Re: Maximization of ARMA−GARCH models

Source: http://sci.tech−archive.net/Archive/sci.stat.math/2007−01/msg00437.html

- *From*: "David Jones" <dajxxx@xxxxxxxxx>

- *Date*: Thu, 25 Jan 2007 10:11:16 −0000

David Jones wrote:

> monnomiznogoud@xxxxxxxxxxxx wrote:
>
>> Thank you for your answer.
>> You're right, the question was about any model (hence the "similar"

i

>> used.)
>>
>> So what you're saying is that using a different distriburion for

the

>> innovations/errors makes another model out of the first one ?

> Yes they would be separate models, unless that is you find amodel

for

> the residual that includes the Student−t distribution and the
> Hyperbolic distribution as special cases. The theory I mentioned
> provides one general way of doing this, but there are probably

others.

>> It would have been great if i could compare directly the ML

function

>> of an ARMA(1,1)−GARCH(1,1) with Student−t distribution with an
>> ARMA(1,1)−GARCH(1,1) with a GED distribution.
>>
>> It is true that comparing ARMA(1,1)−GARCH(1,1) with

ARMA(1,1)−APARCH(1,1) might not be evident, but i can't see why the
first example could not be compared directly (thus preferring the

one

with the maximum value)

The problem is that of finding the valid distribution for the test−statistic. Standard maximum likelihood theory does not provide this. If you really do want to do a test using the difference of the log−likelihoods you can't easily do the obvious thing of deriving

the

critical region for a test by doing simulations since this would entail you finding a pair of models from each class that have the

same

"true" likelihood. However it is possible you could make use of the theory in my long−ago paper to help you construct a reasonable test

of

the difference in log−likelihoods: see Jones DA (1983) Statistical analysis of empirical models fitted by optimisation, Bimometrika, 70(1), 67−88. It may need some consideable adaptation, but Section 5 seems to relate.

Note that the "testing separate families of hypotheses" approach I mentioned previously does not do a direct test of one model being better than another. Instead it works by supplying two tests: taking each model in turn it asks whether there is evidence that the given model needs to be expanded into the combined model.

David Jones

A subsequent thought .... if both the following are true, you may be able to do something simpler and more intuitively reasonable. If:

(i) the sample size is reasonably large so that both (a) the effect of parameter estimation errors is small and (b) you can divide the data set into a reasonably large number of subsets (say 20);

(ii) the models are such that you can pre−preocess the data with any difference operators to lead to series with fairly short temporal dependence.

Then:

(i) fit the two models to the full (prepocessed) data set;

(ii) Specificy subsets of the data .. the first m observations, the
next m observations etc.

(iii) calculate log−likelihoods for each subset of data (for the
parameter values fitted to the complete data−set)... giving L1i, L2i.
If you work with conditional likelihoods this should be
straightforward to define (ie likelihoods of each observation given
past observations).

(iv) Calculate differences Di=L1i−l2i.

(v) Do a test that the mean of the Di's is zero, on the basis of the
sample mean and sample variance of the Di's and assuming that the Di's
are effectively uncorrelated. For the last to be reasonable you need
both the assumption about short range dependence and the choice of m
above in (ii) to be reasonably matched. The idea here is closely
related to the suggestion of Moran (1975) (Biometrika 69 19−27).

David Jones

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