1 Tests

1.1 Data sets

- Set 1: Poisson-distributed data. Regression design ($\beta = \{1, 2\}$), $x \sim U[0, 1]$. 10 blocks, 10 reps per block. Random intercept with $\sigma = 1$.
- Set 2: as above but random slope with $\sigma_s = 0.5$.
- Set 3: `epil2` data set from `glmmADMB`

1.2 Models

- 0: Data set 1: intercept-only model, random intercepts.
- 1: Data set 1: `y~x`, random intercepts.
- 2: Data set 1: `y~x`, random slopes.
- 3–5: as 0–2, but with data set 2
- 6: `epil2` data, `y~Base*trt+Age+Visit`, random slopes (`Visit`) by subject, negative binomial
- 7: as 6, but Poisson (bad model, but useful for comparison with `lme4`)

All models with multiple random effects (i.e. 2, 5, 6, 7) are fitted with diagonal variance-covariance matrix (i.e. default `corStruct="diag"` in glmmADMB, non-default `(1|group)+(0+x|group)` in glmer).

Note that random effects as stored in `glmm.admb` objects are unscaled; those in `mer` are scaled by the standard deviation of the relevant random effect.

Would like to test `cbpp` data from `lme4`, but it's binomial with $N > 1$ so not currently possible with glmmADMB.

2 Comparisons

```
> load("singlerand_batch.RData")
```

```
> library(glmmADMB) ## MUST load this first!
> library(lme4) ## handy for glmer accessors
```

All fits OK, *except*:

- Warnings (`Estimated covariance matrix may not be positive definite`) for models 0-5, 7 with old glmmADMB. (Is this a real difference or a reporting difference? Doesn't seem to be in the TPL file, hence must (?) be coming from ADMB, hence must (?) be real ...)
- new glmmADMB fails on model 6

2.0.1 Model 0

sumfun	glmmADMB(orig)	glmmADMB(new)	glmer
(Intercept)	2.1390000	2.1526000	2.1524974
var(RE).(Intercept)	0.6777200	0.7055200	0.7009971
logLik	−399.4830000	−401.1910000	−214.4328451
U.(Intercept).min	−1.0550612	−1.0701833	−1.0698071
U.(Intercept).mean	0.0061092	0.0072664	0.0074201
U.(Intercept).max	1.1101358	1.0956339	1.0956924
time	1.1800000	2.6900000	0.2100000

Conclusions:

- Precision of glmmADMB results is truncated, presumably from printing/reading intermediate files in lowered precision. This applies throughout: not a big deal, but would be nice (and presumably not too hard) to fix.
- new glmmADMB and glmer agree on intercept, intercept variance, random effects
- Log-likelihood is obviously computed differently for glmer and glmmADMB; new and old glmmADMB differ by a disturbing amount. (Don't know whether this is computation or poorer fit; could check this.)

2.0.2 Model 1

sumfun	glmmADMB(orig)	glmmADMB(new)	glmer
(Intercept)	1.0205000	1.0205000	1.0204996
x	1.9001000	1.9001000	1.9001000
var(RE).(Intercept)	0.8814500	0.8814800	0.8758217
logLik	−260.5250000	−260.5080000	−73.7496189
U.(Intercept).min	−1.2520579	−1.2520793	−1.2517375
U.(Intercept).mean	0.0073972	0.0073992	0.0074799
U.(Intercept).max	1.1961021	1.1961225	1.1961017
time	2.0500000	2.9100000	0.2200000

Conclusions:

- All three agree on coefficients, REs
- glmmADMBs agree very closely on RE var (although glmer is pretty close too)

2.0.3 Model 2

sumfun	glmmADMB(orig)	glmmADMB(new)	glmer
(Intercept)	1.0205000	1.0205000	1.0205034
x	1.9001000	1.9001000	1.9000974
var(RE).(Intercept)	0.8758000	0.8758200	0.8758227
var(RE).x	0.0000069	0.0000000	0.0000000
logLik	−260.5250000	−260.5080000	−73.7496189
U.(Intercept).min	−1.2517821	−1.2517964	−1.2517391
U.(Intercept).mean	0.0074624	0.0074597	0.0074779
U.(Intercept).max	1.1960995	1.1961131	1.1960996
U.x.min	−0.0000429	0.0000000	0.0000000
U.x.mean	0.0000000	0.0000000	0.0000000
U.x.max	0.0000215	0.0000000	0.0000000
time	4.3600000	6.0200000	0.3600000

Conclusions:

- Like model 2: all agree closely

2.0.4 Model 3

sumfun	glmmADMB(orig)	glmmADMB(new)	glmer
(Intercept)	2.0834000	2.0838000	2.0836934
var(RE).(Intercept)	0.5827200	0.5834800	0.5797371
logLik	−356.0520000	−356.0700000	−169.5313261
U.(Intercept).min	−1.0267969	−1.0273135	−1.0268995
U.(Intercept).mean	0.0075214	0.0072689	0.0074029
U.(Intercept).max	1.1822172	1.1819185	1.1819182
time	1.6900000	2.1800000	0.1300000

Conclusions:

- Like model 0: new glmmADMB agrees with glmer (is this those two getting stuck at a slightly suboptimal fit?)
- log-likelihoods are all over the map

2.0.5 Model 4

sumfun	glmmADMB(orig)	glmmADMB(new)	glmer
(Intercept)	1.1121000	1.1121000	1.1120779
x	1.6540000	1.6540000	1.6539967
var(RE).(Intercept)	0.7214300	0.7214500	0.7168210
logLik	−256.1680000	−256.1500000	−69.6112380
U.(Intercept).min	−1.0584853	−1.0585849	−1.0582890
U.(Intercept).mean	0.0074023	0.0073990	0.0074787
U.(Intercept).max	1.2705731	1.2705907	1.2705182
time	1.8700000	2.6800000	0.3200000

Conclusions:

- Like model 1

2.0.6 Model 5

sumfun	glmmADMB(orig)	glmmADMB(new)	glmer
(Intercept)	1.1121000	1.1121000	1.1120757
x	1.6540000	1.6540000	1.6540212
var(RE).(Intercept)	0.7168000	0.7168200	0.7168311
var(RE).x	0.0000085	0.0000002	0.0000000
logLik	−256.1690000	−256.1500000	−69.6112380
U.(Intercept).min	−1.0582159	−1.0583153	−1.0583266
U.(Intercept).mean	0.0074648	0.0074599	0.0074658
U.(Intercept).max	1.2704686	1.2704863	1.2705328
U.x.min	−0.0000215	−0.0000004	0.0000000
U.x.mean	0.0000001	0.0000000	0.0000000
U.x.max	0.0000592	0.0000011	0.0000000
time	3.1900000	5.0700000	0.3600000

Conclusions:

- Like model 2 (but now slope variances are non-zero)

2.0.7 Model 6

glmer can’t do this one (negative binomial), and new glmmADMB fails.

2.0.8 Model 7

sumfun	glmmADMB(orig)	glmmADMB(new)	glmer
(Intercept)	−1.3002000	−1.3473000	−1.3472663
Base	0.8585700	0.8842300	0.8842334
trtprogabide	−0.9503100	−0.9276200	−0.9276255
Age	0.4655000	0.4705200	0.4705255
Visit	−0.2946100	−0.2670900	−0.2670821
Base:trtprogabide	0.3619500	0.3379000	0.3378860
var(RE).(Intercept)	0.2308500	0.2493100	0.2493143
var(RE).Visit	0.4636700	0.5457200	0.5422212
logLik	−645.2420000	−655.4100000	−272.4580894
U.(Intercept).min	−0.8921820	−0.9266186	−0.9266283
U.(Intercept).mean	0.0228518	0.0243157	0.0243575
U.(Intercept).max	1.0992639	1.1104644	1.1105139
U.Visit.min	−1.2499890	−1.3866675	−1.3815736
U.Visit.mean	0.0002485	0.0002641	0.0002481
U.Visit.max	0.8402035	1.0461875	1.0447351
time	10.7200000	22.8300000	2.1900000

Conclusions:

- As before: glmer and new glmmADMB agree

3 To do

- Try to figure out if glmer/new glmmADMB are getting stuck (e.g. evaluate likelihoods from scratch at both sets of parameter values, or evaluate likelihoods from each set in the other package/version
- incorporate timings
- incorporate fits from glmmML (can do intercept-only RE Poisson/binomial models, with Laplace [runs done, just have to do reporting]