TSA FINAL REPORT:

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Introduction

Method (Data Processing)

Data

Three datasets used in the project were collected from EDI Data Portal, including:

- 1. North Temperate Lakes LTER: Phytoplankton Madison Lakes Area 1995 current; (Magnuson & H.Stanley, 2022)
- 2. North Temperate Lakes LTER: Physical Limnology of Primary Study Lakes 1981 current;
- 3. North Temperate Lakes LTER: Chemical Limnology of Primary Study Lakes: Nutrients, pH and Carbon 1981 current.

The three files respectively record the water body phytoplankton information, physical information and chemical information of multiple lakes in the Wisconsin range. We analyzed these data at the beginning stage to screen out suitable research subjects, including the target lake, and primary algae responsible for blooms. First, we chose Mendota Lake (ME) for this project, as it has more time measurement data compared to other lakes, which might be more conducive to time series analysis and obtaining more reliable results (Table 1). Second, to obtain information on dominant species that may cause water blooms, we accumulated the biomass of algae from different divisions and considered the algae with the highest total biomass to

be the main contributor to water bloom outbreaks. It is worth noting that the original data records the biomass of specific algal species on the observation day. Therefore, to obtain division-level data, we summed the biomass of all species within the same division on the same day to obtain the biomass information for the division. The result shows that the dominant division is Cyanophyta, which is also consistent with other studies (Table 2)[Brock (2012)](Beversdorf, 2015).

Table 1: Site Information

Site	Observation Date Count
ME	402
MO	355
WI	23
$_{\mathrm{FI}}$	1

Table 2: Division level Total Biomass (mg/L)

Division	Count	Total Biomass	Max Biomass	Min Biomass	Mean Biomass
Cyanophyta	8581	1824.25213	76.0000	0.00e+00	0.2125920
Bacillariophyta	1914	378.01888	13.4028	3.19 e-05	0.1975020
Chlorophyta	4368	244.95205	84.6924	0.00e+00	0.0560788
Cryptophyta	1876	76.11009	2.9630	3.63 e-05	0.0405704
Pyrrhophyta	415	29.12950	5.3194	0.00e+00	0.0701916

After identifying the target lake and algal division, we cleaned and combined the three data tables. The following are the data cleaning steps:

- a. Integrate the phytoplankton data according to lake id, sampledate, depth range, and division to obtain the biomass information of each division on the observation day. Then, filter out all data with a lake id of Mendota and a division of Cyanophyta.
- b. Filter out the physical and chemical information of Lake Mendota. Considering that the original data records information at different depths on the same observation day, we calculated the average of all environmental data at depths of 0-8m, which correspond to the depths mentioned in the algae information. It is worth noting that on some dates, the depth of the algae information is 0-2m, and in these cases, we used the average environmental data for 0-2m.
- c. Based on the sampling date and depth range, we combined these data together (Table 3).

Table 3: rawdata

lakeid	sampledate	total_biomass	Temperature	date_diff	TN	TP
ME	1995-01-24	0.0128965	NA	NA	NA	NA
ME	1995-03-28	0.0013183	NA	63	NA	NA

lakeid	sample date	$total_biomass$	Temperature	${\rm date_diff}$	TN	TP
ME	1995-04-11	0.0017578	NA	14	NA	NA
ME	1995-04-24	0.0019157	NA	13	NA	NA
ME	1995-05-23	0.8052959	13.64444	29	0.7305	0.0895000
ME	1995-06-06	0.0738443	16.84444	14	0.7195	0.0756667

- d. We averaged the data monthly and used the zoo function (na.approx, rule = 2) to fill in NA values. Due to this method is not suitable for filling in NA values at the beginning of data, data before 1996 were removed.
- e. The final dataset includes dates (from 1996 to December 2020), temperature, total nitrogen, total phosphorus, and biomass (Table 4).

Table 4: Final Data

date	Temperature	TN	ТР	Biomass
1996-01-01	3.702222	0.7277500	0.1163333	0.4872730
1996-02-01	5.104444	0.7835000	0.1096667	0.1878542
1996-03-01	6.506667	0.8120556	0.1080556	0.1224752
1996-04-01	7.908889	0.8406111	0.1064444	0.0570962
1996-05-01	9.311111	0.8691667	0.1048333	0.0817296

Result ()

#Load/install required package here

library(lubridate)

library(ggplot2)

library(forecast)

```
## Registered S3 method overwritten by 'quantmod':
```

method from

as.zoo.data.frame zoo

library(Kendall)

library(tseries)

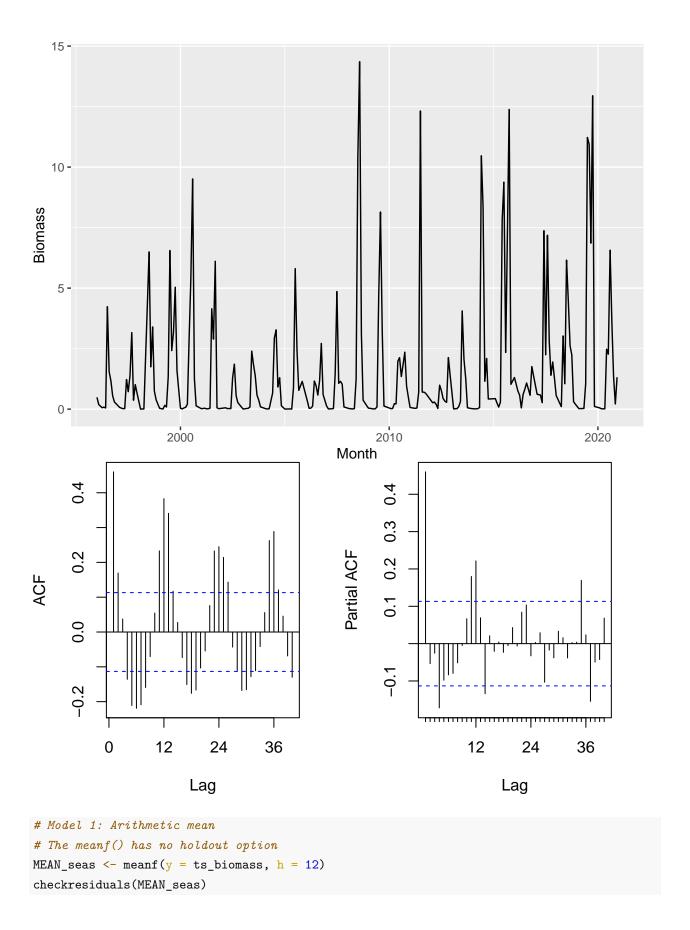
library(outliers)

library(tidyverse)

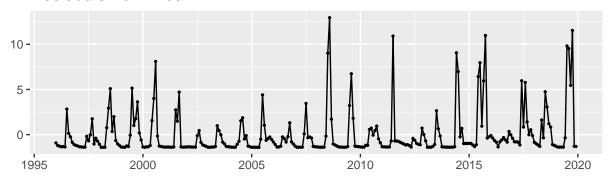
library(smooth)

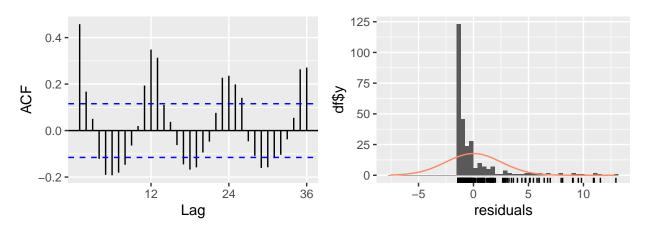
Loading required package: greybox

```
## Package "greybox", v1.0.7 loaded.
##
## Attaching package: 'greybox'
## The following object is masked from 'package:lubridate':
##
##
       hm
## The following object is masked from 'package:tidyr':
##
##
       {\tt spread}
## This is package "smooth", v3.2.0
#New package for M9 to assist with tables
#install.packages("kableExtra")
library(kableExtra)
##
## Attaching package: 'kableExtra'
## The following object is masked from 'package:dplyr':
##
##
       group_rows
Original (1996-2020)
```



Residuals from Mean

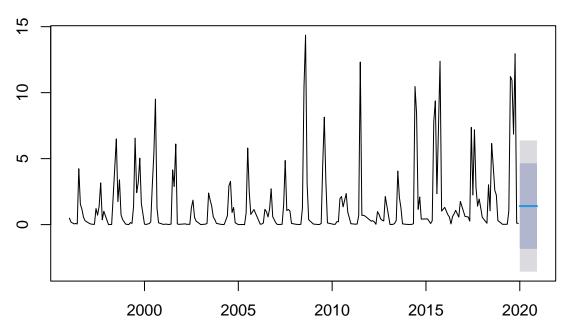




```
##
## Ljung-Box test
##
## data: Residuals from Mean
## Q* = 258.95, df = 23, p-value < 2.2e-16
##
## Model df: 1. Total lags used: 24</pre>
```

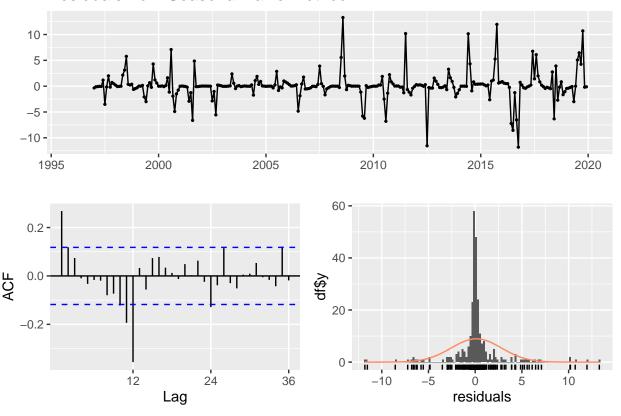
plot(MEAN_seas)

Forecasts from Mean



Model 2: Seasonal naive
SNAIVE_seas <- snaive(ts_biomass, h=12, holdout=FALSE)
checkresiduals(SNAIVE_seas)</pre>

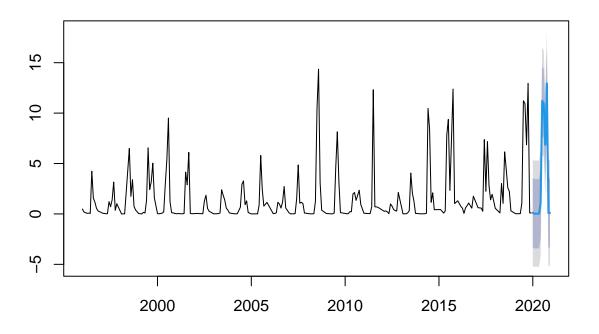
Residuals from Seasonal naive method



```
##
## Ljung-Box test
##
## data: Residuals from Seasonal naive method
## Q* = 93.651, df = 24, p-value = 3.556e-10
##
## Model df: 0. Total lags used: 24
```

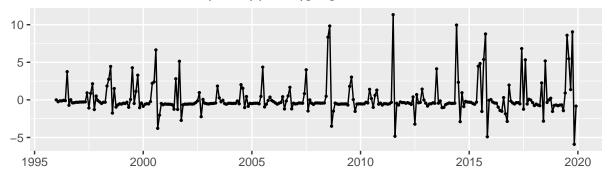
plot(SNAIVE_seas)

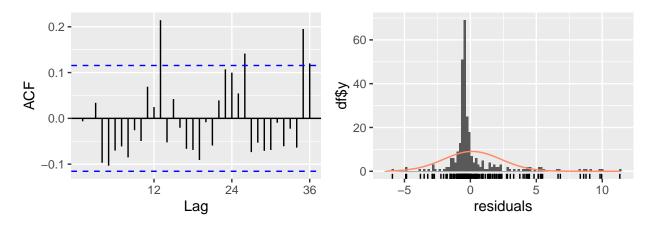
Forecasts from Seasonal naive method



Model 3: SARIMA
SARIMA_autofit <- auto.arima(ts_biomass)
checkresiduals(SARIMA_autofit)</pre>

Residuals from ARIMA(1,1,1)(0,0,1)[12]



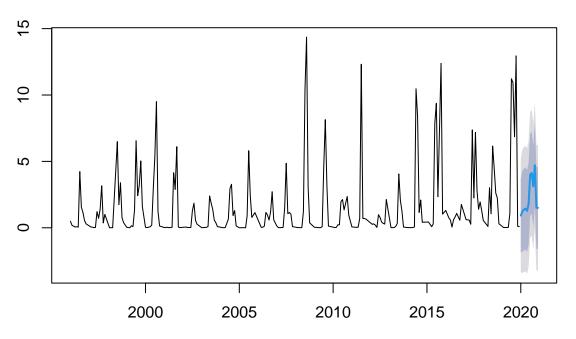


```
##
## Ljung-Box test
##
## data: Residuals from ARIMA(1,1,1)(0,0,1)[12]
## Q* = 42.8, df = 21, p-value = 0.003333
##
## Model df: 3. Total lags used: 24
```

```
\#Generating\ forecasts
```

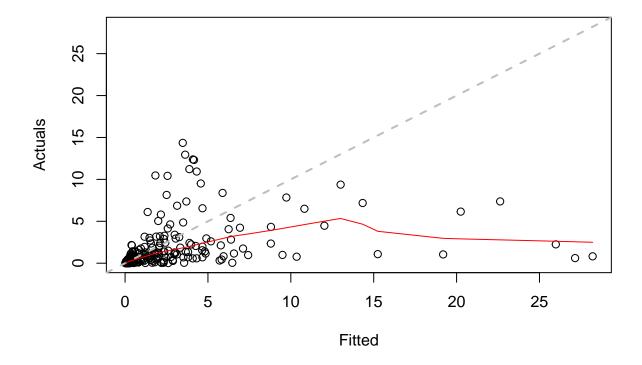
 $\label{thm:continuous} \begin{tabular}{ll} \$

Forecasts from ARIMA(1,1,1)(0,0,1)[12]

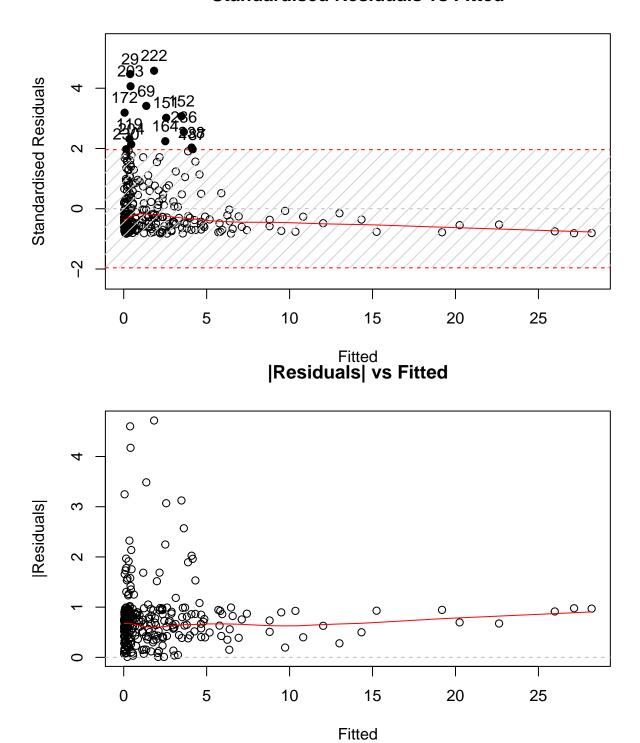


Model 4: SS Exponential smoothing
SSES_seas <- es(ts_biomass,model="ZZZ",h=12,holdout=FALSE)
plot(SSES_seas)</pre>

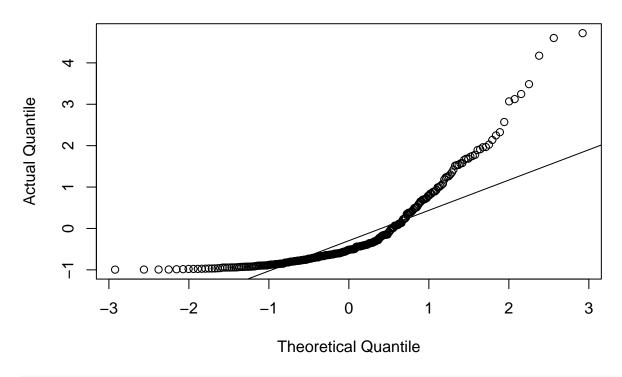
Actuals vs Fitted



Standardised Residuals vs Fitted

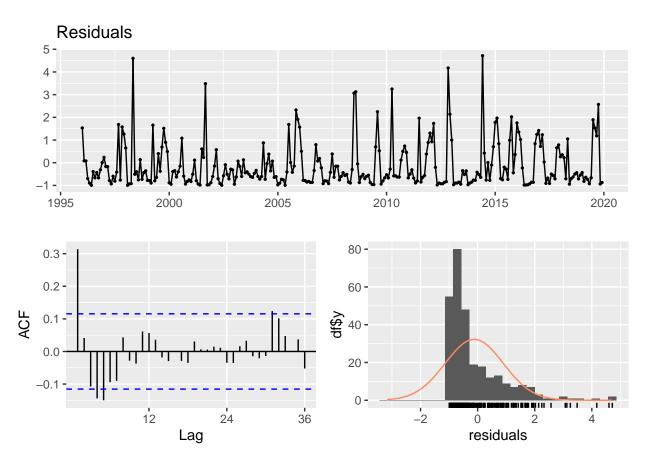


QQ plot of Normal distribution



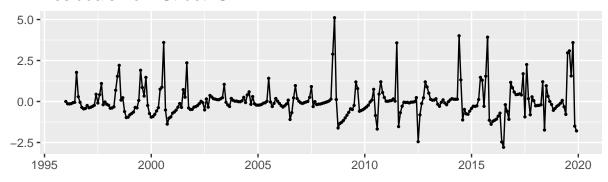
 ${\tt checkresiduals}({\tt SSES_seas})$

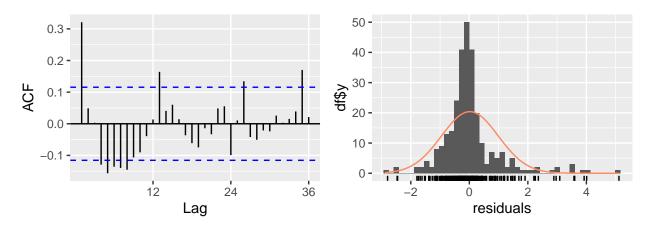
Warning in modeldf.default(object): Could not find appropriate degrees of
freedom for this model.



Warning in modeldf.default(object): Could not find appropriate degrees of
freedom for this model.

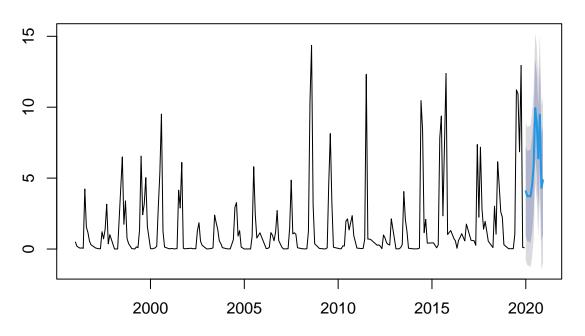






#Generating forecasts
StructTS() does not call the forecast() internally so we need one more step
SS_for <- forecast(SS_seas,h=12)
plot(SS_for)</pre>

Forecasts from Basic structural model



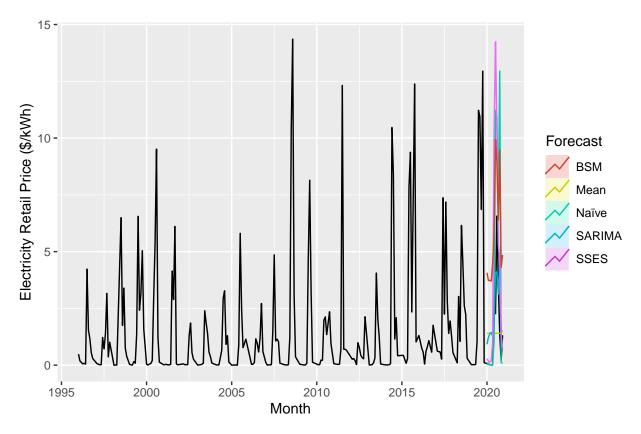
```
#Model 1: Arithmetic mean
MEAN_scores <- accuracy(MEAN_seas$mean,last_obs) #store the performance metrics</pre>
#Model 2: Seasonal naive
SNAIVE_scores <- accuracy(SNAIVE_seas$mean,last_obs)</pre>
# Model 3: SARIMA
SARIMA_scores <- accuracy(SARIMA_for$mean,last_obs)</pre>
# Model 4: SSES
SSES_scores <- accuracy(SSES_seas$forecast,last_obs)</pre>
# Model 5: BSM
SS_scores <- accuracy(SS_for$mean,last_obs)</pre>
#create data frame
seas_scores <- as.data.frame(rbind(MEAN_scores, SNAIVE_scores, SARIMA_scores, SSES_scores, SS_scores))</pre>
row.names(seas_scores) <- c("MEAN", "SNAIVE", "SARIMA", "SSES", "BSM")</pre>
#choose model with lowest RMSE
best_model_index <- which.min(seas_scores[,"RMSE"])</pre>
cat("The best model by RMSE is:", row.names(seas_scores[best_model_index,]))
```

The best model by RMSE is: SARIMA

Table 5: Forecast Accuracy for Seasonal Data

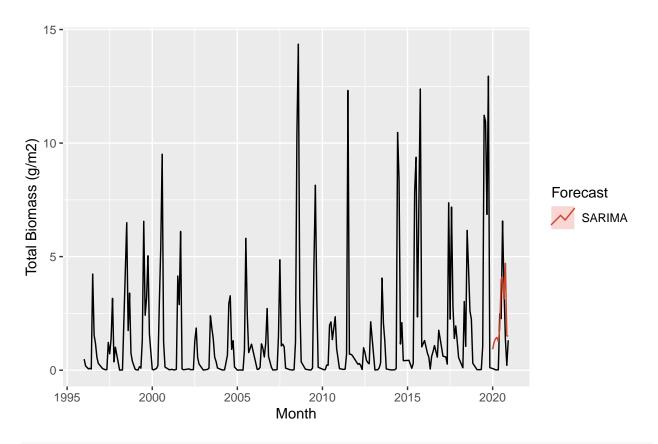
	ME	RMSE	MAE	MPE	MAPE
MEAN	0.09077	1.91972	1.45817	-2993.9993	3030.8195
SNAIVE	-2.12360	4.54636	2.58677	-122.4177	164.9659
SARIMA	-0.75532	1.58841	1.35418	-2867.0051	2879.9488
SSES	-2.55079	4.40694	2.64893	-998.5011	1005.9502
BSM	-4.29032	4.61610	4.29032	-8743.8441	8743.8441

```
autoplot(ts_biomass_data) +
  autolayer(MEAN_seas, PI=FALSE, series="Mean") +
  autolayer(SNAIVE_seas, PI=FALSE, series="Naïve") +
  autolayer(SARIMA_for, PI=FALSE, series="SARIMA") +
  autolayer(SSES_seas$forecast, series="SSES") +
  autolayer(SS_for, PI=FALSE, series="BSM") +
  xlab("Month") + ylab("Electricity Retail Price ($/kWh)") +
  guides(colour=guide_legend(title="Forecast"))
```



```
autoplot(ts_biomass_data) +

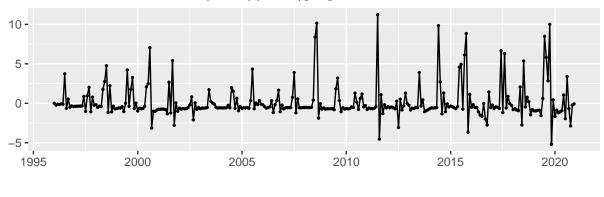
autolayer(SARIMA_for,PI=FALSE, series="SARIMA") +
    xlab("Month") + ylab("Total Biomass (g/m2)") +
    guides(colour=guide_legend(title="Forecast"))
```

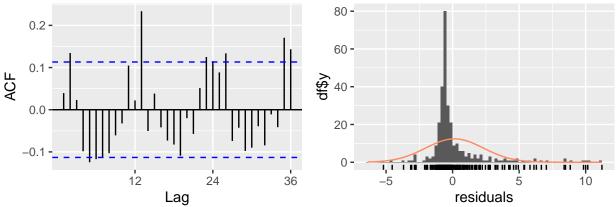


Forecast

SARIMA_autofit_new <- auto.arima(ts_biomass_data)
checkresiduals(SARIMA_autofit_new)</pre>

Residuals from ARIMA(0,1,2)(0,0,1)[12]

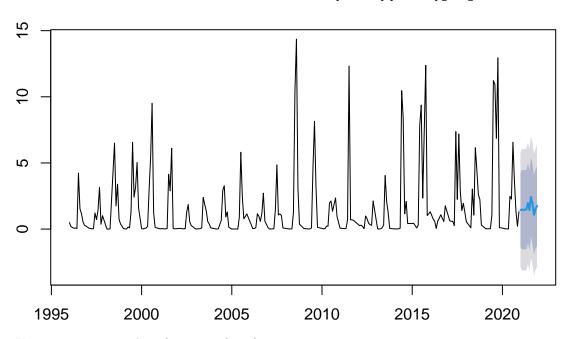




```
##
## Ljung-Box test
##
## data: Residuals from ARIMA(0,1,2)(0,0,1)[12]
## Q* = 68.766, df = 21, p-value = 5.534e-07
##
## Model df: 3. Total lags used: 24
```

```
SARIMA_for_new <- forecast(SARIMA_autofit_new, h=12)
plot(SARIMA_for_new)</pre>
```

Forecasts from ARIMA(0,1,2)(0,0,1)[12]



Use recent ten-year data (2010-2020) to forecast

```
# Change the time span

# Transform to time series format

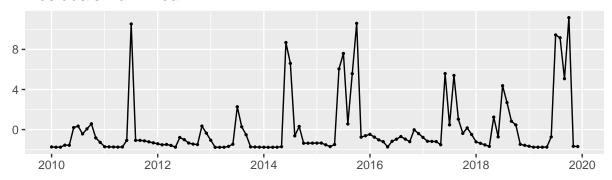
ts_biomass_data <- ts(
    biomass_data_frame[169:300,2],
    start=c(year(biomass_data_frame$Month[169]),month(biomass_data_frame$Month[169])),
    frequency=12)

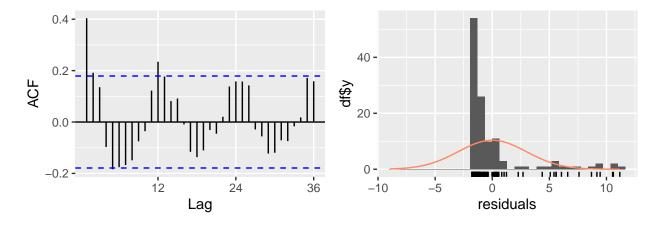
ts_biomass <- ts(
    biomass_data_frame[169:288,2],
    start=c(year(biomass_data_frame$Month[169]),month(biomass_data_frame$Month[169])),
    frequency=12)

last_obs <- ts_biomass_data[121:132]</pre>
```

```
# Model 1: Arithmetic mean
# The meanf() has no holdout option
MEAN_seas <- meanf(y = ts_biomass, h = 12)
checkresiduals(MEAN_seas)</pre>
```

Residuals from Mean

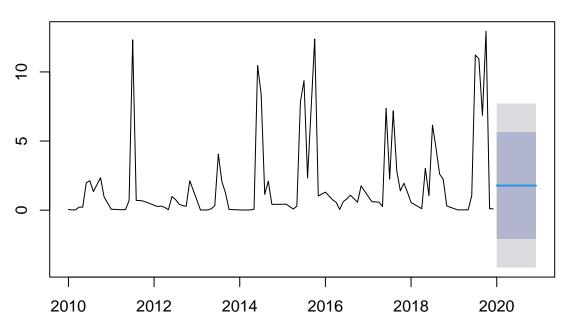




```
##
## Ljung-Box test
##
## data: Residuals from Mean
## Q* = 73.247, df = 23, p-value = 3.795e-07
##
## Model df: 1. Total lags used: 24
```

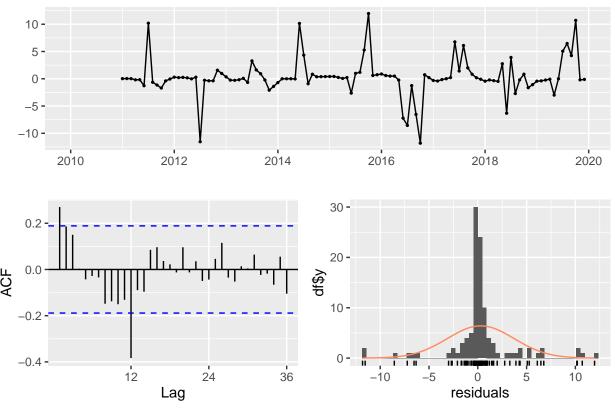
plot(MEAN_seas)

Forecasts from Mean



Model 2: Seasonal naive
SNAIVE_seas <- snaive(ts_biomass, h=12, holdout=FALSE)
checkresiduals(SNAIVE_seas)</pre>

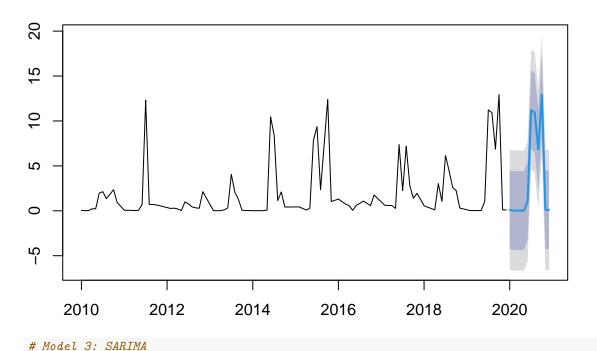
Residuals from Seasonal naive method



```
##
## Ljung-Box test
##
## data: Residuals from Seasonal naive method
## Q* = 49.511, df = 24, p-value = 0.001633
##
## Model df: 0. Total lags used: 24
```

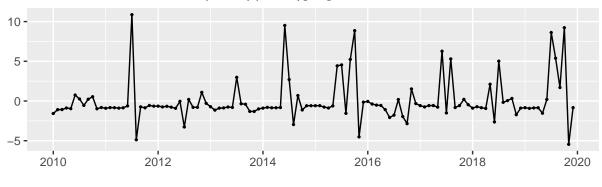
plot(SNAIVE_seas)

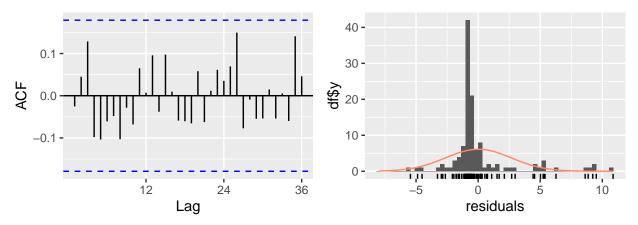
Forecasts from Seasonal naive method



```
SARIMA_autofit <- auto.arima(ts_biomass)
checkresiduals(SARIMA_autofit)
```

Residuals from ARIMA(1,0,0)(1,0,0)[12] with non-zero mean



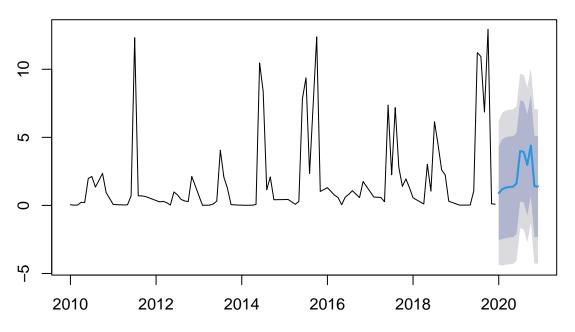


```
##
## Ljung-Box test
##
## data: Residuals from ARIMA(1,0,0)(1,0,0)[12] with non-zero mean
## Q* = 14.711, df = 22, p-value = 0.8743
##
## Model df: 2. Total lags used: 24
```

```
#Generating forecasts
```

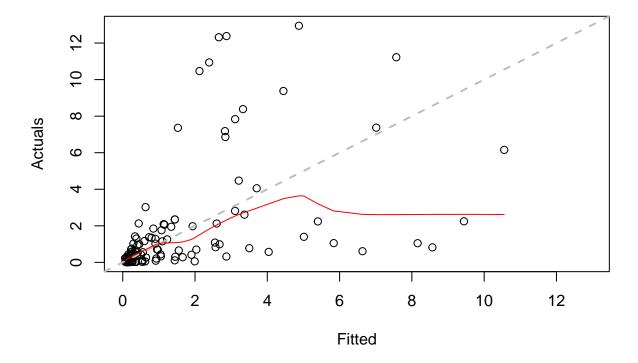
 $\label{thm:continuous} \begin{tabular}{ll} \$

Forecasts from ARIMA(1,0,0)(1,0,0)[12] with non-zero mean

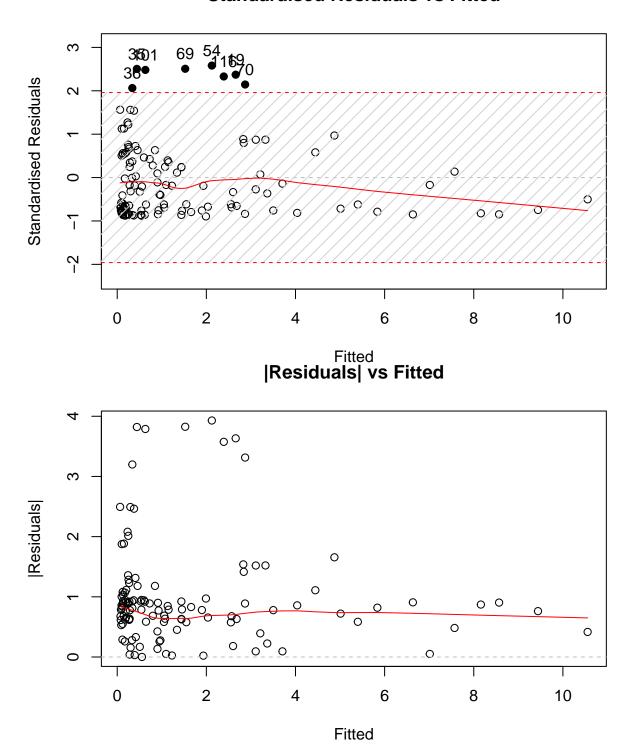


Model 4: SS Exponential smoothing
SSES_seas <- es(ts_biomass,model="ZZZ",h=12,holdout=FALSE)
plot(SSES_seas)</pre>

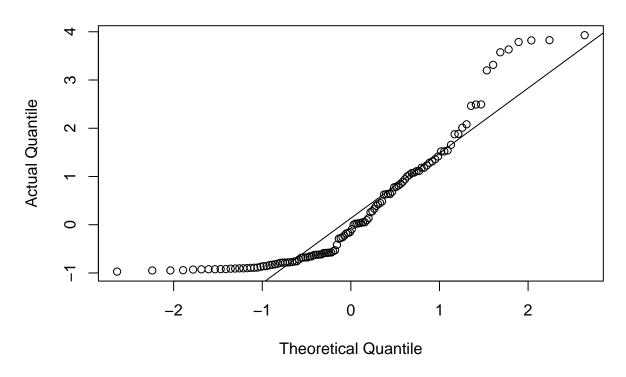
Actuals vs Fitted



Standardised Residuals vs Fitted

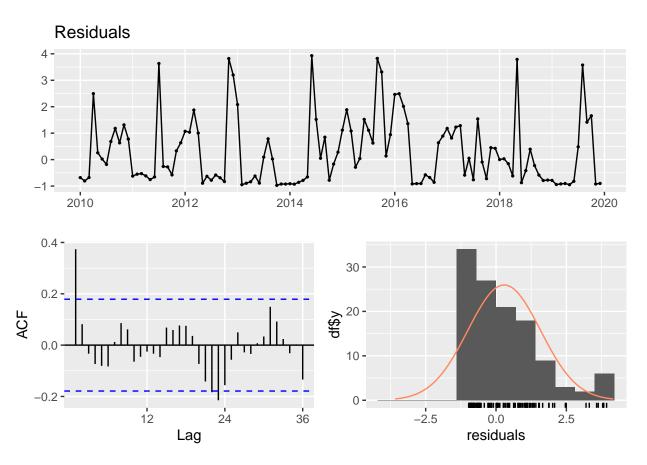


QQ plot of Normal distribution



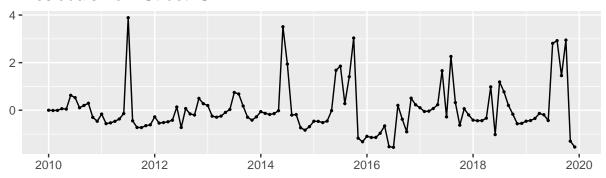
checkresiduals(SSES_seas)

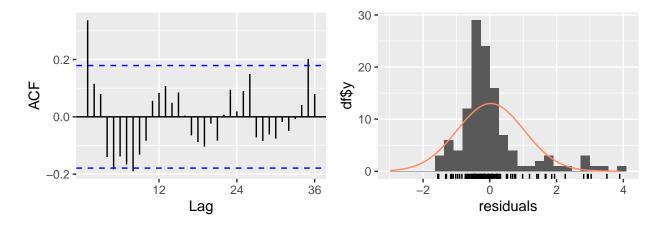
Warning in modeldf.default(object): Could not find appropriate degrees of
freedom for this model.



Warning in modeldf.default(object): Could not find appropriate degrees of
freedom for this model.

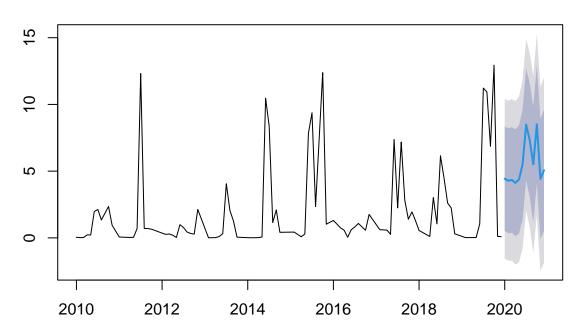
Residuals from StructTS





#Generating forecasts
StructTS() does not call the forecast() internally so we need one more step
SS_for <- forecast(SS_seas,h=12)
plot(SS_for)</pre>

Forecasts from Basic structural model



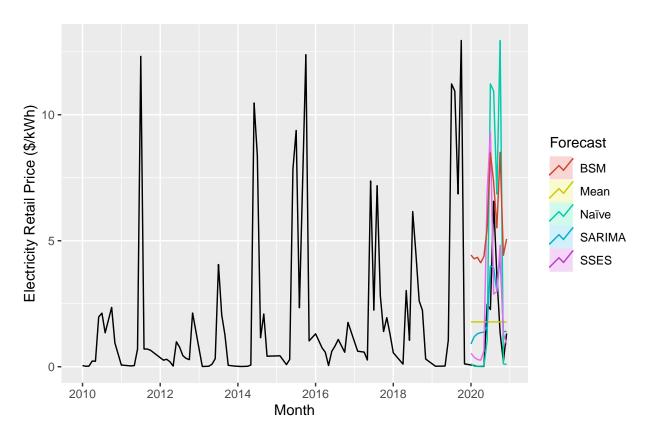
```
#Model 1: Arithmetic mean
MEAN_scores <- accuracy(MEAN_seas$mean,last_obs) #store the performance metrics</pre>
#Model 2: Seasonal naive
SNAIVE_scores <- accuracy(SNAIVE_seas$mean,last_obs)</pre>
# Model 3: SARIMA
SARIMA_scores <- accuracy(SARIMA_for$mean,last_obs)</pre>
# Model 4: SSES
SSES_scores <- accuracy(SSES_seas$forecast,last_obs)</pre>
# Model 5: BSM
SS_scores <- accuracy(SS_for$mean,last_obs)</pre>
#create data frame
seas_scores <- as.data.frame(rbind(MEAN_scores, SNAIVE_scores, SARIMA_scores, SSES_scores, SS_scores))</pre>
row.names(seas_scores) <- c("MEAN", "SNAIVE", "SARIMA", "SSES", "BSM")</pre>
#choose model with lowest RMSE
best_model_index <- which.min(seas_scores[,"RMSE"])</pre>
cat("The best model by RMSE is:", row.names(seas_scores[best_model_index,]))
```

The best model by RMSE is: SARIMA

Table 6: Forecast Accuracy for Seasonal Data

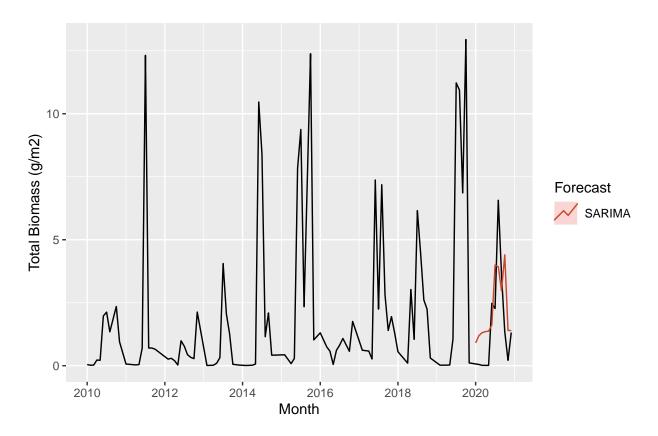
	ME	RMSE	MAE	MPE	MAPE
MEAN	-0.28323	1.93838	1.58284	-3817.5199	3846.3960
SNAIVE	-2.12360	4.54636	2.58677	-122.4177	164.9659
SARIMA	-0.65751	1.55783	1.34461	-2824.6163	2839.9915
SSES	-1.10662	2.85708	1.89745	-919.7008	937.4871
BSM	-4.03626	4.34690	4.03626	-9410.6202	9410.6202

```
autoplot(ts_biomass_data) +
  autolayer(MEAN_seas, PI=FALSE, series="Mean") +
  autolayer(SNAIVE_seas, PI=FALSE, series="Naïve") +
  autolayer(SARIMA_for,PI=FALSE, series="SARIMA") +
  autolayer(SSES_seas$forecast, series="SSES") +
  autolayer(SS_for,PI=FALSE,series="BSM") +
  xlab("Month") + ylab("Electricity Retail Price ($/kWh)") +
  guides(colour=guide_legend(title="Forecast"))
```



```
autoplot(ts_biomass_data) +

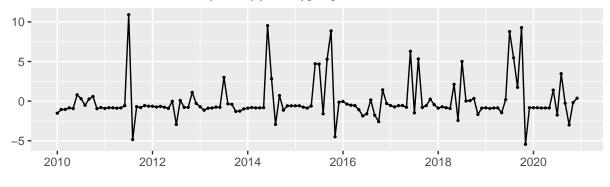
autolayer(SARIMA_for,PI=FALSE, series="SARIMA") +
    xlab("Month") + ylab("Total Biomass (g/m2)") +
    guides(colour=guide_legend(title="Forecast"))
```

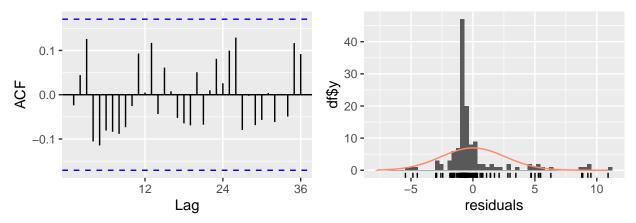


Forecast

SARIMA_autofit_new <- auto.arima(ts_biomass_data)
checkresiduals(SARIMA_autofit_new)</pre>

Residuals from ARIMA(1,0,0)(1,0,0)[12] with non-zero mean

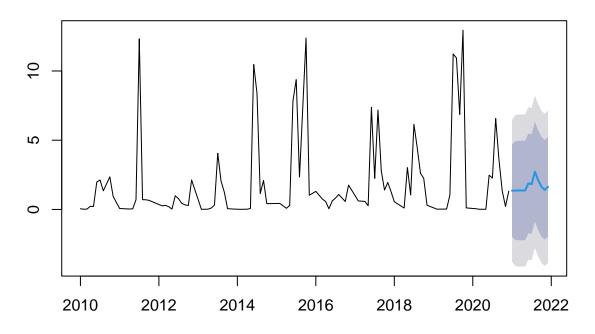




```
##
## Ljung-Box test
##
## data: Residuals from ARIMA(1,0,0)(1,0,0)[12] with non-zero mean
## Q* = 18.099, df = 22, p-value = 0.7001
##
## Model df: 2. Total lags used: 24
```

```
SARIMA_for_new <- forecast(SARIMA_autofit_new,h=12)
plot(SARIMA_for_new)</pre>
```

Forecasts from ARIMA(1,0,0)(1,0,0)[12] with non-zero mean



Discussion

Reference

" " r

#To add reference, you need first add reference in reference in reference.bib.
#Than use"[@uniqueID]" to site it.

Beversdorf, T. R. M., Lucas J; Miller. (2015). Long-term monitoring reveals carbon–nitrogen metabolism key to microcystin production in eutrophic lakes. *Frontiers in Microbiology*, 6, 456.

Brock, T. D. (2012). A eutrophic lake: Lake mendota, wisconsin. Springer Science & Business Media. Magnuson, S. R. C., J.J., & H.Stanley, E. (2022). North temperate lakes LTER: Phytoplankton - madison lakes area 1995 - current. Retrieved from https://portal.edirepository.org/nis/mapbrowse?scope=knb-lter-ntl&identifier=88&revision=31