Examples of focused model comparison: skew-normal models

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Abstract

The following example (from **?**) illustrates how focused model comparison can be performed using the **fic** package in a situation where:

- a novel class of models is defined and fitted by custom R functions
- a simple model is extended in two different directions to define the models being compared

Keywords: models.

An outcome y_i and a covariate x_i are observed for individuals $i = 1, \ldots, n$. Four different models are compared: two normal models with a constant variance, one without (1) and one with (2) a linear regression term, and two "skew-normal" models without (3) and with (4) the linear regression term. The skew-normal model is defined by an error term $\sigma\epsilon_i$, where the ϵ_i are independently distributed with a density $f(u|\lambda) = \lambda\Phi(u)^{\lambda-1}\phi(u)$. All four models are nested in the "wide" model (4).

(1) $y_i \sim N(\beta_0, \sigma^2)$

(2) $y_i \sim N(\beta_0 + \beta_1 x_i, \sigma^2)$

(3) $y_i = \beta_0 + \sigma\epsilon_i$

(4) $y_i = \beta_0 + \beta_1 x_i + \sigma\epsilon_i$

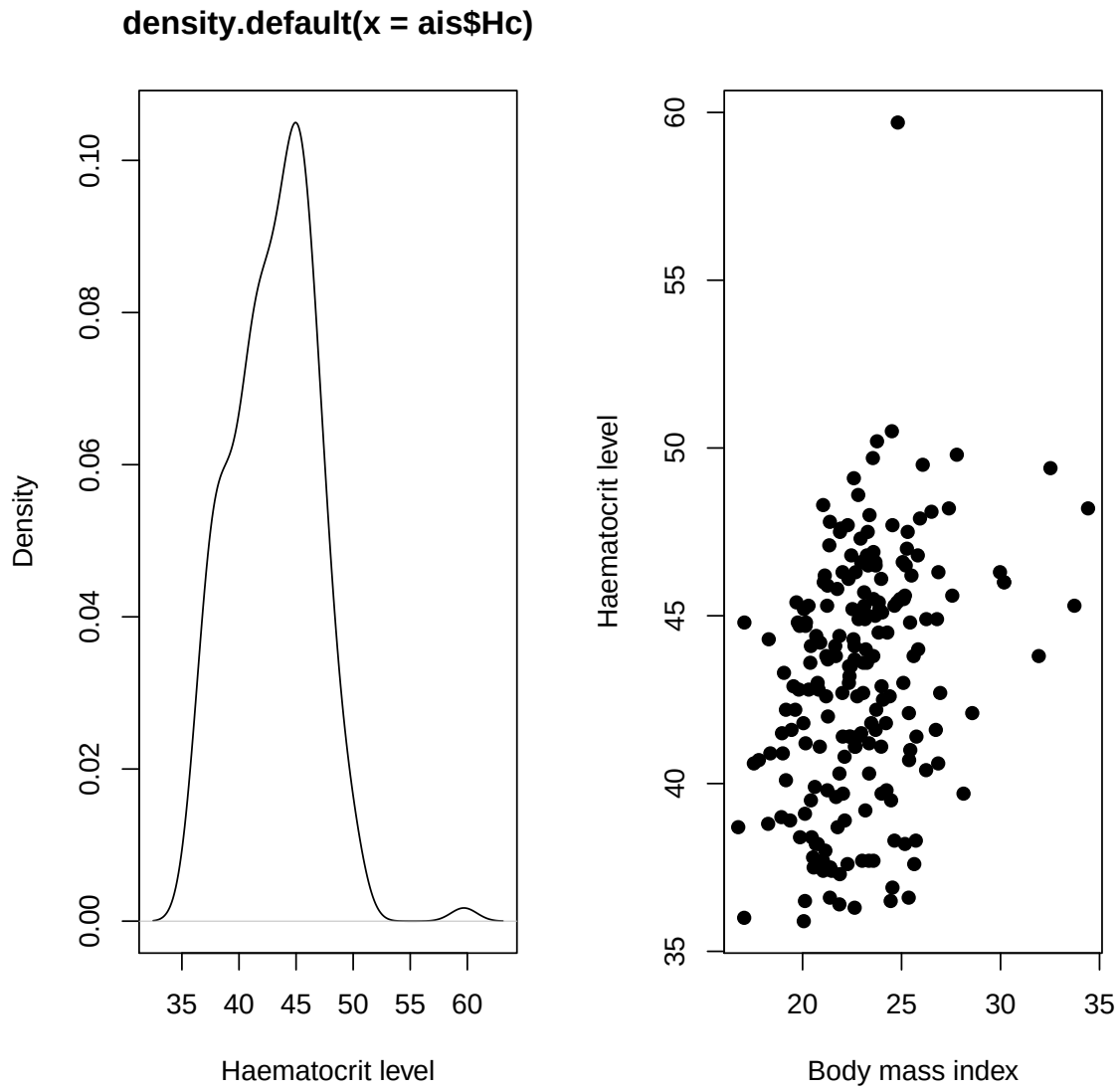
1. Fitting the models

To implement this class of models in R, firstly we define the log density function of the general skew-normal model with mean, scale and skewness parameters μ, σ, λ indicated by arguments `mean`, `sigma` and `lambda`. This defines the distribution of y_i in model (3) with mean $\mu_i = \beta_0$, and in (4) with $\mu_i = \beta_0 + \beta_1 x_i$. Models (1) and (2) are defined by setting $\lambda = 1$ in models (3) and (4) respectively.

```
ldsnorm <- function(x, mean, sd, lambda){
    log(lambda) + (lambda-1)*pnorm(x, mean, sd, log=TRUE) +
        dnorm(x, mean, sd, log=TRUE)
}
```

The models are fitted to data from the Australian Institute of Sports (Cook and Weisberg, 1994 REF), available as `ais` from the **sn** package REF. The outcome y_i is haematocrit level `Hc`, and the covariate is body mass index `BMI`. Figure ?? illustrates the skewed distribution of the outcome and a mild association between the variables.

```
if (!require("sn"))
    stop("The `sn` package should be installed to run code in this vignette")
data(ais)
par(mfrow=c(1,2))
plot(density(ais$Hc), xlab="Haematocrit level")
plot(ais$BMI, ais$Hc, pch=19,
     xlab="Body mass index", ylab="Haematocrit level")
```



The following defines the minus log likelihood for these data as a function of four parameters

β_0, β_1, σ and λ.

```
mloglik <- function(b0, b1, sd, lambda){
    -sum(ldsnorm(ais$Hc, b0 + b1*ais$BMI, sd, lambda))
}
```

Then to obtain the maximum likelihood estimates under models 1 to 4, `mloglik` is rewritten as a function of a single vector `par`, containing either 2, 3 or 4 parameters to be minimised over, depending on the model. Note here that models 1 and 3 have β_2 fixed at 0, and models 1 and 2 have λ fixed at 1. The positive parameters σ and λ will be estimated by unconstrained maximisation on the log scale. These functions can be passed to the `nlm` function for optimisation.

```
fn1 <- function(par) mloglik(par[1], 0, exp(par[2]), 1)
fn2 <- function(par) mloglik(par[1], par[2], exp(par[3]), 1)
fn3 <- function(par) mloglik(par[1], 0, exp(par[2]), exp(par[3]))
fn4 <- function(par) mloglik(par[1], par[2], exp(par[3]), exp(par[4]))
```

`nlm` also requires plausible initial values for the parameters. A vector of these (`ini`) is obtained as follows by fitting model (2) with `lm` and extracting the coefficients with `coef` (for β_0 and β_1) and the residual standard deviation for $\log(\sigma)$. An initial value of 0 is used for $\log(\lambda)$. [1]

```
lm2 <- lm(Hc ~ BMI, data=ais)
cf <- unname(coef(lm2))
ini <- c(beta0=cf[1], beta1=cf[2],
         logsigma=log(summary(lm2)$sigma), loglambda=0)
```

The appropriate objective function (`fn1`–`fn4`) is then optimised for each model, starting from the given initial values[2].

```
opt1 <- nlm(fn1, ini[c("beta0","logsigma")], hessian=TRUE)
opt2 <- nlm(fn2, ini[c("beta0","beta1","logsigma")], hessian=TRUE)
opt3 <- nlm(fn3, ini[c("beta0","logsigma","loglambda")], hessian=TRUE)
opt4 <- nlm(fn4, ini, hessian=TRUE)
```

Finally, the information required by the `fic` function (the estimates and covariance matrices) is extracted from the `nlm` results and arranged into a list, for each of the four models.

[1] Note these are the exact maximum likelihood estimates for model 2. The added value of `nlm` in fitting models 1 and 2, compared to simply using `lm`, is to conveniently provide the covariance matrix at the maximum likelihood estimates, which is required for focused model comparison

[2] A warning message of `NA/Inf replaced by maximum positive value` can be ignored and is the result of `nlm` trying out extreme and implausible values on the way to finding the maximum likelihood.

```
mod1 <- list(est=opt1$estimate, vcov=solve(opt1$hessian) )
mod2 <- list(est=opt2$estimate, vcov=solve(opt2$hessian) )
mod3 <- list(est=opt3$estimate, vcov=solve(opt3$hessian) )
mod4 <- list(est=opt4$estimate, vcov=solve(opt4$hessian) )
```

dsn also provided with sn package

2. Focused model comparison

We now perform a focused comparison of the four models. Two alternative focuses are investigated: the mean and median outcome at a covariate value of interest. Expressions for the mean and median of the skew normal, in the parameterisation used here, are given by **?** and encoded in the following R functions:

```
mean_snorm <- function(mu, sigma, lambda){
    f <- function(u){u*exp(ldsnorm(u, 0, 1, lambda))}
    mu + sigma * integrate(f, -Inf, Inf)$value
}
median_snorm <- function(mu, sigma, lambda){
    mu + sigma * qnorm(0.5^(1/lambda))
}
```

As described in the main package vignette (Section ??) the focus function supplied to `fic` should have arguments defined by a vector `par` of parameters of the biggest model (in this case the four-parameter model 4), and a matrix of covariate values `X`, and return the corresponding focus quantity. In this example, the two focus functions are

```
focus1 <- function(par, X){
    mean_snorm(mu = X %*% par[1:2], sigma=exp(par[3]), lambda=exp(par[4]))
}
focus2 <- function(par, X){
    median_snorm(mu = X %*% par[1:2], sigma = exp(par[3]), lambda = exp(par[4]))
}
```

The `inds` matrix, required by `fic` is now constructed. Recall this indicates which parameters (columns) are included in each of the models (rows) being compared. The narrow model is in the first row, and the wide model in the last. The functions `fns` required to extract the estimates and covariance matrix from the fitted model objects are then defined.

Finally `fic` is called to compare the four models for focuses defined by the mean and median for average men and women, with covariate values defined by `med.bmi`

TODO do we really need an intercept? Shouldn't

```
inds <- rbind(c(1,0,1,0),
              c(1,1,1,0),
              c(1,0,1,1),
```

```
              c(1,1,1,1))

fns <- list(coef=function(x)x$est,
            vcov=function(x)x$vcov,
            nobs=function(x)nrow(ais))

med.bmi <- rbind(male=c(1, 23.56),
                 female=c(1, 21.82))

focus0 <- function(par){X %*% par[1:2]}
fic(mod2, inds=rbind(c(1,0,1),c(1,1,1)), fns=fns, focus=focus0, X=med.bmi, FIC=TRUE,
    sub=list(mod1, mod2))
```

```
##     vals mods  rmse rmse.adj   bias    se   FIC focus
## 1   male    1 0.347    0.347 -0.248 0.244 12.39  43.1
## 4   male    2 0.249    0.249  0.000 0.249  1.07  43.3
## 2 female    1 0.525    0.525  0.466 0.244 43.80  43.1
## 5 female    2 0.262    0.262  0.000 0.262  3.79  42.6
## 3    ave    1 0.439    0.439  0.365 0.244 26.99  43.1
## 6    ave    2 0.256    0.256  0.000 0.256  1.32  43.0
```

```
fmean <- fic(mod4, inds=inds, fns=fns, focus=focus1, X=med.bmi, FIC=TRUE,
    sub=list(mod1, mod2, mod3, mod4))
fmean
```

```
##      vals mods  rmse rmse.adj   bias    se   FIC focus
## 1    male    1 0.349    0.349 -0.250 0.244 12.61  43.1
## 4    male    2 0.249    0.249  0.000 0.249  1.05  43.3
## 7    male    3 0.340    0.340 -0.237 0.244 11.85  43.1
## 10   male    4 0.249    0.249  0.000 0.249  1.05  43.3
## 2  female    1 0.515    0.515  0.454 0.244 41.62  43.1
## 5  female    2 0.262    0.262  0.000 0.262  3.73  42.6
## 8  female    3 0.513    0.513  0.452 0.244 43.09  43.1
## 11 female    4 0.262    0.262  0.000 0.262  3.78  42.6
## 3     ave    1 0.433    0.433  0.358 0.244 26.02  43.1
## 6     ave    2 0.256    0.256  0.000 0.256  1.30  43.0
## 9     ave    3 0.435    0.435  0.360 0.244 26.38  43.1
## 12    ave    4 0.256    0.256  0.000 0.256  1.32  43.0
```

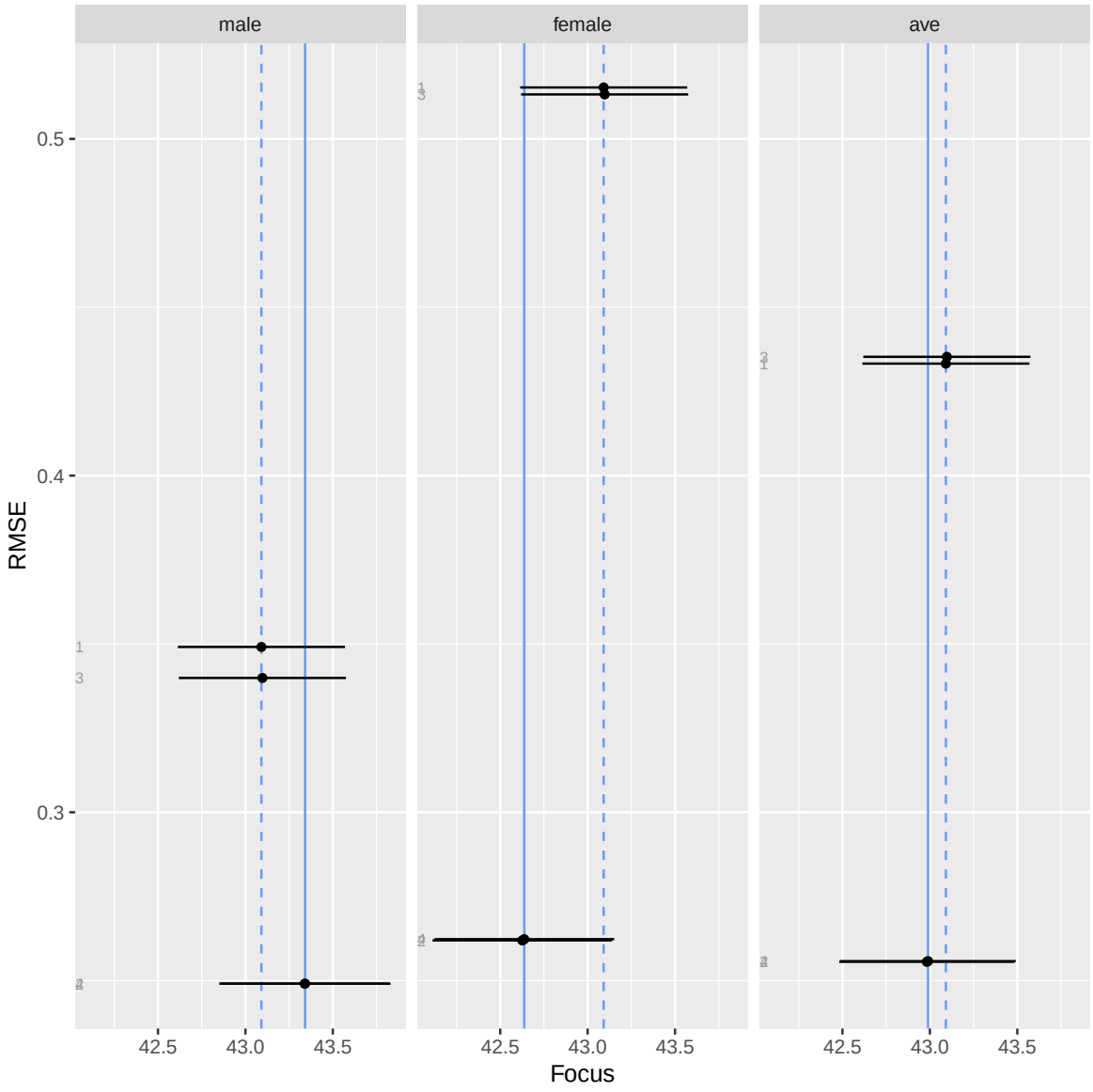
```
fmed <- fic(mod4, inds=inds, fns=fns, focus=focus2, X=med.bmi,
    sub=list(mod1, mod2, mod3, mod4))
fmed
```

```
##      vals mods  rmse rmse.adj   bias    se focus
## 1    male    1 0.299    0.299 -0.174 0.244  43.1
## 4    male    2 0.242    0.249  0.000 0.249  43.3
```

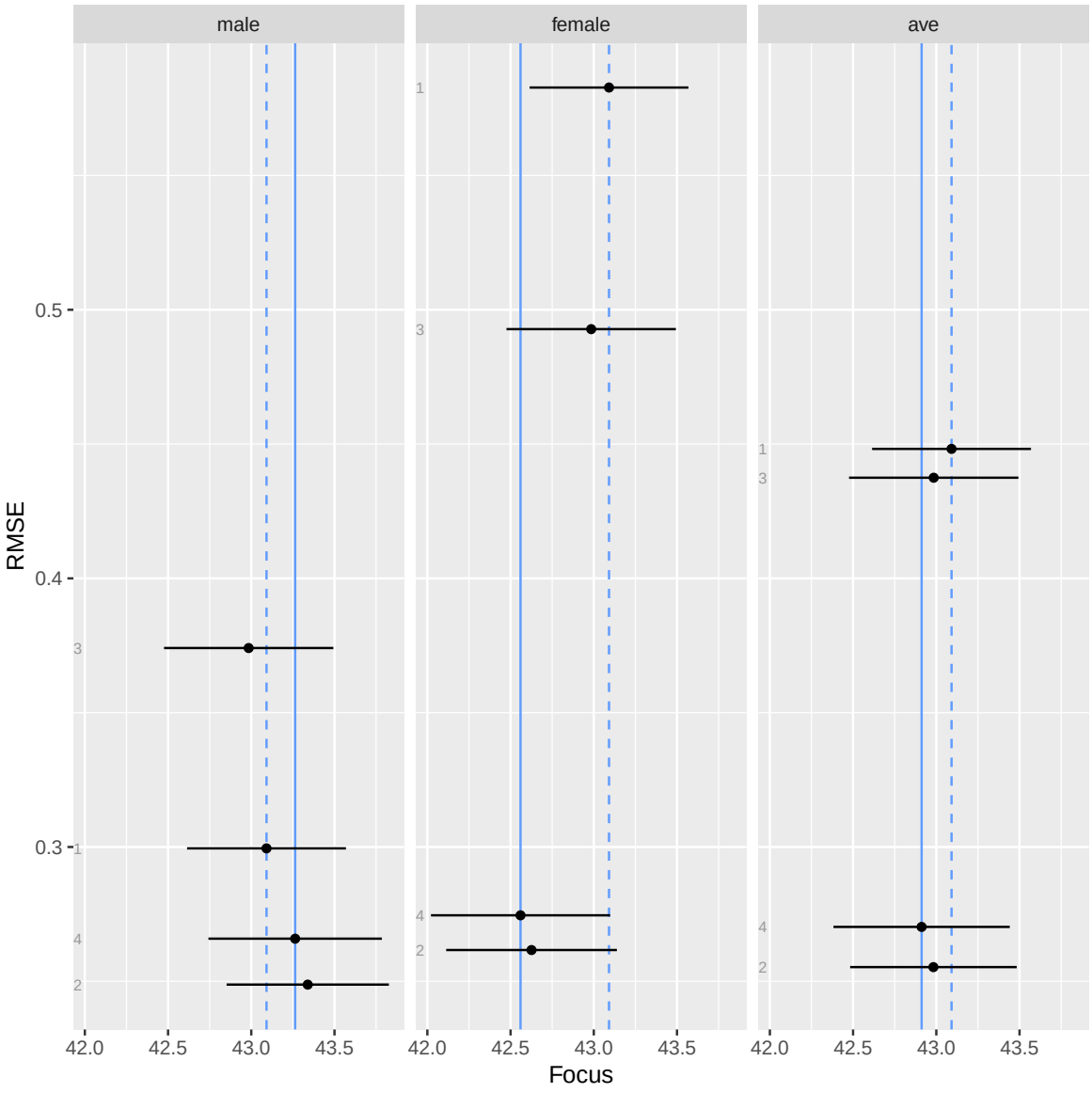
```
## 7    male    3 0.374    0.374 -0.269 0.260  43.0
## 10   male    4 0.266    0.266  0.000 0.266  43.3
## 2  female    1 0.583    0.583  0.529 0.244  43.1
## 5  female    2 0.256    0.262  0.000 0.262  42.6
## 8  female    3 0.493    0.493  0.419 0.260  43.0
## 11 female    4 0.275    0.275  0.000 0.275  42.6
## 3     ave    1 0.448    0.448  0.376 0.244  43.1
## 6     ave    2 0.249    0.255  0.000 0.255  43.0
## 9     ave    3 0.437    0.437  0.352 0.260  43.0
## 12    ave    4 0.270    0.270  0.000 0.270  42.9

library(ggplot2)

ggplot_fic(fmean)
```




```
ggplot_fic(fmed)
```



TODO name the models TODO shrink the plots TODO if nobs is supplied then set FIC true

mean: we need the covariate, but not necessarily the skewness as well. these conclusions don't depend on cov "For estimating the mean there is no award in involving the Îż aspects of the data, as the added complexity does not alter the large-sample performance of estimators."

fic values close to book, not exactly, for mean when wide excludes skew

median: we need the covariate again, but skew model has worse rmse

makes sense for measures of central tendency. median more robust to skew?

todo check vs book , hmm book selects wide model for median

refer to algebraic results in book

Very different FICs from book for median can we check the omegas against book?

TODO teach people to make a S3 method for their new class

TODO can't refit submodels - only works for standard cov selection problems