

Stats and Probability Information

April 27, 2014

Continuous and marginal distributions

The marginal distribution of x in a two-variable distribution is equal to the sum of the joint distribution over y .

$$Pr(X = x) = \sum_y Pr(X = x, Y = y) = \sum_y Pr(X = x|Y = y)Pr(Y = y) \quad (1)$$

From [Wikipedia](#)

For the continuous case

$$p_X(x) = \int_y p_{X,Y}(x, y)dy = \int_y p_{X|Y}(x|y)p_Y(y)dy \quad (2)$$

There are three related distributions: the marginal, the joint and the conditional.

1 Mixture Model

This is a probabilistic model that relates some random variables to some other variables. The model has sub-populations. The properties of the sub-population are different from those of the parent. The sub-populations may not be observable. For example, the distribution of returns may be different in different sub-population or regime.

A *mixture distribution* is the probability distribution of a random variable whose values are derived from an underlying set of random variables. The *mixture components* are individual distributions with *mixture weights*. Even in cases where the mixture components have a normal distribution, the mixture distribution is likely to be non-normal. Mixture models are used to

understand the sub-population when there is only access to the information about the pooled population.

The mixture model will be comprised of N random variables distributed according to K components, with each component belonging to the same distribution. The k mixture weights sum to one. Each component will have parameters (mean and variance in the case of normal distribution).

The method will try to estimate the all the parameters of the model from the data. The underlying data is known (x_i); the number of mixture components is set (K); the parameters of the distribution of each mixture component ($\theta_{i=1...K}$); mixture weight ($\Phi_{i=1...K}$); Φ K -dimensional vector summing to 1; $F(x|\theta)$ probability distribution of observations parameterised on θ ; α shared hyperparameter for component weights; β shared hyperparameter for mixture weights; $H(\theta|\alpha)$ prior probability distribution of component parameters;

2 Adjusted R squared

Adjusted R squared applied a penalty to the basic R squared to account for additional variables. The equation is

$$R_A^2 = 1 - \left[\frac{(n-1)}{(n-k)} \right] [1 - R^2] \quad (3)$$

Adding a regressor to the equation will increase (reduce) the R_A^2 when the absolute value of the t-statistic is greater (less) than one. Adding a group of regressors to the model will reduce (increase) the R_A^2 when the absolute value of the F-statistic is greater than one.

Proof <http://davegiles.blogspot.com/2014/04/proof-of-result-about-adjusted.html>

3 Monte Carlo Simulation

This comes from **Revolutionary Analytics**. The analysis is in annual terms.

$$\mu\Delta t + \sigma Z\sqrt{\Delta t} \quad (4)$$

where μ is the drift or average annual return, Z is a standard Normal random variable, t is measured in years so for monthly returns Δt equals $\frac{1}{12}$.

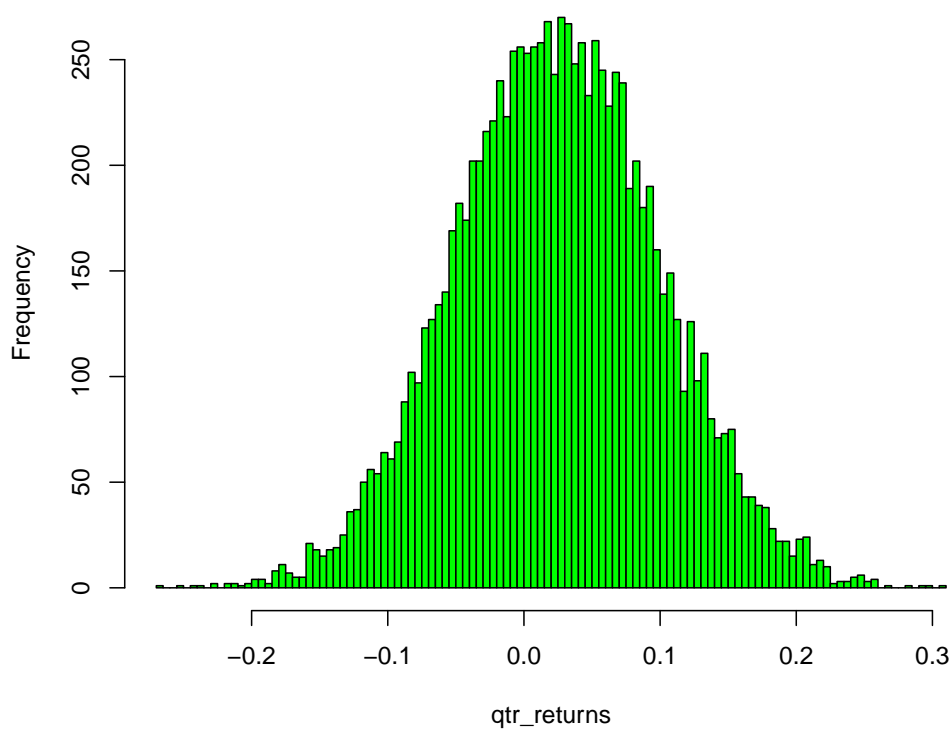
```
n <- 10000
# Fixing the seed gives us a consistent set of simulated returns
set.seed(106)
```

```

z <- rnorm(n) # mean = 0 and sd = 1 are defaults
mu <- 0.1
sd <- 0.15
delta_t <- 0.25
# apply to expression (*) above
qtr_returns <- mu * delta_t + sd * z * sqrt(delta_t)
hist(qtr_returns, breaks = 100, col = "green")

```

Histogram of qtr_returns



Now the descriptive statistics can be uncovered from the simulated results.

```

stats <- c(mean(qtr_returns) * 4, sd(qtr_returns) * 2) # sqrt(4)
names(stats) <- c("mean", "volatility")
stats

##      mean volatility
## 0.09901    0.14976

```

This is the basic model. It would also be possible to simulate two variables and to include some relationship between the two in the analysis. It would also be possible to simulate an asset in two different regimes. A Monte-Carlo Markov Model (MCMM) would require another set of μ and σ inputs as well as a transition matrix of the probabilities that there is a switch from one regime to another.

4 Generalised Lambda Distribution

This is from [Revolutionary Analytics](#). The four parameters λ_1 , λ_2 , λ_3 and λ_4 indicate the location, scale, skew and kurtosis of the distribution.

```
require(GLDEX)
require(quantmod)
getSymbols("SPY", from = "1994-02-01")

## [1] "SPY"

SPY.Close <- SPY[, 4] # Closing prices
SPY.vector <- as.vector(SPY.Close)
# Calculate log returns
sp500 <- diff(log(SPY.vector), lag = 1)
sp500 <- sp500[-1] # Remove the NA in the first position
# Set normalise='Y' so that kurtosis is calculated with reference to
# kurtosis = 0 under Normal distribution
fun.moments.r(sp500, normalise = "Y")

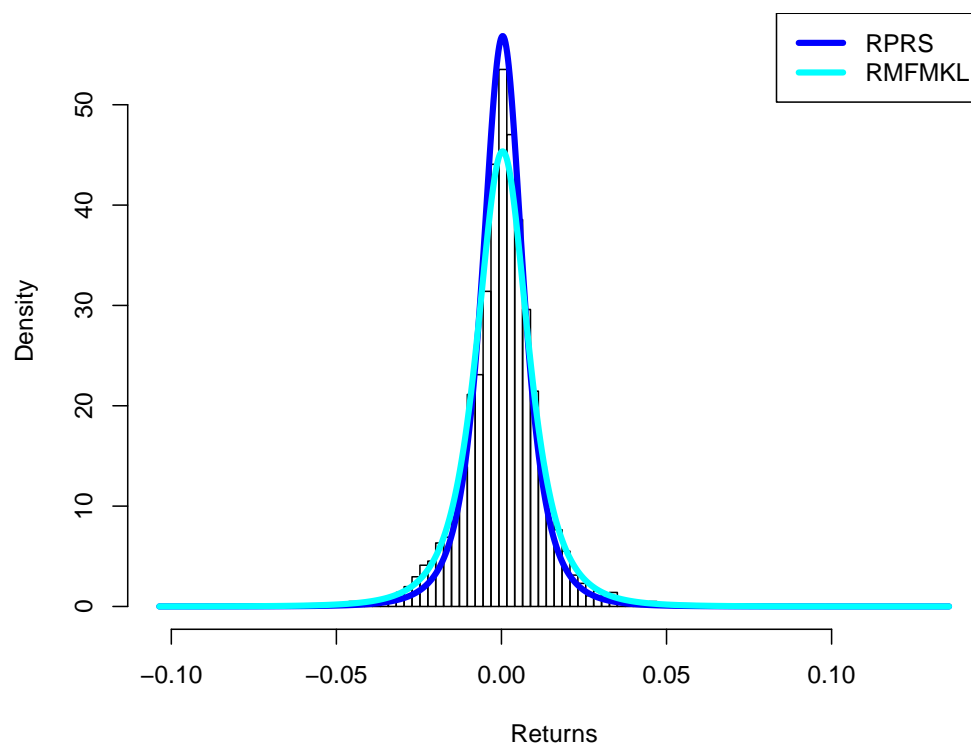
##          mean    variance  skewness  kurtosis
## 0.0002633 0.0001532 -0.0960976  9.5131553
```

Now fit the GLD with the function `fun.data.fit.mm`. There are warnings but these can be ignored.

```
spLambdaDist = fun.data.fit.mm(sp500)
spLambdaDist

##          RPRS      RMFMKL
## [1,] 3.846e-04 0.000321
## [2,] -4.228e+01 203.501581
## [3,] -1.675e-01 -0.169657
## [4,] -1.640e-01 -0.161483
```

```
fun.plot.fit(fit.obj = spLambdaDist, data = sp500, nclass = 100, param = c("rs"
  "fmkl"), xlab = "Returns")
```



Now it is possible to generate simulated results using the function `rgl()`. Lambdas need to be identified.

```
lambda_params_rs <- spLambdaDist[, 1]
lambda1_rs <- lambda_params_rs[1]
lambda2_rs <- lambda_params_rs[2]
lambda3_rs <- lambda_params_rs[3]
lambda4_rs <- lambda_params_rs[4]
lambda_params_fmkl <- spLambdaDist[, 2]
lambda1_fmkl <- lambda_params_fmkl[1]
lambda2_fmkl <- lambda_params_fmkl[2]
lambda3_fmkl <- lambda_params_fmkl[3]
lambda4_fmkl <- lambda_params_fmkl[4]
```

Now generate simulations of each variety.

There are problems with the `rgl` function. I am not sure what this does. It is 10 million simulations. I think that the `rgl` just uses extra hardware to make the change. It may be useful to re-do this last section using a different method.

```
require(gld)

## Loading required package: gld

require(GLDEX)

## Loading required package: GLDEX
## Loading required package: cluster
##
## Attaching package: 'GLDEX'
##
## The following objects are masked from 'package:gld':
##
##      dgl, pgl, qdgl, qgl, rgl, starship, starship.adaptivegrid,
##      starship.obj

# RS version:
set.seed(100) # Set seed to obtain a reproducible set
rs_sample <- rgl(n = 1e+07, lambda1 = lambda1_rs, lambda2 = lambda2_rs, lambda3 =
  lambda4 = lambda4_rs, param = "rs")
# Moments of simulated returns using RS method:
fun.moments.r(rs_sample, normalise = "Y")

##      mean      variance      skewness      kurtosis
## 2.633e-04 9.774e-05 -1.043e-01 9.955e+00

# Moments calculated from market data:
fun.moments.r(sp500, normalise = "Y")

##      mean      variance      skewness      kurtosis
## 0.0002633 0.0001532 -0.0960976 9.5131553

# FKML version:
set.seed(100) # Set seed to obtain a reproducible set
fmkl_sample <- rgl(n = 1e+05, lambda1 = lambda1_fmkl, lambda2 = lambda2_fmkl,
  lambda3 = lambda3_fmkl, lambda4 = lambda4_fmkl, param = "fmkl")
# Moments of simulated returns using FKML method:
fun.moments.r(fmkl_sample, normalise = "Y")
```

```
##          mean    variance    skewness    kurtosis
## 0.0002403 0.0001547 -0.0862244  8.5839659

# Moments calculated from market data:
fun.moments.r(sp500, normalise = "Y")

##          mean    variance    skewness    kurtosis
## 0.0002633 0.0001532 -0.0960976  9.5131553
```

Compare the moments to the S&P500 market data

```
fun.moments.r(rs_sample, normalise = "Y")

##          mean    variance    skewness    kurtosis
## 2.633e-04 9.774e-05 -1.043e-01  9.955e+00

fun.moments.r(sp500, normalise = "Y")

##          mean    variance    skewness    kurtosis
## 0.0002633 0.0001532 -0.0960976  9.5131553

fun.moments.r(fmkl_sample, normalise = "Y")

##          mean    variance    skewness    kurtosis
## 0.0002403 0.0001547 -0.0862244  8.5839659

fun.moments.r(sp500, normalise = "Y")

##          mean    variance    skewness    kurtosis
## 0.0002633 0.0001532 -0.0960976  9.5131553
```

5 Lasso method

Rob Tibshirani Cancer example that requires identification of appropriate cell. There are 20 cases that are being used as a training set. Train a classifier to identify whether the cells are cancerous or not. There are 11,000 features. It would be useful to use as few of the features as possible. Therefore, also want to know which features are important for the classification.

Sparcity means that the features are reduced by only using those that pass a particular level of significance. [More here.](#)