

# 1

## Empirical Findings

### 1.1 Density of the returns

#### 1.1.1 MLE distribution parameters

In table 1.1 we can see the estimated parameters of the unconditional distribution functions. They are presented for the Skewed Generalized T-distribution (SGT) and limiting cases thereof previously discussed. Additionally, maximum likelihood score and the Aikake Information Criterion (AIC) is reported to compare goodness of fit of the different distributions. We find that the SGT-distribution has the highest maximum likelihood score of all. All other distributions have relatively similar likelihood scores, though slightly lower and are therefore not the optimal distributions. However, when considering AIC it is a tie between SGT and SGED. This provides some indication that we have a valid case to test the suitability of different SGED-GARCH VaR models as an alternative for the SGT-GARCH VaR models. While sacrificing some goodness of fit, the SGED distribution has the advantage of requiring one less parameter, which could possibly result in less errors due to misspecification and easier implementation. For the SGT parameters the standard deviation and skewness are both significant at the 1% level. For the SGED parameters, the standard deviation and the skewness are both significant

at respectively the 1% and 5% level. Both distributions are right-skewed. For both distributions the shape parameters are significant at the 1% level, though the  $q$  parameter was not estimated as it is by design set to infinity due to the SGED being a limiting case of SGT.<sup>1</sup>

Additionally, for every distribution fitted with MLE, plots are generated to compare the theoretical distribution with the observed returns. We see that except for the normal distribution which is quite off, the theoretical distributions are close to the actual data, except that they are too peaked. This problem is the least present for the SGT distribution.

**Table 1.1:** Maximum likelihood estimates of unconditional distribution functions

$\theta$	$\alpha$	$\beta$	$\xi$	$\kappa$	$\eta$	$LLH$	AIC
SGT	0.02 (0.013)	1.321 (0.026)***	-0.04 (0.013)***	1.381 (0.071)***	3.314 (0.538)***	-13973.01	27956.01
SGED	0.019 (0.013)	1.274 (0.016)***	-0.018 (0.01)***	0.916 (0.017)***	Inf	-14008.63	27956.01
GED	0.032 (0.009)***	1.276 (0.016)***	0	0.911 (0.017)***	Inf	-14009.52	28025.04
ST	0.019 (0.014)	1.481 (0.054)***	-0.052 (0.013)***	2	2.793 (0.098)***	-13997.35	28002.71
T	0.056 (0.01)***	1.494 (0.056)***	0	2	1.383 (0.097)***	-14005.14	28016.29
Normal	0.017 (0.014)	1.307 (0.01)***	0	2	Inf	-15101.73	30207.46

Table contains parameter estimates for SGT-distribution and some of its limiting cases. The underlying data is the daily return series of the Eurostoxx 50 for the period between December 31. 1986 and April 27. 2021. Standard errors are reported between brackets.  $L$  is the maximum log-likelihood value. \*, \*\* and \*\*\* point out significance at 10

<sup>1</sup>To check whether the relative ranking of distributions still holds in different periods, we have calculated the maximum likelihood score and AIC for three smaller periods: The period up to the dotcom collapse (1987-2001), up to the GFC (2002-2009) and up to the present Covid-crash (2009-2021). There is no qualitative difference in relative ranking with these subsamples. Results are reported in the appendix.

## 1.2 Results of GARCH with constant higher moments

```
require(plyr)

Table.GARCH.function <- function(GARCHfit.object = garchfit.eGARCH){
  #Making objects to fill
  list.table.3.tmp <- vector(mode = "list", length = length(distributions)*2)
  list.table.3 <- vector(mode = "list", length = length(distributions))
  names(list.table.3) <- distributions
  ref.distr <- seq(from = 1, to = length(distributions)*2, by = 2)
  #Retriving all the data from the original lists
  for(i in 1:length(distributions)){
    list.table.3.tmp[[ref.distr[i]]] <- GARCHfit.object[[i]]@fit$coef
    list.table.3.tmp[[ref.distr[i]+1]] <- GARCHfit.object[[i]]@fit$tval
  }
  #From list of vectors of different lengths to list of matrixes with empty spaces
  for(i in 1:length(distributions)){
    list.table.3[[i]] <- cbind(list.table.3.tmp[[ref.distr[i]]], list.table.3.tmp[[ref.distr[i]+1]])
  }
  #Function to rearrange the list from a list of matrices to list of vectors
  list.restructure <- function(object = list.table.3){
    len.table <- length(object)
    len.inside.list <- rep(NA, len.table)
    for(i in 1:len.table){len.inside.list[i] <- nrow(object[[i]])}
    adj.list <- vector(mode = "list", length = len.table)
    ref.list <- vector(mode = "list", length = len.table)
    names.list <- vector(mode = "list", length = len.table)
    for(i in 1:len.table){ref.list[[i]] <- seq(from = 1, to = len.inside.list[i]*2, by = 2)}
    for(i in 1:len.table){adj.list[[i]] <- names.list[[i]] <- rep(NA, len.inside.list[i])}
```

```

for(i in 1:len.table){
  adj.list[[i]][ref.list[[i]]] <- round(object[[i]][,1],3)
  adj.list[[i]][ref.list[[i]]+1] <- paste0("(", round(object[[i]][,2],3),")")
}
for(i in 1:len.table){
  names.list[[i]][ref.list[[i]]] <- rownames(object[[i]])
  names.list[[i]][ref.list[[i]]+1] <- paste0("p-val ",rownames(object[[i]]))
  #names.list[[i]][ref.list[[i]]+1] <- ""
}
names(adj.list) <- distributions
for(i in 1:len.table){names(adj.list[[i]]) <- names.list[[i]]}
return(adj.list)
}

#Unlisting and removing NAs
adj.list <- list.restructure(object = list.table.3)
table.3.matrix <- matrix(unlist(lapply(adj.list, `length<-`, max(lengths(adj.list)))
colnames(table.3.matrix) <- names(adj.list)
table.3.matrix[is.na(table.3.matrix)] <- ""
table.3.matrix[table.3.matrix=="(NA)"] <- ""

#Adjustments for std & ged distributions
table.3.matrix[c(length(table.3.matrix[,2])-1,length(table.3.matrix[,2])),2] <- tai
table.3.matrix[c(length(table.3.matrix[,2])-3,length(table.3.matrix[,2])-2),2] <- "
table.3.matrix[c(length(table.3.matrix[,4])-1,length(table.3.matrix[,4])),4] <- tai
table.3.matrix[c(length(table.3.matrix[,4])-3,length(table.3.matrix[,4])-2),4] <- "

#Log-Likelyhoods
LLH <- rep(NA, length(distributions))
for(i in 1:length(distributions)){LLH[i] <- GARCHfit.object[[i]]@fit$LLH}
names.table.3 <- revalue(names(adj.list[[3]]), c("mu"="$\\alpha_0$", "ar1"="$\\alpha_1$", "
kappa.object <- cbind(matrix(data = "", nrow = 2, ncol = 3) ,table.3.matrix[(nrow(t
eta <- cbind(table.3.matrix[(nrow(table.3.matrix)-1):(nrow(table.3.matrix)),1:3], m

```

```

table.3.matrix[(nrow(table.3.matrix)-1):(nrow(table.3.matrix)),] <- kappa.object
table.3.matrix <- rbind(table.3.matrix, eta, round(LLH,3))
table.3.matrix <- cbind(c(names.table.3,"$\\eta$","p-val eta","$LLH$"), table.3.mat
table.3.matrix <- as.data.frame(table.3.matrix, row.names = c(names.table.3,"$\\eta$
return(table.3.matrix)
}

```

### *#PARTIAL RESULTS*

```

Table.3.iGARCH <- Table.GARCH.function(GARCHfit.object = garchfit.iGARCH)
Table.3.eGARCH <- Table.GARCH.function(GARCHfit.object = garchfit.eGARCH)
Table.3.gjrGARCH <- Table.GARCH.function(GARCHfit.object = garchfit.gjrGARCH)
Table.3.sGARCH <- Table.GARCH.function(GARCHfit.object = garchfit.sGARCH)
Table.3.EWMA <- Table.GARCH.function(GARCHfit.object = garchfit.EWMA)
Table.3.fGARCH.AVGARCH <- Table.GARCH.function(GARCHfit.object = garchfit.fGARCH.AV
Table.3.fGARCH.NAGARCH <- Table.GARCH.function(GARCHfit.object = garchfit.fGARCH.NA
Table.3.fGARCH.TGARCH <- Table.GARCH.function(GARCHfit.object = garchfit.fGARCH.TGA

Table.3.function <- function(distribution = "sstd"){
ref <- which(names(Table.3.eGARCH)==distribution)#Reference column
#Taking all the relevant values
AVGARCH <- Table.3.fGARCH.AVGARCH[,c(1,ref)]
iGARCH <- Table.3.iGARCH[,c(1,ref)]
eGARCH <- Table.3.eGARCH[,c(1,ref)]
sGARCH <- Table.3.sGARCH[,c(1,ref)]
gjrGARCH <- Table.3.gjrGARCH[,c(1,ref)]
EWMA <- Table.3.EWMA[,c(1,ref)]
NAGARCH <- Table.3.fGARCH.NAGARCH[,c(1,ref)]
TGARCH <- Table.3.fGARCH.TGARCH[,c(1,ref)]
#Assigning the right names to columns

```

```

colnames(AVGARCH)[-1] <- rep("AVGARCH", length(colnames(AVGARCH)[-1]))
colnames(iGARCH)[-1] <- rep("iGARCH", length(colnames(iGARCH)[-1]))
colnames(eGARCH)[-1] <- rep("eGARCH", length(colnames(eGARCH)[-1]))
colnames(sGARCH)[-1] <- rep("sGARCH", length(colnames(sGARCH)[-1]))
colnames(gjrGARCH)[-1] <- rep("gjrGARCH", length(colnames(gjrGARCH)[-1]))
colnames(EWMA)[-1] <- rep("EWMA", length(colnames(EWMA)[-1]))
colnames(NAGARCH)[-1] <- rep("NAGARCH", length(colnames(NAGARCH)[-1]))
colnames(TGARCH)[-1] <- rep("TGARCH", length(colnames(TGARCH)[-1]))
#Binding all the columns & cleaning & ordering data
Table3 <- full_join(full_join(full_join(full_join(full_join(full_join(full_join(sGA
Table3[is.na(Table3)] <- ""
Table3 <- rbind(Table3[Table3[,1]!="$LLH$",], Table3[Table3[,1]=="$LLH$",])
Table3[substr(Table3[,1],1,5)=="p-val",1] <- ""
colnames(Table3) <- c("", colnames(Table3)[-1])
return(Table3)
}

Table.3 <- vector(mode = "list", length = length(distributions))
names(Table.3) <- c("Norm", "T", "ST", "GED", "SGED")
for(i in 1:length(distributions)){
  Table.3[[i]] <- suppressMessages(Table.3.function(distribution = distributions[i]
}

#Testing the kabling
knitr::kable(Table.3$ST)

print("iGARCH")
garchfit.iGARCH[[1]]@fit$coef
garchfit.iGARCH[[1]]@fit$se.coef

```

```
print("EWMA")
garchfit.EWMA[[1]]@fit$coef
c(garchfit.EWMA[[1]]@fit$se.coef[1:2], NA, garchfit.EWMA[[1]]@fit$se.coef[3], NA)
```

```
print("eGARCH")
garchfit.eGARCH[[1]]@fit$coef
garchfit.eGARCH[[1]]@fit$se.coef
```

```
print("gjrGARCH")
garchfit.gjrGARCH[[1]]@fit$coef
garchfit.gjrGARCH[[1]]@fit$se.coef
```

```
print("NAGARCH")
garchfit.fGARCH.NAGARCH[[1]]@fit$coef
garchfit.fGARCH.NAGARCH[[1]]@fit$se.coef
```

```
print("TGARCH")
garchfit.fGARCH.TGARCH[[1]]@fit$coef
garchfit.fGARCH.TGARCH[[1]]@fit$se.coef
```

```
garchfit.fGARCH.AVGARCH[[1]]@fit$coef
garchfit.fGARCH.AVGARCH[[1]]@fit$se.coef
```

**Table 1.2:** Model selection according to AIC

	SGARCH	IGARCH	EWMA	EGARCH	GJRGARCH	NAGARCH	TGARCH	AVGARCH
norm	2.995	2.998	3.034	2.962	2.967	2.955	2.957	2.954
std	2.924	2.924	2.935	2.900	2.904	2.897	2.896	2.896
sstd	2.920	2.920	2.930	2.895	2.900	2.891	2.891	2.890
ged	2.930	2.930	2.944	2.907	2.911	2.903	7.705	7.702
sged	2.927	2.927	2.940	2.902	2.906	2.898	7.675	7.672

Notes

<sup>1</sup> This table shows the AIC value for the respective model

```
# VaR table, unconditional coverage
```

```
# VaRTest(Egarch)
```

## 1.3 Results of GARCH with time-varying higher moments

```
require(racd)
require(rugarch)
require(parallel)
require(xts)

# ACD specification
sGARCH_ACDspec = acdspec(mean.model = list(armaOrder = c(1, 0)), variance.model = list(armaOrder = c(1, 0)),
distribution.model = list(model = 'jsu', skewOrder = c(1, 1, 1), shapeOrder = c(1, 1, 1)))

# sGARCH
cl = makePSOCKcluster(10)
fit = acdfit(sGARCH_ACDspec, as.data.frame(R), solver = 'msoptim', solver.control = list(maxit = 10000))

# par(mfrow = c(2, 2), mai = c(0.75, 0.75, 0.3, 0.3))
# cm <- plot.zoo(xts(fit@model$modeldata$data, fit@model$modeldata$index), auto.g = F, col = 'grey')
# cm <- lines(fitted(fit), col = 2)
# cm
# cs <- plot(xts(abs(fit@model$modeldata$data), fit@model$modeldata$index), auto.g = F, col = 'grey')
# minor.ticks = FALSE, main = 'Conditional Sigma', yaxis.right = F, col = 'grey')
# cs <- lines(sigma(fit), col = 'steelblue')
# cs
# plot(racd::skewness(fit), col = 'steelblue', yaxis.right = F, main = 'Conditional Skewness')
# plot(racd::kurtosis(fit), col = 'steelblue', yaxis.right = F, main = 'Conditional Kurtosis')

# pnl <- function(fitted(fit), xts(fit@model$modeldata$data, fit@model$modeldata$index), col = 'steelblue') {
#   panel.number <- parent.frame()$panel.number
#   if (panel.number == 1) lines(fitted(fit), xts(fit@model$modeldata$data, fit@model$modeldata$index), col = 'steelblue')
#   lines(fitted(fit), xts(fit@model$modeldata$data, fit@model$modeldata$index), col = 'steelblue')
# }
```



```
# }  
# plot(xts(fit$model$modeldata$data, fit$model$modeldata$index), auto.grid = T, mi  
# # lines(fitted(fit), col = 2) + grid()  
#  
# plot(xts(fit$model$modeldata$data, fit$model$modeldata$index), auto.grid = T, mi
```