0.534
50% weekend removal	0.523	0.518

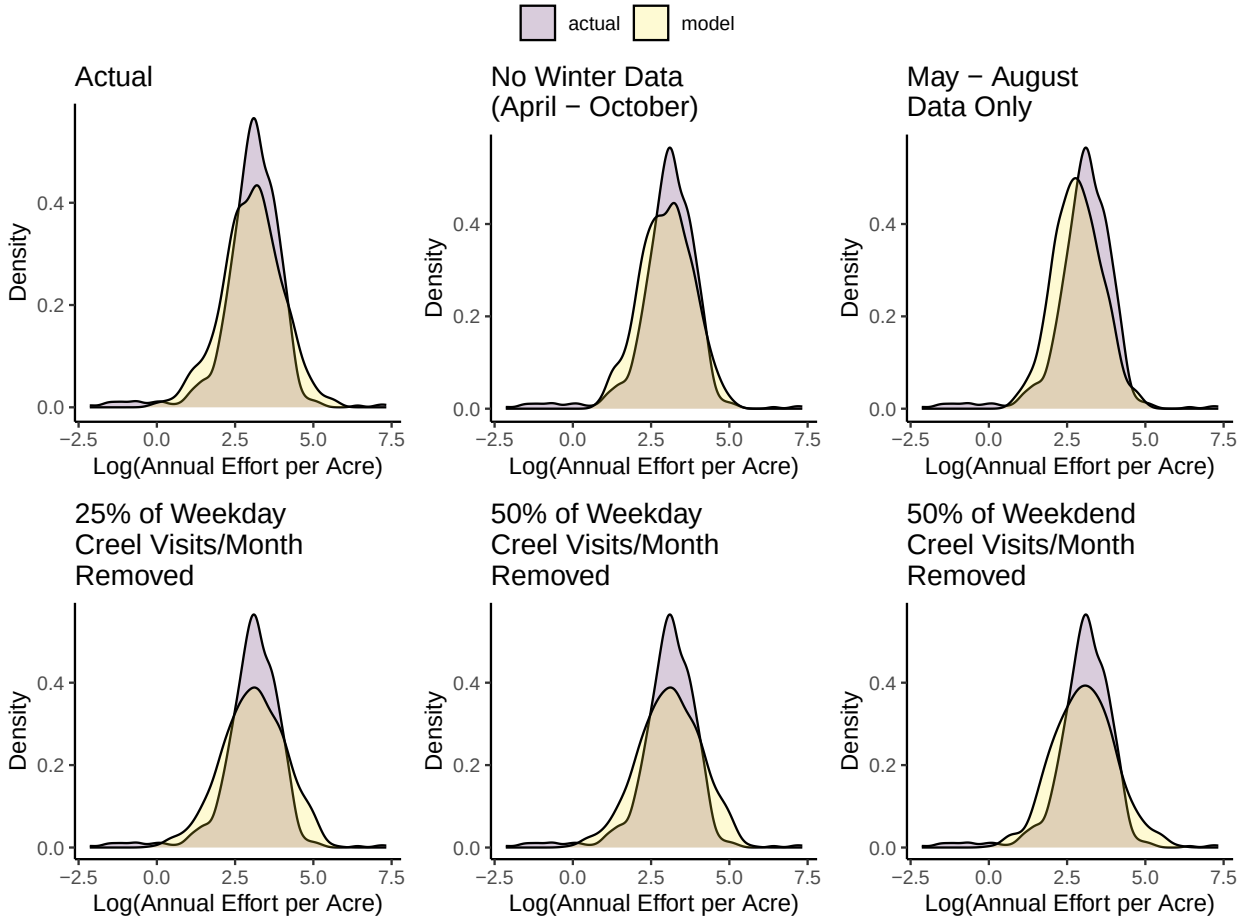


Figure 4: Comparison of the distribution of actual annual effer per acre estimates calculated from creel data and annual effort per acre estimated calculated from simulated creel data for each data reduction scenario and the resulting median parameter values for their respective model fits.

Table 3: Bayesian p-values for the comparison between the actual data and the scenario-specific model fit to a lognormal distribution. This test is asking whether the scenario-specific model can approximate the actual data. When true this signals no effect of the data reduction for that scenario on the resulting annual effort per acre estimate. Two metrics are assessed here, coefficient of variation (CV) and standard devidation (SD).

Scenario	CV p-value	SD p-value
Actual	0.523	0.518
No Winter	0.003	0.001
May-August	0.000	0.000
25% weeday removal	0.514	0.516
50% weekday removal	0.565	0.553
50% weekend removal	0.523	0.518

or decrease beyond 0.5. Generally, the rule of thumb is that p-values < 0.10 or > 0.90 signal unacceptable fits. However, these cutoffs can be set based on the objectives of the study at hand and the values of the decision makers.

The results of these tests suggest that when using coefficient of variation as the variance metric to assess model fit and the < 0.10 or > 0.90 rule that the no winter and may-august data reduction models are unable to approximate the data, but the 3 percentage reductions are able to (Table 3). When using standard deviation the same pattern holds true (Table 3).

What's likely going on here is the difference between removing a chunk of data as in the seasonal removals and having the removals spread evenly acros the entire year.

1.3.4 Year Specific Analyses

Instead of modeling the full population of annual effort estimates as was done above, here I have done the model fitting on individual creel-years so that I can see how the removal of data for a creel-year (which is a comparatively large amount of missing data since only 16-20 lakes are creeled each year) impacts the annual effort per acre estimated that year. This analysis will follow the same routine as the whole-population analyses above but only consider one creel-year at a time.

I first started with some basic analyses of the data on a year by year basis to understand how the data changes from year to year and if any lake characteristics explained variation (if there is any) in annual effort per acre estimates across data reduction scenarios for specific creel-years (Figure 5).

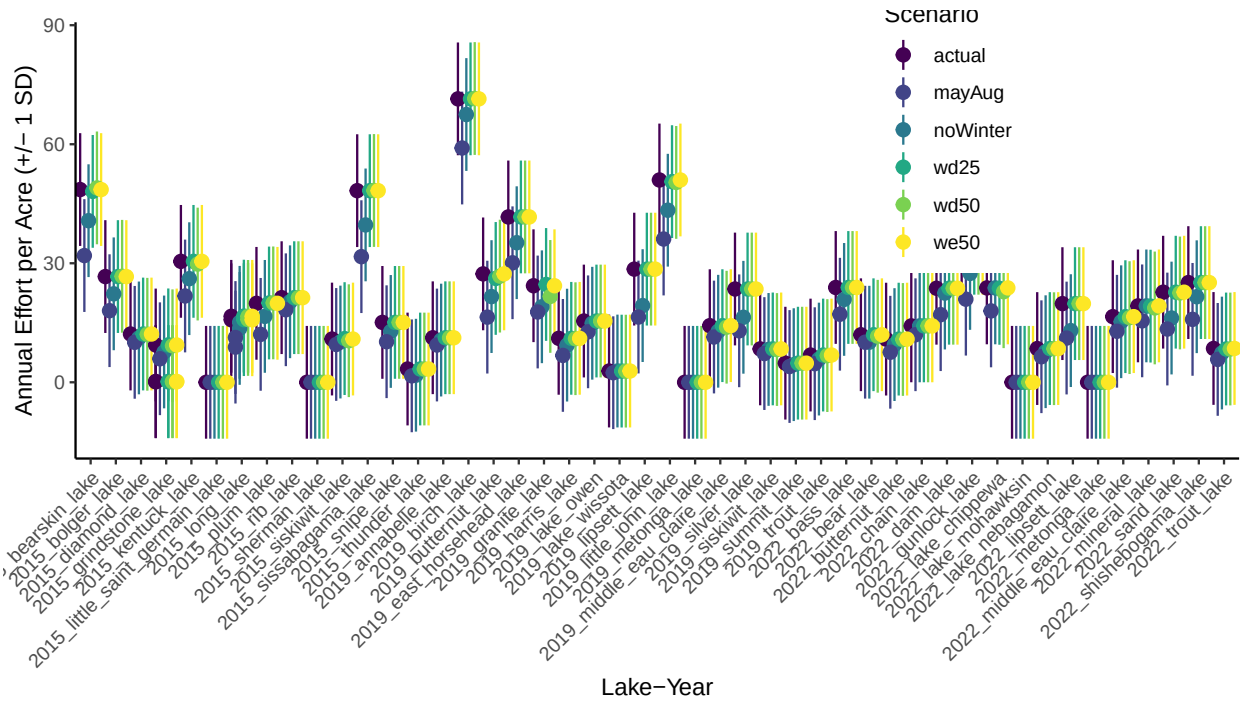


Figure 5: Comparison of the annual effort per acre estimated from the reduced data for a handful of creel surveys. Most data reductions do not result in annual effort per acre estimates that are much different from the actual data (most are within 1 SD of the effort estimate for that treatment). Colors represent data reduction scenarios, points are mean annual effort per acre estimates across all months of that creel survey and vertical lines represent 1 standard deviation.

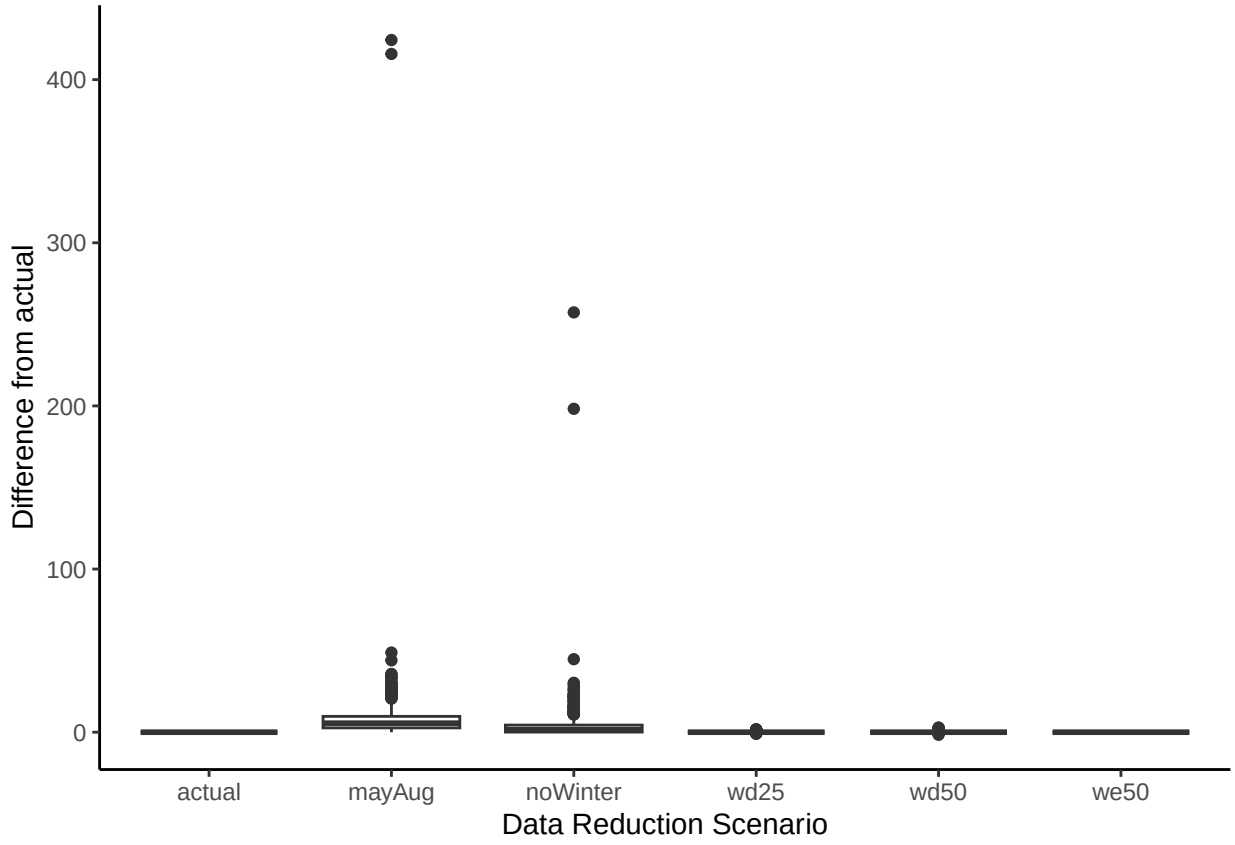
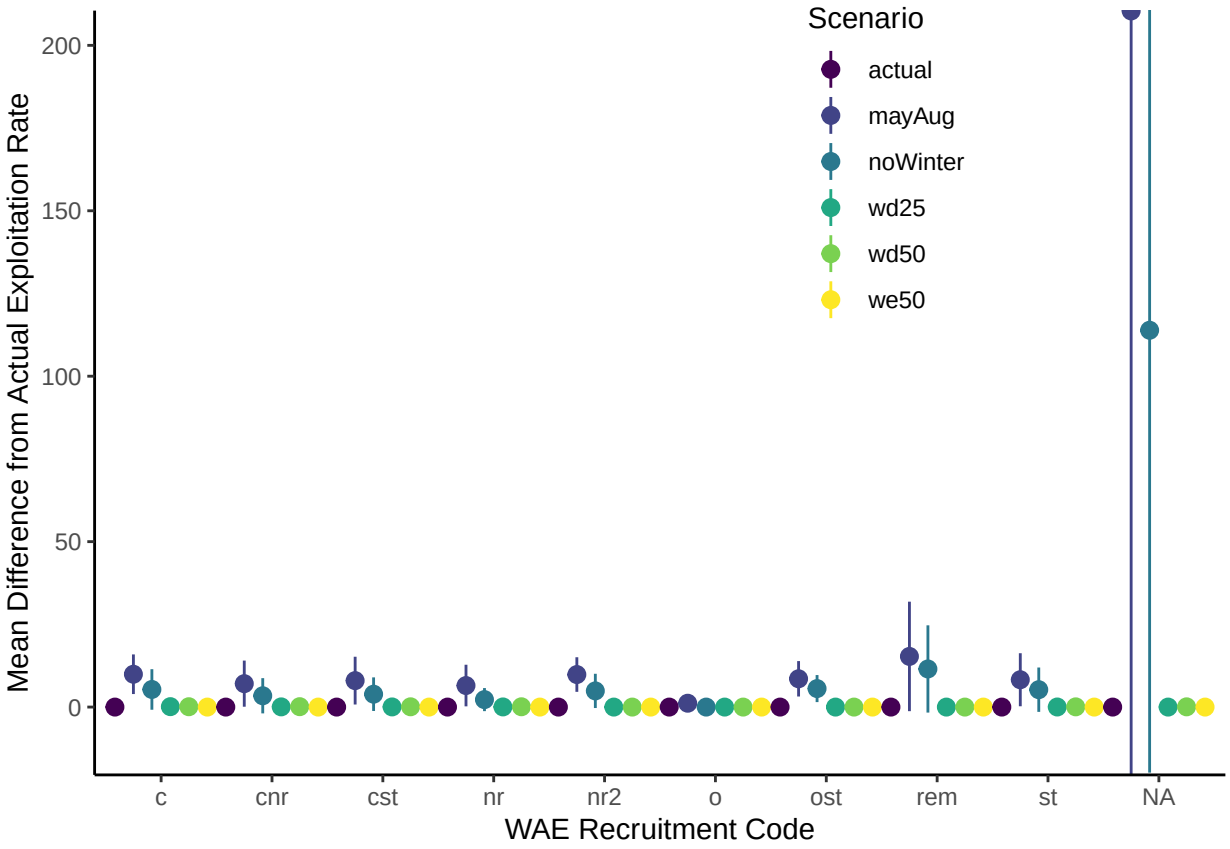
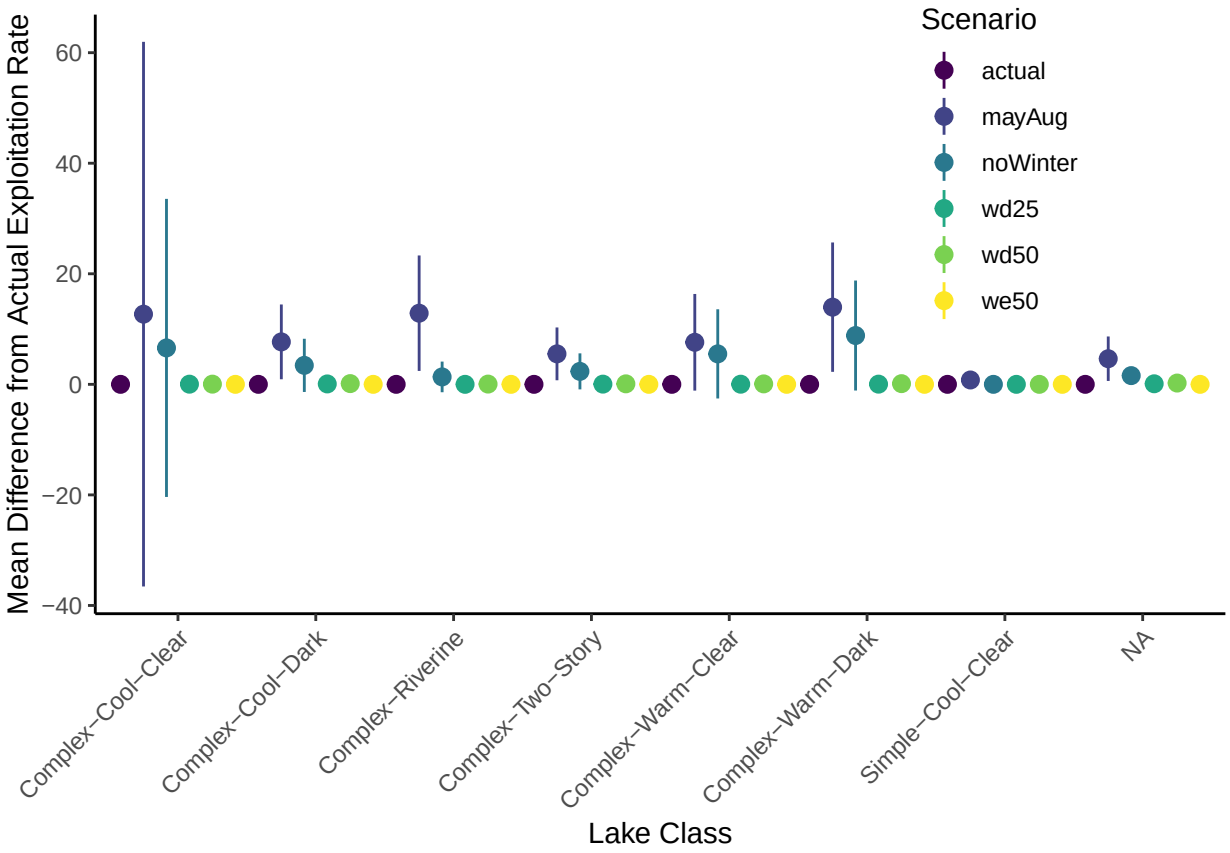


Figure 6: Boxplot of the difference between the actual annual effort per acre estimate and the data-reduced annual effort per acre estimate for each creel survey in the creel dataset. Most of the data exhibits differences very near 0 except the seasonal reductions, dots represent outliers (x<|> x's percentile-1.5*interquartile range)


Scenario
actual
mayAug
noWinter
wd25
wd50
we50
Mean Difference from Actual Exploitation Rate
200
150
100
50
0
c
cnr
cst
nr
nr2
o
ost
rem
st
NA
WAE Recruitment Code




```
# MODELING EFFECTS OF DATA REDUCTION ON INDIVIDUAL YEARS

# likelihoods to fit
effLL.we50 = function(param) {
    alpha = param[1]
    beta = param[2]

    efs = rlnorm(nrow(tdat[tdat$treat == "we50", ]), meanlog = alpha,
        sdlog = beta)
    ll = dlnorm(tdat$total.eff[tdat$treat == "we50"], meanlog = mean(log(efs)),
        sdlog = sd(log(efs)), log = T)
    return(sum(ll))
}
effLL.wd50 = function(param) {
    alpha = param[1]
    beta = param[2]

    efs = rlnorm(nrow(tdat[tdat$treat == "wd50", ]), meanlog = alpha,
        sdlog = beta)
    ll = dlnorm(tdat$total.eff[tdat$treat == "wd50"], meanlog = mean(log(efs)),
        sdlog = sd(log(efs)), log = T)
    return(sum(ll))
}
effLL.wd25 = function(param) {
    alpha = param[1]
    beta = param[2]
```

```
    efs = rlnorm(nrow(tdat[tdat$treat == "wd25", ]), meanlog = alpha,
        sdlog = beta)
    ll = dlnorm(tdat$total.eff[tdat$treat == "wd25"], meanlog = mean(log(efs)),
        sdlog = sd(log(efs)), log = T)
    return(sum(ll))
}
effLL.ma = function(param) {
    alpha = param[1]
    beta = param[2]

    efs = rlnorm(nrow(tdat[tdat$treat == "mayAug", ]), meanlog = alpha,
        sdlog = beta)
    ll = dlnorm(tdat$total.eff[tdat$treat == "mayAug"], meanlog = mean(log(efs)),
        sdlog = sd(log(efs)), log = T)
    return(sum(ll))
}
effLL.nw = function(param) {
    alpha = param[1]
    beta = param[2]

    efs = rlnorm(nrow(tdat[tdat$treat == "noWinter", ]), meanlog = alpha,
        sdlog = beta)
    ll = dlnorm(tdat$total.eff[tdat$treat == "noWinter"], meanlog = mean(log(efs)),
        sdlog = sd(log(efs)), log = T)
    return(sum(ll))
}
effLL.a = function(param) {
    alpha = param[1]
    beta = param[2]

    efs = rlnorm(nrow(tdat[tdat$treat == "actual", ]), meanlog = alpha,
        sdlog = beta)
    ll = dlnorm(tdat$total.eff[tdat$treat == "actual"], meanlog = mean(log(efs)),
        sdlog = sd(log(efs)), log = T)
    return(sum(ll))
}

# removing 0s
ttrExp = ttrExp[ttrExp$total.eff != 0, ]
loopY = sort(unique(ttrExp$year))

bpval.comp.y = data.frame(year = NA, scenario = NA, coef.var.pval = NA,
    sd.pval = NA)

bpval.self.y = data.frame(year = NA, scenario = NA, coef.var.pval = NA,
    sd.pval = NA)
grMetrics.y = data.frame(year = NA, scenario = NA, gr.prsf = NA,
    gr.par1 = NA, gr.par2 = NA)

for (y in 1:length(loopY)) {
    # first get to year-specific data
    tdat = ttrExp[ttrExp$year == loopY[y], ]
    # Bayesian Model Fitting ACTUAL
```

```
prior = createTruncatedNormalPrior(mean = c(mean(log(ttrExp$total.eff[ttrExp$treat ==
    "actual"])), sd(log(ttrExp$total.eff[ttrExp$treat ==
    "actual"]))), sd = c(1, 1), lower = c(-15, 0), upper = c(15,
    5))

setup.a = createBayesianSetup(effLL.a, prior = prior)

settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
t.a = runMCMC(bayesianSetup = setup.a, sampler = "DEzs",
    settings = settings)
# NW

prior = createTruncatedNormalPrior(mean = c(mean(log(ttrExp$total.eff[ttrExp$treat ==
    "noWinter"])), sd(log(ttrExp$total.eff[ttrExp$treat ==
    "noWinter"]))), sd = c(1, 1), lower = c(-15, 0), upper = c(15,
    5))

setup.nw = createBayesianSetup(effLL.nw, prior = prior)

settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
t.nw = runMCMC(bayesianSetup = setup.nw, sampler = "DEzs",
    settings = settings)
# MA

prior = createTruncatedNormalPrior(mean = c(mean(log(ttrExp$total.eff[ttrExp$treat ==
    "mayAug"])), sd(log(ttrExp$total.eff[ttrExp$treat ==
    "mayAug"]))), sd = c(1, 1), lower = c(-15, 0), upper = c(15,
    5))

setup.ma = createBayesianSetup(effLL.ma, prior = prior)

settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
t.ma = runMCMC(bayesianSetup = setup.ma, sampler = "DEzs",
    settings = settings)
# WD.25

prior = createTruncatedNormalPrior(mean = c(mean(log(ttrExp$total.eff[ttrExp$treat ==
    "wd25"])), sd(log(ttrExp$total.eff[ttrExp$treat == "wd25"]))),
    sd = c(1, 1), lower = c(-15, 0), upper = c(15, 5))

setup.wd25 = createBayesianSetup(effLL.wd25, prior = prior)

settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
t.25wd = runMCMC(bayesianSetup = setup.wd25, sampler = "DEzs",
    settings = settings)
```

```
# WD.50

prior = createTruncatedNormalPrior(mean = c(mean(log(ttrExp$total.eff[ttrExp$treat ==
    "wd50"])), sd(log(ttrExp$total.eff[ttrExp$treat == "wd50"]))),
    sd = c(1, 1), lower = c(-15, 0), upper = c(15, 5))

setup.wd50 = createBayesianSetup(effLL.wd50, prior = prior)

settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
t.50wd = runMCMC(bayesianSetup = setup.wd50, sampler = "DEzs",
    settings = settings)

# WE.50

prior = createTruncatedNormalPrior(mean = c(mean(log(ttrExp$total.eff[ttrExp$treat ==
    "we50"])), sd(log(ttrExp$total.eff[ttrExp$treat == "we50"]))),
    sd = c(1, 1), lower = c(-15, 0), upper = c(15, 5))

setup.we50 = createBayesianSetup(effLL.we50, prior = prior)

settings = list(iterations = 10000, nrChains = 3, message = F,
    burnin = 5000)
set.seed(10)
t.50we = runMCMC(bayesianSetup = setup.we50, sampler = "DEzs",
    settings = settings)

## GR Diagnostics

gr.a = gelmanDiagnostics(t.a)
gr.ma = gelmanDiagnostics(t.ma)
gr.nw = gelmanDiagnostics(t.nw)
gr.wd25 = gelmanDiagnostics(t.25wd)
gr.wd50 = gelmanDiagnostics(t.50wd)
gr.we50 = gelmanDiagnostics(t.50we)

## BAYESIAN P-VALUE CALCS

pars.a = getSample(t.a)
pars.nw = getSample(t.nw)
pars.ma = getSample(t.ma)
pars.wd25 = getSample(t.25wd)
pars.wd50 = getSample(t.50wd)
pars.we50 = getSample(t.50we)

#### Pb ACTUAL ####
pval.actual = data.frame(alpha = rep(NA, nrow(pars.a)), beta = NA,
    cv = NA, sd = NA)
set.seed(10)
for (i in 1:nrow(pars.a)) {
    tempdat = rlnorm(n = length(tdat$total.eff[tdat$treat ==
        "actual"]), meanlog = pars.a[i, 1], sdlog = pars.a[i,
```

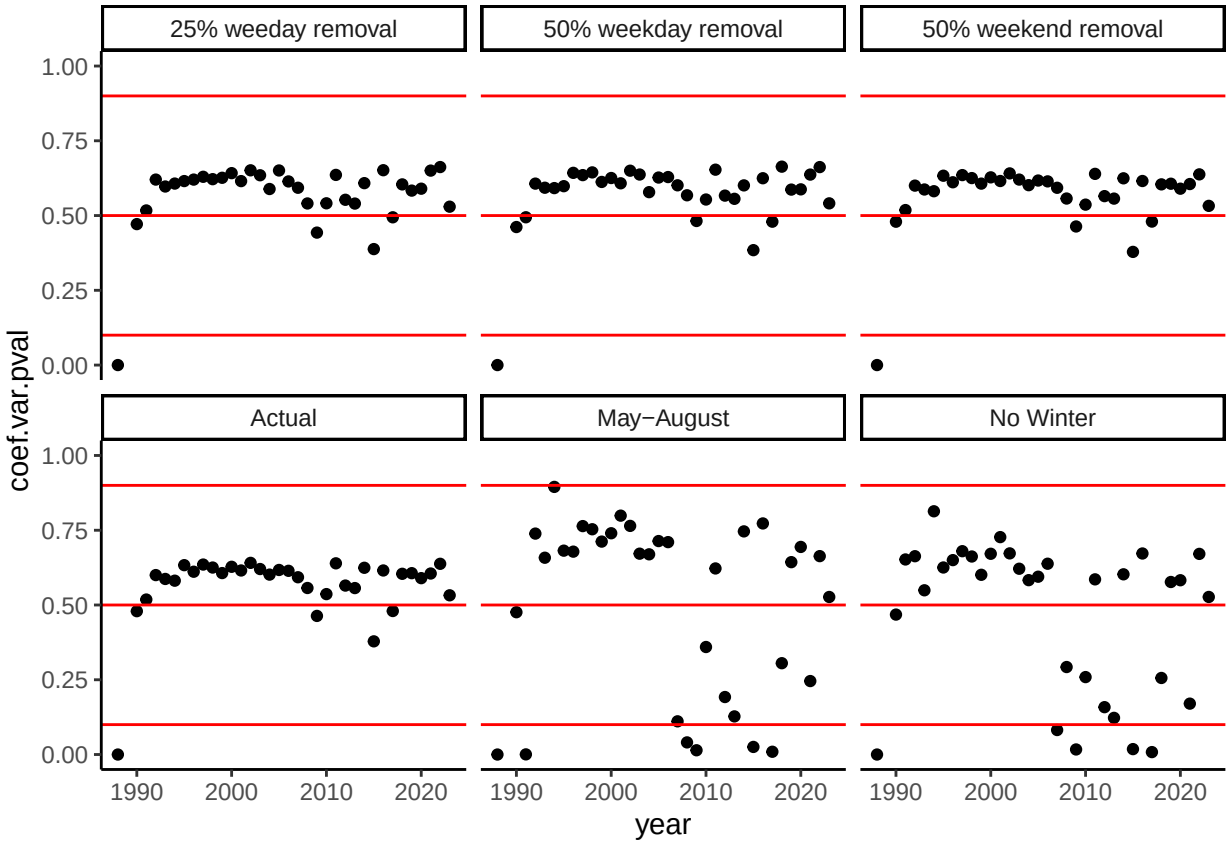
```
        2])
    pval.actual$alpha[i] = pars.a[i, 1]
    pval.actual$beta[i] = pars.a[i, 2]
    pval.actual$cv[i] = sd(log(tempdat))/mean(log(tempdat))
    pval.actual$sd[i] = sd(log(tempdat))
}

# now calculate the number of times the cv or sd
# exceeds that of the real data

pval.actual$cvExceed = 0
pval.actual$sdExceed = 0

actual.cv = sd(log(tdat$total.eff[tdat$treat == "actual"]))/mean(log(tdat$total.eff[tdat$treat ==
    "actual"]))
actual.sd = sd(log(tdat$total.eff[tdat$treat == "actual"]))

pval.actual$cvExceed[pval.actual$cv > actual.cv] = 1
pval.actual$sdExceed[pval.actual$sd > actual.sd] = 1

#### Pb NO WINTER ####
pval.noWinter = data.frame(alpha = rep(NA, nrow(pars.nw)),
    beta = NA, cv = NA, sd = NA)
set.seed(10)
for (i in 1:nrow(pars.nw)) {
    tempdat = rlnorm(n = length(tdat$total.eff[tdat$treat ==
        "noWinter"]), meanlog = pars.nw[i, 1], sdlog = pars.nw[i,
        2])
    pval.noWinter$alpha[i] = pars.nw[i, 1]
    pval.noWinter$beta[i] = pars.nw[i, 2]
    pval.noWinter$cv[i] = sd(log(tempdat))/mean(log(tempdat))
    pval.noWinter$sd[i] = sd(log(tempdat))
}

# now calculate the number of times the cv or sd
# exceeds that of the real data

pval.noWinter$cvExceed = 0
pval.noWinter$sdExceed = 0

noWinter.cv = sd(log(tdat$total.eff[tdat$treat == "noWinter"]))/mean(log(tdat$total.eff[tdat$treat =
    "noWinter"]))
noWinter.sd = sd(log(tdat$total.eff[tdat$treat == "noWinter"]))

pval.noWinter$cvExceed[pval.noWinter$cv > noWinter.cv] = 1
pval.noWinter$sdExceed[pval.noWinter$sd > noWinter.sd] = 1

#### Pb MAYAUGUST ####
pval.mayAug = data.frame(alpha = rep(NA, nrow(pars.ma)),
    beta = NA, cv = NA, sd = NA)
set.seed(10)
for (i in 1:nrow(pars.ma)) {
    tempdat = rlnorm(n = length(tdat$total.eff[tdat$treat ==
```

```
        "mayAug"]), meanlog = pars.ma[i, 1], sdlog = pars.ma[i,
        2])
    pval.mayAug$alpha[i] = pars.ma[i, 1]
    pval.mayAug$beta[i] = pars.ma[i, 2]
    pval.mayAug$cv[i] = sd(log(tempdat))/mean(log(tempdat))
    pval.mayAug$sd[i] = sd(log(tempdat))
}

# now calculate the number of times the cv or sd
# exceeds that of the real data

pval.mayAug$cvExceed = 0
pval.mayAug$sdExceed = 0

mayAug.cv = sd(log(tdat$total.eff[tdat$treat == "mayAug"]))/mean(log(tdat$total.eff[tdat$treat ==
    "mayAug"]))
mayAug.sd = sd(log(tdat$total.eff[tdat$treat == "mayAug"]))

pval.mayAug$cvExceed[pval.mayAug$cv > mayAug.cv] = 1
pval.mayAug$sdExceed[pval.mayAug$sd > mayAug.sd] = 1

#### Pb WD25 ####
pval.wd25 = data.frame(alpha = rep(NA, nrow(pars.wd25)),
    beta = NA, cv = NA, sd = NA)
set.seed(10)
for (i in 1:nrow(pars.wd25)) {
    tempdat = rlnorm(n = length(tdat$total.eff[tdat$treat ==
        "wd25"]), meanlog = pars.wd25[i, 1], sdlog = pars.wd25[i,
        2])
    pval.wd25$alpha[i] = pars.wd25[i, 1]
    pval.wd25$beta[i] = pars.wd25[i, 2]
    pval.wd25$cv[i] = sd(log(tempdat))/mean(log(tempdat))
    pval.wd25$sd[i] = sd(log(tempdat))
}

# now calculate the number of times the cv or sd
# exceeds that of the real data

pval.wd25$cvExceed = 0
pval.wd25$sdExceed = 0

wd25.cv = sd(log(tdat$total.eff[tdat$treat == "wd25"]))/mean(log(tdat$total.eff[tdat$treat ==
    "wd25"]))
wd25.sd = sd(log(tdat$total.eff[tdat$treat == "wd25"]))

pval.wd25$cvExceed[pval.wd25$cv > wd25.cv] = 1
pval.wd25$sdExceed[pval.wd25$sd > wd25.sd] = 1

#### Pb WD50 ####
pval.wd50 = data.frame(alpha = rep(NA, nrow(pars.wd50)),
    beta = NA, cv = NA, sd = NA)
set.seed(10)
for (i in 1:nrow(pars.wd50)) {
```

```
    tempdat = rlnorm(n = length(tdat$total.eff[tdat$treat ==
        "wd50"]), meanlog = pars.wd50[i, 1], sdlog = pars.wd50[i,
        2])
    pval.wd50$alpha[i] = pars.wd50[i, 1]
    pval.wd50$beta[i] = pars.wd50[i, 2]
    pval.wd50$cv[i] = sd(log(tempdat))/mean(log(tempdat))
    pval.wd50$sd[i] = sd(log(tempdat))
}

# now calculate the number of times the cv or sd
# exceeds that of the real data

pval.wd50$cvExceed = 0
pval.wd50$sdExceed = 0

wd50.cv = sd(log(tdat$total.eff[tdat$treat == "wd50"]))/mean(log(tdat$total.eff[tdat$treat ==
    "wd50"]))
wd50.sd = sd(log(tdat$total.eff[tdat$treat == "wd50"]))

pval.wd50$cvExceed[pval.wd50$cv > wd50.cv] = 1
pval.wd50$sdExceed[pval.wd50$sd > wd50.sd] = 1

#### Pb WE50 ####
pval.we50 = data.frame(alpha = rep(NA, nrow(pars.we50)),
    beta = NA, cv = NA, sd = NA)
set.seed(10)
for (i in 1:nrow(pars.we50)) {
    tempdat = rlnorm(n = length(tdat$total.eff[tdat$treat ==
        "we50"]), meanlog = pars.we50[i, 1], sdlog = pars.we50[i,
        2])
    pval.we50$alpha[i] = pars.we50[i, 1]
    pval.we50$beta[i] = pars.we50[i, 2]
    pval.we50$cv[i] = sd(log(tempdat))/mean(log(tempdat))
    pval.we50$sd[i] = sd(log(tempdat))
}

# now calculate the number of times the cv or sd
# exceeds that of the real data

pval.we50$cvExceed = 0
pval.we50$sdExceed = 0

we50.cv = sd(log(tdat$total.eff[tdat$treat == "we50"]))/mean(log(tdat$total.eff[tdat$treat ==
    "we50"]))
we50.sd = sd(log(tdat$total.eff[tdat$treat == "we50"]))

pval.we50$cvExceed[pval.we50$cv > we50.cv] = 1
pval.we50$sdExceed[pval.we50$sd > we50.sd] = 1

# df to hold pvals for model comparison to self, a way
# of knowing the model fit the data well
t.pself = data.frame(year = rep(loopY[y], 6), scenario = c("Actual",
    "No Winter", "May-August", "25% weeday removal", "50% weekday removal",
```

```
    "50% weekend removal"), coef.var.pval = NA, sd.pval = NA)
# adding self comparison pvals
t.pself$coef.var.pval = c(sum(pval.actual$cvExceed)/nrow(pval.actual),
    sum(pval.noWinter$cvExceed)/nrow(pval.noWinter), sum(pval.mayAug$cvExceed)/nrow(pval.mayAug),
    sum(pval.wd25$cvExceed)/nrow(pval.wd25), sum(pval.wd50$cvExceed)/nrow(pval.wd50),
    sum(pval.we50$cvExceed)/nrow(pval.we50))
t.pself$sd.pval = c(sum(pval.actual$sdExceed)/nrow(pval.actual),
    sum(pval.noWinter$sdExceed)/nrow(pval.noWinter), sum(pval.mayAug$sdExceed)/nrow(pval.mayAug),
    sum(pval.wd25$sdExceed)/nrow(pval.wd25), sum(pval.wd50$sdExceed)/nrow(pval.wd50),
    sum(pval.we50$sdExceed)/nrow(pval.we50))
bpval.self.y = rbind(bpval.self.y, t.pself)
## p-value tests comparing the scenarios to actual to
## show that some scenarios approximate the actual
## quite well.

t.pcomp = data.frame(year = rep(loopY[y], 6), scenario = c("Actual",
    "No Winter", "May-August", "25% weeday removal", "50% weekday removal",
    "50% weekend removal"), coef.var.pval = NA, sd.pval = NA)

pval.actual$cvComp = 0
pval.actual$sdComp = 0
pval.actual$cvComp[pval.actual$cv > actual.cv] = 1
pval.actual$sdComp[pval.actual$sd > actual.sd] = 1

pval.noWinter$cvComp = 0
pval.noWinter$sdComp = 0
pval.noWinter$cvComp[pval.noWinter$cv > actual.cv] = 1
pval.noWinter$sdComp[pval.noWinter$sd > actual.sd] = 1

pval.mayAug$cvComp = 0
pval.mayAug$sdComp = 0
pval.mayAug$cvComp[pval.mayAug$cv > actual.cv] = 1
pval.mayAug$sdComp[pval.mayAug$sd > actual.sd] = 1

pval.wd25$cvComp = 0
pval.wd25$sdComp = 0
pval.wd25$cvComp[pval.wd25$cv > actual.cv] = 1
pval.wd25$sdComp[pval.wd25$sd > actual.sd] = 1

pval.wd50$cvComp = 0
pval.wd50$sdComp = 0
pval.wd50$cvComp[pval.wd50$cv > actual.cv] = 1
pval.wd50$sdComp[pval.wd50$sd > actual.sd] = 1

pval.we50$cvComp = 0
pval.we50$sdComp = 0
pval.we50$cvComp[pval.we50$cv > actual.cv] = 1
pval.we50$sdComp[pval.we50$sd > actual.sd] = 1

t.pcomp$coef.var.pval = c(sum(pval.actual$cvComp)/nrow(pval.actual),
    sum(pval.noWinter$cvComp)/nrow(pval.noWinter), sum(pval.mayAug$cvComp)/nrow(pval.mayAug),
    sum(pval.wd25$cvComp)/nrow(pval.wd25), sum(pval.wd50$cvComp)/nrow(pval.wd50),
    sum(pval.we50$cvComp)/nrow(pval.we50))
```

```
    t.pcomp$sd.pval = c(sum(pval.actual$sdComp)/nrow(pval.actual),
        sum(pval.noWinter$sdComp)/nrow(pval.noWinter), sum(pval.mayAug$sdComp)/nrow(pval.mayAug),
        sum(pval.wd25$sdComp)/nrow(pval.wd25), sum(pval.wd50$sdComp)/nrow(pval.wd50),
        sum(pval.we50$sdComp)/nrow(pval.we50))
    bpval.comp.y = rbind(bpval.comp.y, t.pcomp)

    # adding GR results to the output dataframe
    t.gr = data.frame(year = rep(loopY[y], 6), scenario = c("Actual",
        "No Winter", "May-August", "25% weeday removal", "50% weekday removal",
        "50% weekend removal"), gr.prsf = c(gr.a[[2]], gr.nw[[2]],
        gr.ma[[2]], gr.wd25[[2]], gr.wd50[[2]], gr.we50[[2]]),
        gr.par1 = c(gr.a[[1]][1, 1], gr.nw[[1]][1, 1], gr.ma[[1]][1,
            1], gr.wd25[[1]][1, 1], gr.wd50[[1]][1, 1], gr.we50[[1]][1,
            1]), gr.par2 = c(gr.a[[1]][2, 1], gr.nw[[1]][2, 1],
            gr.ma[[1]][2, 1], gr.wd25[[1]][2, 1], gr.wd50[[1]][2,
                1], gr.we50[[1]][2, 1]))
    grMetrics.y = rbind(grMetrics.y, t.gr)
}

# saving big loop's output since it takes a while to run
yearLoopOutput = list(bpval.self.y, bpval.comp.y, grMetrics.y)
# saveRDS(yearLoopOutput, file =
# 'yearLoopOutput_effort_3.13.25.RData')
```



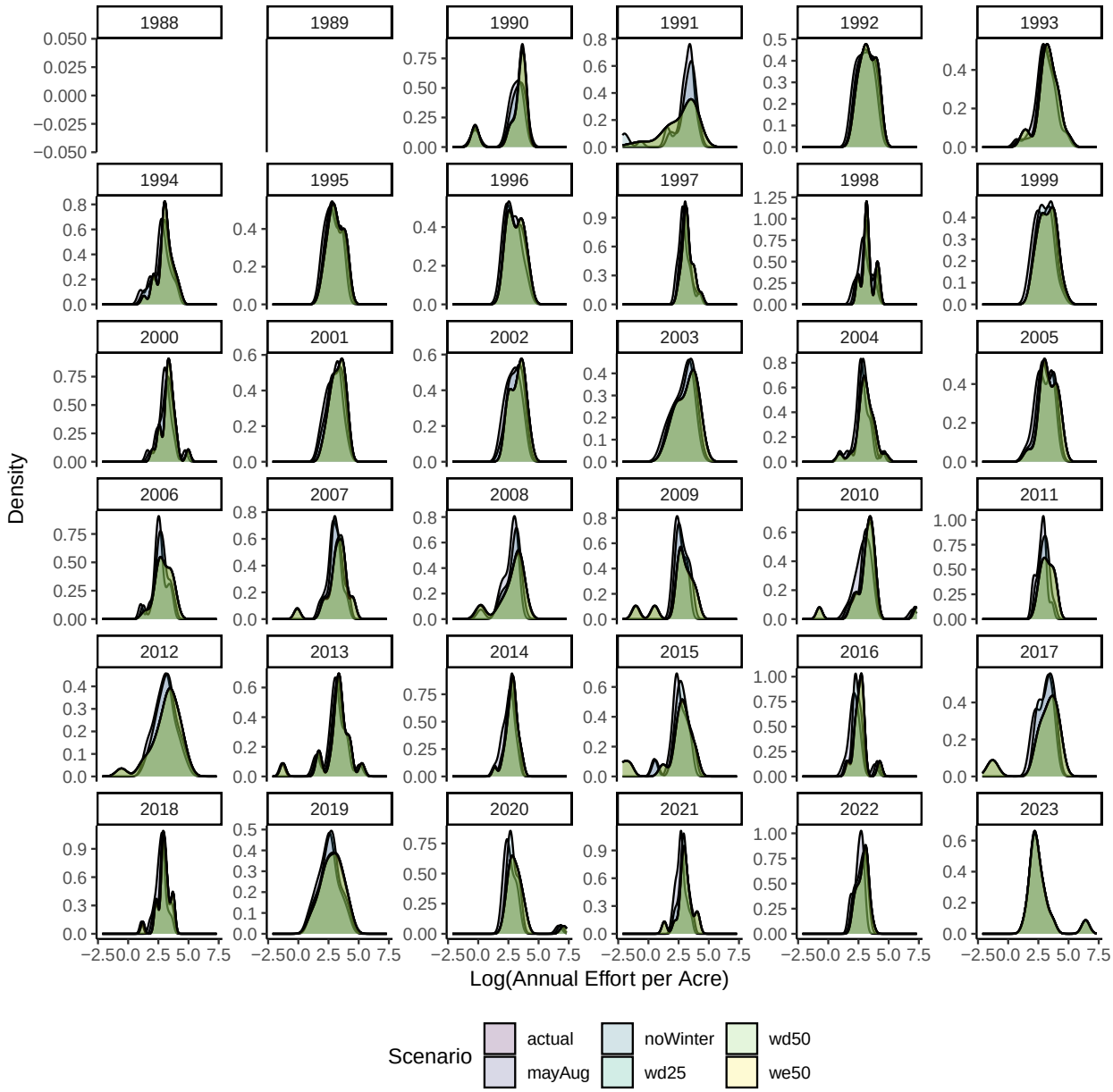


Figure 7: Distribution of exploitation rates across years in the creel data set. Different data reduction scenarios are noted with varying colors.

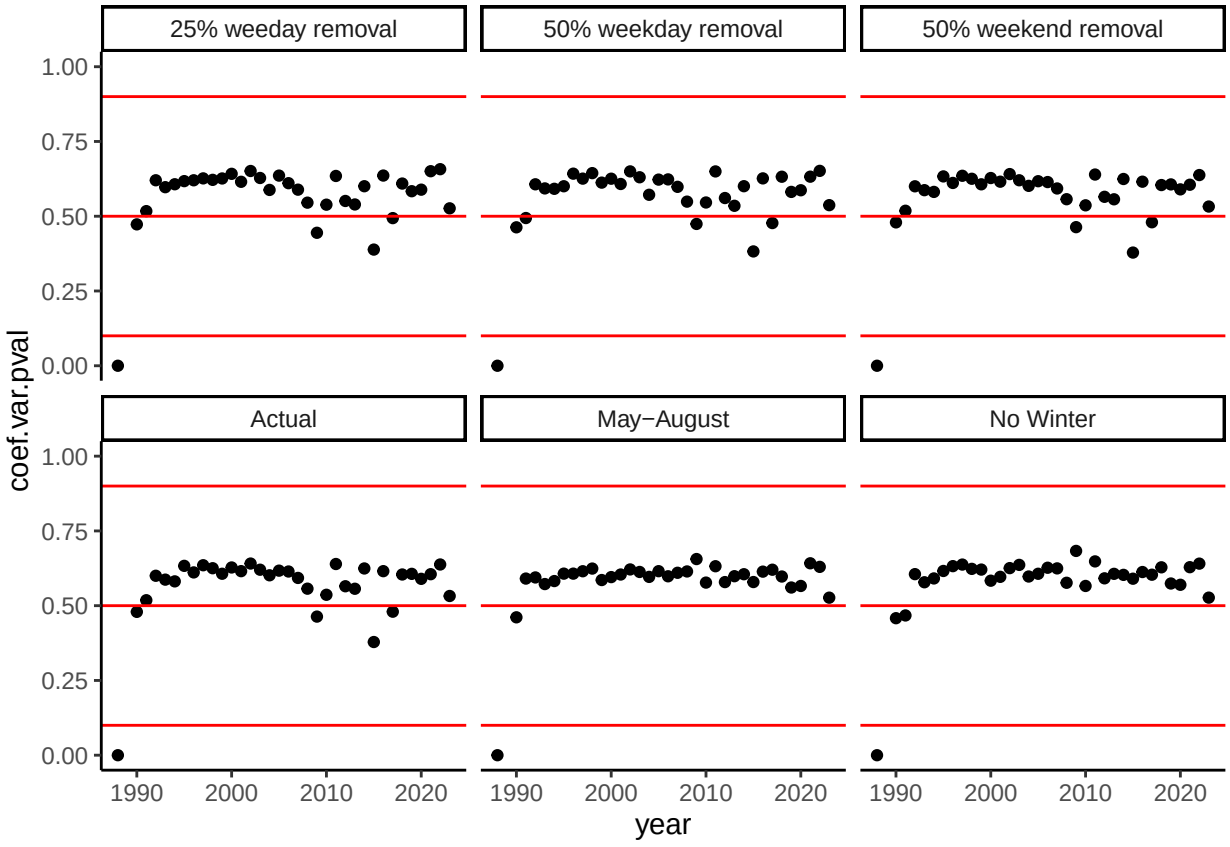
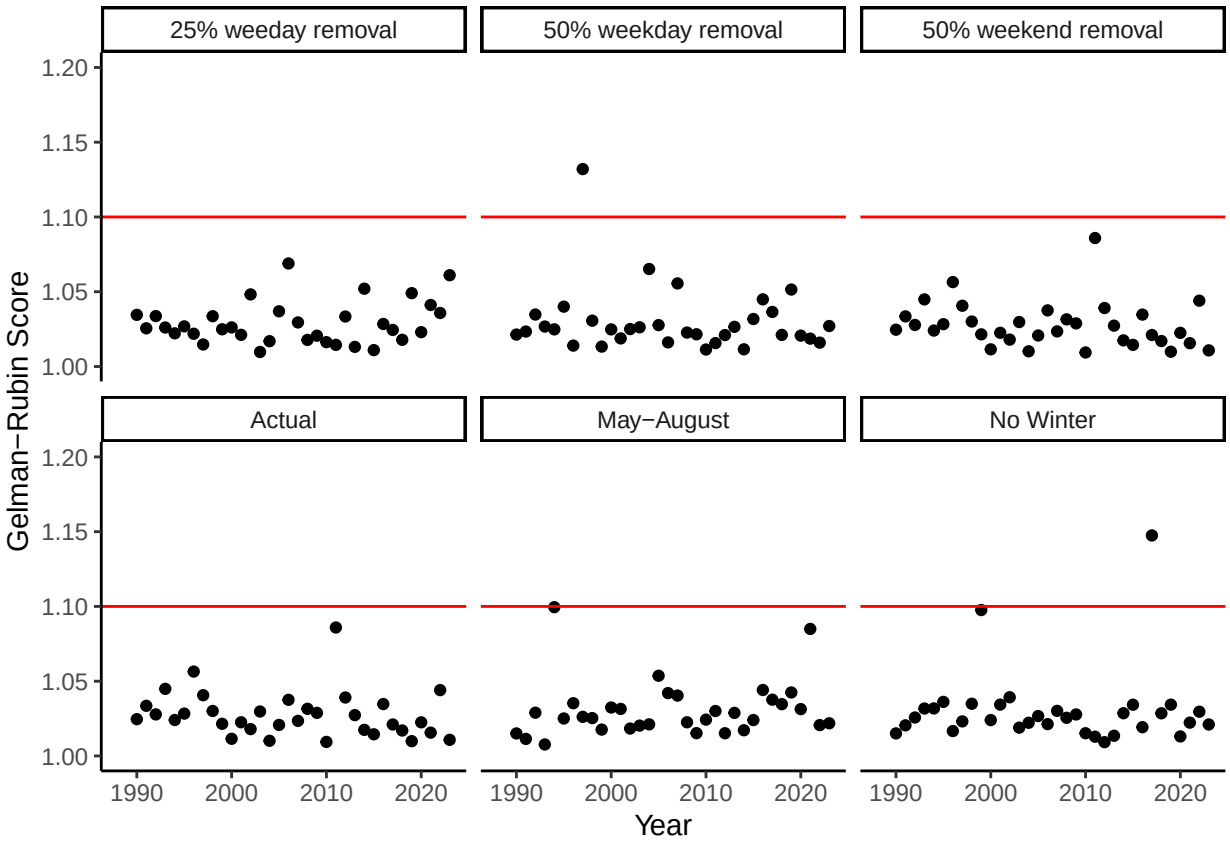


Figure 8: Comparison of coefficient of variations for bayesian p-values comparing the actual data to the simulated data for the creel year and data reduction scenario.



The results of these creel-year specific analyses suggest that even on an individual creel year level, the estimated annual effort per acre from the data-reduced scenario generally is not significantly different from the annual effort per acres calculated from the full data set (Figure **??**). Compared to the same analysis for the full population of creel data all at once instead of on a year-by-year basis, the estimated exploitation rates from the reduced data here don't match the actual quite as well for the seasonal data removals, but the majority of years still fall within the typical bounds of acceptance for this test. All models do appear to fit well and converge (Figure **??**).

There did not appear to be any obvious characteristics of the lakes themselves or their walleye populations that correlated with the magnitude of the difference between the actual estimated annual effort per acre and the reduced-data estimation. Walleye recruitment code (Figure **??**) and lake class (Figure **??**) were examined and showed no clear trend. This may be in large part due to the relatively small differences between each estimate of annual effort per acre and the reduced-data estimate that could make it hard to see an effects, which would further point towards there being minimal effect of data reductions on annual effort per acre estimate even at the individual creel-year level.

1.3.5 Important Caveats

Here are the important caveats for this analysis. These are things that I would expect another researcher to raise as potential weak points of this work. Number 1 can be addressed by me in consultation with other researchers and the scientific literature. Numbers 2 and 3 are probably better informed by the legal context of the situation. These don't have 'right' answers in the way that the other two do. Here the 'right' answer will be values-based and likely depends on what the group, or legal system, decides.

1. Accuracy measure. In order to compare the exploitation rate estimates from the reduced data to the actual data I used 1 standard deviation as my measure. This means that a reduced-data exploitation

rate estimate that is within 1 SD of the actual data exploitation rate estimate was considered to be 'the same'. There may be better metrics to use here, and different people may have different opinions about the best metric to use. My rationale for using this metric has been outlined above.

2. Bayesian p-value metrics. when calculating the Bayesian p-value to understand if the data from the reduced scenarios resembled that of the actual data I used the coefficient of variation and standard deviation. In reality any variance metric could be used to compare the two data sets. I chose these two because I felt that were intuitive enough for anyone to understand and defensible. But that may be others that should be explored and the results of the p-value tests may differ based on the metric used.
3. Related to the p-value metric are the cutoffs to use to decide whether there is a meaningful difference between the actual exploitation rate and the data reduced rate. The rule of thumb for this test is values <0.1 or >0.9 indicate a significant difference between the actual data estimate and the reduced data estimate. In reality it is up to the user to decide what those cutoffs should be based on the context of their problem. Whether or not we consider the reduced data exploitation rates similar or different from the actual can obviously be influenced by the cutoff numbers we chose.

1.4 Appendix

1.4.1 Alternative modeling distributions

Instead of the lognormal distribution there is one other probability distributions that could be used to model this data based on the characteristics of the data and the data characteristics assumed by each of the distributions.

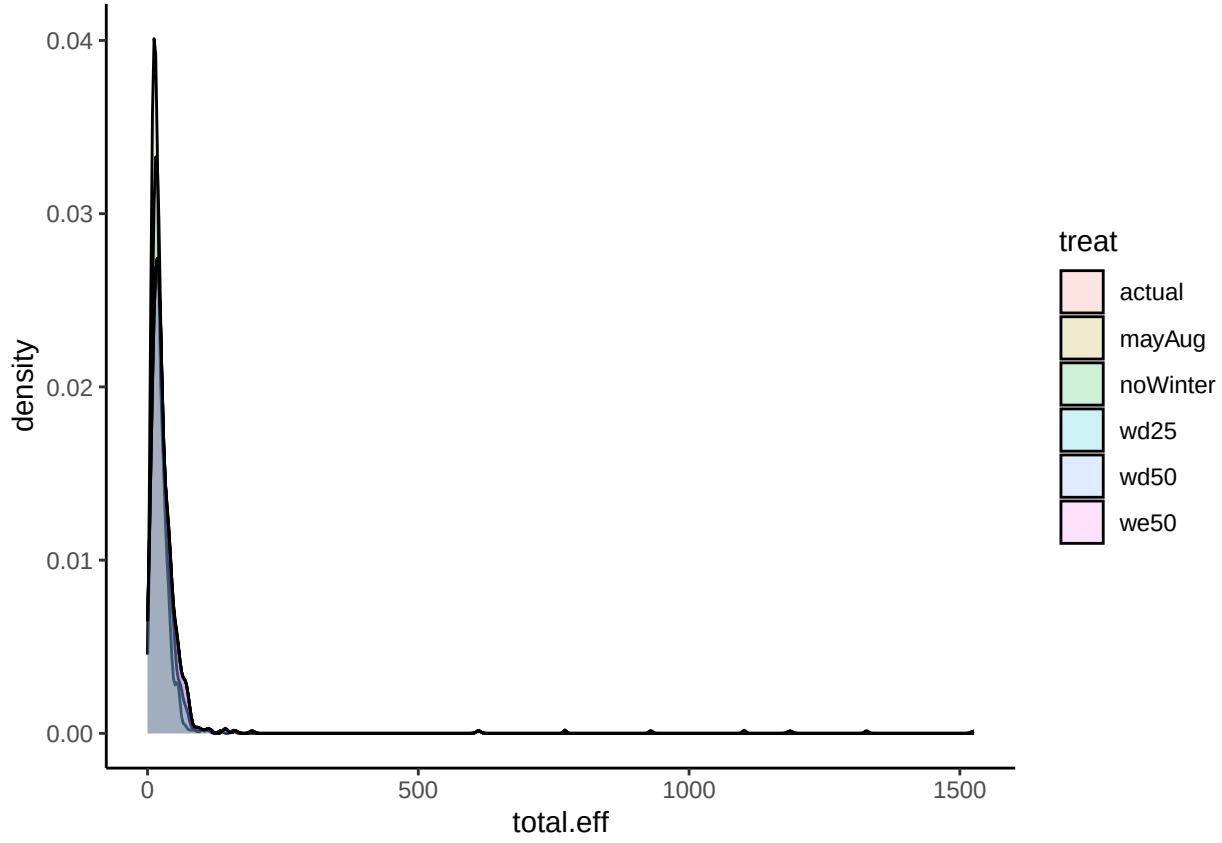
Table of data distributions and their definitions:

Distribution	Definition
Lognormal	Continuously distributed quantities with nonnegative values. Random variables with the property that their logs are normally distributed.
Gamma	Any continuous quantity that is nonnegative. Continuous version of a Poisson distribution.

The following analyses will compare the ability of models using the lognormal and gamma distributions to fit the full data and each of the reduced data set. A cursory look at the ability of gamma distributed models showed no real difference from beta and lognormal and the definition of the beta better represents the data we're dealing with than the gamma definition so further analyses with this family of models was not pursued (Figure 9). The purpose of the comparison between lognormal and beta family models is not to see which model provided the most convenient answer but to compare their ability to fit the data. All comparisons presented in this analysis are comparing a model's ability to fit the data **within** each dataset and **not** across data sets which is what is necessary to gain inference on the effect of any data reductions.

Table 5: Bayesian p-values for a gamma distributed model. Each p-value describes whether or not there is a significant difference between data generated by the fitted model and the actual data for that scenario. Two metrics are assessed here, coefficient of variation (CV) and standard devidation (SD).

Scenario	CV p-value	SD p-value
Actual	0	0
No Winter	0	0
May-August	0	0
25% weeday removal	0	0
50% weekday removal	0	0
50% weekend removal	0	0



Gelman-Rubin convergence diagnostics indicate all models have converged. Seems like the gamma models could be a potential alternative, the bayesian p values should help confirm this.

```
### MODEL CHECKNG ####

gelmanDiagnostics(eff.actual.gamma)  # 1 converged
gelmanDiagnostics(eff.nw.gamma)  # 1 converged
gelmanDiagnostics(eff.ma.gamma)  # 1 converged
gelmanDiagnostics(eff.25wd.gamma)  # 1 converged
gelmanDiagnostics(eff.50wd.gamma)  # 1.01 converged
gelmanDiagnostics(eff.50we.gamma)  # 1 converged
```

The Bayesian p-values in the table presented here suggests the gamma models do a poor job of reproducing

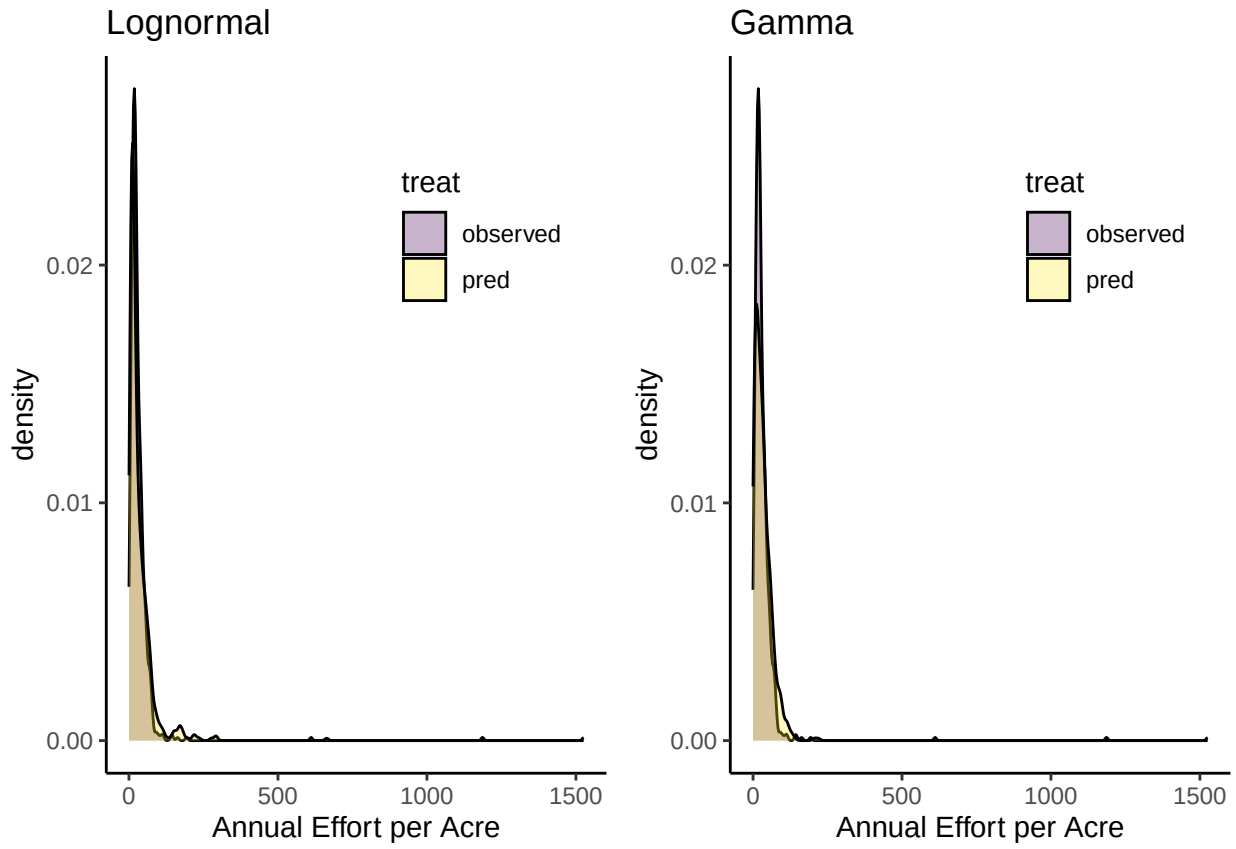


Figure 9: Comparison of model fits for lognormal and gamma, family of models. This rough look at the models suggests there are no obvious differences between the choice of modeling distribution. This will be evaluated statistically using bayesian p values later on.

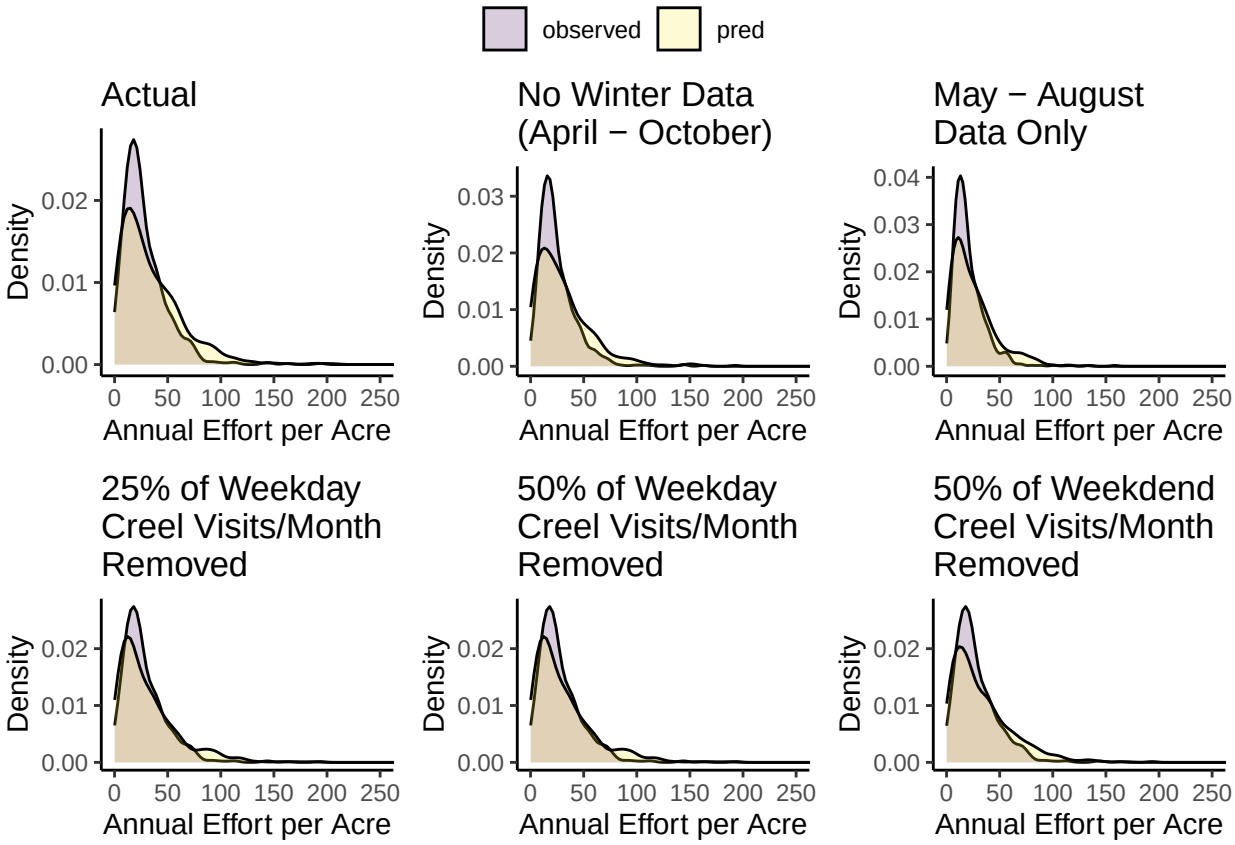


Figure 10: Visualization of the model fit to the data for each scenario using a gamma distribution instead of a lognormal distribution.

the data they were fit to (Table 5). This inference comes from the lack of p-values between 0.1 - 0.9 for the CV and SD metrics. Because this model is unable to reproduce the data it was fit to, we know that this model is not a useful one for fitting these data. This means that the gamma distribution not likely to be appropriate for making comparisons between the actual data and the reduced data to understand whether or not creel effort reductions result in significantly different annual angler effort per acre estimates or not.

1.4.2 P-value sensitivity analysis

Another important area of uncertainty in this analysis is the choice of metric to calculate Bayesian p-values for. In the main text of this document I've chosen the coefficient of variation and standard deviation as two metrics to assess. However any metric could be chosen as along as the choice can be justified in the context of the data and question at hand.

In this analysis I've chosen 3 additional test statistics to compare alongside the CV and SD. The test statistics used are summarized in Table 6. Here I've fit the models using the lognormal distribution as above and then calculated Bayesian p-values for each of the 5 test statistics and 6 data scenarios. I've also done a separate test using the χ^2 goodness of fit test to see how often the modeled data is significantly different from the observed data for each of the parameter values in the Markov-Chain Monte Carlo output from the model fitting algorithm.

1.4.2.1 Interpreting each statistic Some more detail on what I'm looking for in each statistic and what the values mean that are used to calculate each Bayesian p-value. It's important to remember that the way the sampling algorithm works in this Bayesian framework the frequency of values in the MCMC output is relative to their support in the data. In other words, parameter values that produce better models fits show up in the chain more often. This is critical to understanding the Bayesian p-values here because each test statistic is calculated for simulated data based on the MCMC output so each test statistic value should appear with a frequency equal to the support provided by the data too. For example, the medians calculated from data sets produced by each parameter set in the MCMC output should produce medians that have frequencies equal to how well those parameters fit the data. Thus medians well below the median of the observed data should be pretty rare (and likewise for medians well above) because the parameter set from the MCMC chain that produces data with said median should be relatively infrequent in the MCMC output. Medians close to the median of the observed data should be more common, if the model is fitting the data well, because the parameters generating those means are more common in the MCMC output due to the better fit to the data they provide. This results in medians that are often close to the median of the observed data and by random chance should be just as likely to be above as below the median of the observed data. This is why Bayesian p-values close to 0.5 signify a good model fit, because about 50% of the time the test statistic is more extreme than the value for the observed data. If this values is extremely high or low then is signals that our model is not adequately representing the observed data.

1.4.2.1.1 Coefficient of Variation Straightforward, the CV is calculated for a data set simulated from each set of parameters in the MCMC chain from the model fit. Each dataset is simulated by drawing from a random lognormal distribution parameterized according to the values at a given place in the MCMC chain. The CV value from each of these simulated datasets is then compared to the CV for the observed data for a given scenario (Actual, No Winter, May-August, etc.). Whether the CV for the simulated data is greater than or less than the CV of the observed data is recorded. **If the model is able to reproduce the observed data well then the CV of the simulated data should be greater than the CV of the observed data about 50% of the time and less than the observed CV about 50% of the time too.**

1.4.2.1.2 Standard Deviation Another straightforward calculation. SD is calculated for a data set drawn from a random lognormal distribution parameterized using the values in the MCMC chain. This is repeated for each set of parameter values in the MCMC chain to create as many simulated data sets as

there are iterations in the MCMC chain. The SD of each of these simulated data sets is compared to the SD for the observed data for that scenario (Actual, No Winter, May - August, etc.). Whether the SD of the simulated data is greater than or less than the SD of the observed data is recorded. **If the model is able to reproduce the observed data well then the SD of the simulated data should be greater than the SD of the observed data about 50% of the time and less than the SD of the observed data about 50% of the time too.**

1.4.2.1.3 Median Simple descriptive statistic here. The median is calculated for each simulated data set produced by drawing values from a random lognormal distribution parameterized using the values in the MCMC output. The number of times the median of the simulated data set exceeds the median of the observed data is calculated and that proportion of times the test statistic exceeds the value for the observed data is the Bayesian p-value. **If the model is adequately representing the data then the medians generated from the simulated data sets should exceed the median of the observed data roughly 50% of the time.**

1.4.2.1.4 Kurtosis This metric essentially measures the shape of a distribution, specifically the tails. Kurtosis is calculated for the simulated data for each set of parameter values in the MCMC output and compared to the kurtosis of the observed data for the given scenario (Actual, No Winter, May - August, etc.). When the kurtosis value of the simulated data is greater than the kurtosis of the observed data this signals more frequent extreme values in the data. In other words the tails of the distribution of the simulated data are thicker than the tails of the distribution of the observed data. The opposite is true when the kurtosis of the simulated data is less than the kurtosis of the observed data. **A well-fitting model will produce data with kurtosis values similar to the the observed data's kurtosis. The kurtosis of the simulated data will exceed that of the observed data roughly 50% of the time. If the kurtosis of the simulated data is more frequently less than the observed data this would signal that the model is not doing well as representing the rare values in the tails of the data distribution. The opposite is true if kurtosis values for the simulated data tend to be larger than the observed data.**

1.4.2.1.5 Chi Square Test (χ^2) This test is performed outside the Bayesian p-value framework. Instead, each simulated data set arising from a set of parameters in the MCMC output is compared to the probability distribution of the observed data to ask whether the simulated data arises from the same distribution as the observed data. Again, because of the way the parameter space is sampled in MCMC algorithms the values that produce better model fits will be more common which means that in the χ^2 test the null hypothesis that the data comes from the supplied probability distribution should be accepted more often than it's rejected. **If the null hypothesis is rejected the majority of the time that would indicate that the model is not adequately representing the data if it can't produce simulated data that would appear to be from the probability distribution of the observed data used to fit the model in the first place.**

1.4.2.1.6 Fisher 'F' Statistic The F statistic is the ratio of variances between the simulated and observed data sets. For this test I'm looking to see if the F statistic for the simulated:observed comparison is greater than or less than 1 (the ratio of the variance for the observed:observed comparison). **The closer the F statistic is to 1 for the simulated:observed comparison the better job the model is doing at adequately representing the data. So the number of times the F statistic exceeds 1 should, if the model is fitting the data well, be about 50% of the time. If the Bayesian p-value is much higher than 0.5 that would indicate that the variance of the simulated data is often greater than the variance of the observed data. The opposite then is true when the p-value is smaller than 0.5**

Table 6: Candidate variance metrics to use for calculation of Bayesian p-values.

Statistic	Description
CV	Ratio of the standard deviation to the mean.
SD	Square root of the variance.
Median	Middle of the data when all values are ordered from smallest to largest. Similar to a mean but less sensitive to
Kurtosis	Measure of the width, or 'tailedness' of a distribution. In other words, do the tails of the distribution contain n
X2	Chi square test statistic for a 'goodness of fit' test is calculated. Here I want to know if frequency of values in t
F	The ratio of the variance between the model simulated data and the observed data.

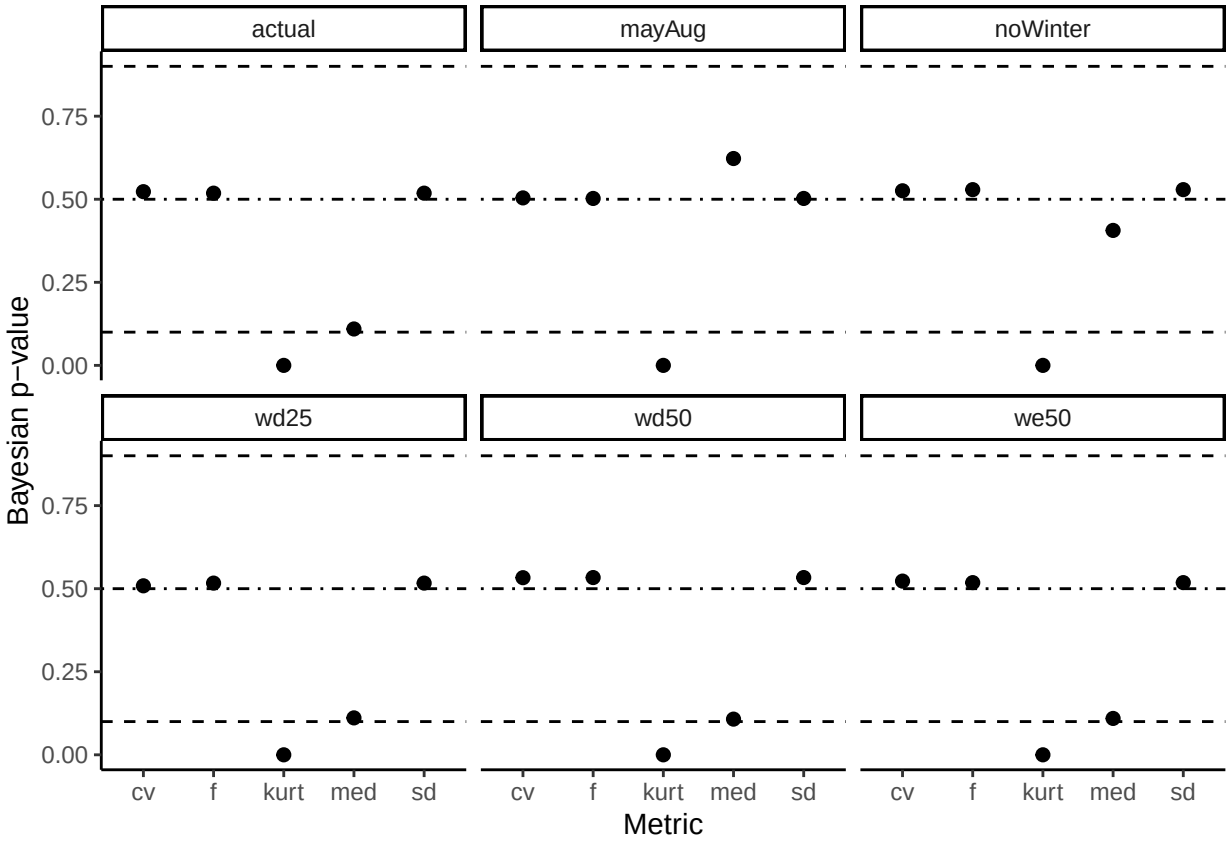


Figure 11: Comparison of multiple metrics for calculating Bayesian p-values. Each panel is a different data scenario. The comparisons in each panel are comparing the model simulated data to the observed data for that same sencario, NOT comparing model simulated data from a reduction scenario tot he actual data. This comparison to self is to understand whether the model is adequately representing the data and whether the choice of statistic influences the answer to that question. Values close to 0.5 are ideal, values more extreme than 0.1 or 0.9 are considered evidence for a poor model fit (i.e. significant difference betweek model simulated data and the observed data).

1.4.3

Figure 11 shows the p-values resulting from each metric for each data scenario. Aside from kurtosis and median, the p-values are quite similar across metrics withing a specific data scenario. This suggests that while kurtosis and median may not be a good choices here, the choice between f statistic, cv, or sd, should have minimal impact on the inference drawn from these models. Digging into kurtosis a bit more, it's not immediately clear why so many of the simulated data sets have thinner tails than observed data. This may have to do with the random sampling function `rlnorm()` which samples randomly from a distribution informed by the MCMC output parameters (as the mean and standard deviation respectively). It may be that the variance term in the function is a tad low and that's preventing some of the outliers from being chosen and creating those thicker tails that are seen in the observed data. It's not immediately clear to me why median performed poorly here either. Interestingly, median is only non-significant for the two seasonal reductions, which are the two that were significantly different for the comparison to the actual data above, but here when comparing to self, median is not significantly different just like many of the other metrics.

The Chi Square Test (χ^2) also returned all Bayesian p-values as 1, meaning highly significant, so that measure lines up with kurtosis and median. Basically seems here like there are 3 for and 3 against non-significance of the lognormal model's ability to reproduce the data it was fit to for 4 out of 6 scenarios.

Finally, the choice of 0.1 and 0.9 as the cutoff values for significance here do not seem to influence the outcomes.