

Author	Citation	Name	m	sd	n	tracking_method	calc_method	hr_estimator	relocated	sex	species	sex.spp	ecoregion	Latitude	Longitude
Aall		Aall, Natha Aall Female Total MCP	0.6556	0.5235	4	Telemetry	MCP	MCP	NO	Female	T. carolina	tc.f	OZARK/OUACHITA-APPALACHIAN FORESTS Aall	38.310454-82.343395"	
Baker		Baker, Jear Baker 95 K Female Total	5.8571	2.6505	14	Telemetry	95 Kernel	Kernel	NO	Female	T. carolina	tc.f	SOUTHEASTERN USA PLAINS	40.122466-87.697554"	
Baker		Baker, Jear Baker MCP Female	10.1643	9.5091	14	Telemetry	MCP	MCP	NO	Female	T. carolina	tc.f	SOUTHEASTERN USA PLAINS	40.122466-87.697554"	
Capitano		Capitano, \Capitano 95K Female	10.72	12.46	7	Telemetry	95 Kernel	Kernel	NO	Female	T. carolina	tc.f	MISSISSIPPI ALLUVIAL AND SOUTHEAST US Capitano	40.775382-72.881087"	
Capitano		Capitano, \Capitano MCP Female	8.1	9.6	7	Telemetry	MCP	MCP	NO	Female	T. carolina	tc.f	MISSISSIPPI ALLUVIAL AND SOUTHEAST US Capitano	40.775382-72.881087"	
Cook		Cook, Robt Cook 95 BN Female	11.43	10.37	25	Telemetry	95 Bivariate Normal	Ellipse	YES	Female	T. carolina	tc.f	MISSISSIPPI ALLUVIAL AND SOUTHEAST US Cook	40.592276-73.891436"	
Cook		Cook, Robt Cook 95 HM Female	5.51	8.42	25	Telemetry	95 HM	HM	YES	Female	T. carolina	tc.f	MISSISSIPPI ALLUVIAL AND SOUTHEAST US Davis	35.987466-83.941978"	
Currylow et al		Currylow, / Currylow post 95 k female	5.02	8.231	8	Telemetry	95 Kernel	Kernel	NO	Female	T. carolina	tc.f	SOUTHEASTERN USA PLAINS	39.139084-77.020463"	Farnsworth and Seigel
Currylow et al		Currylow, / Currylow post MCP female	9.87	7.948	8	Telemetry	MCP	MCP	NO	Female	T. carolina	tc.f	SOUTHEASTERN USA PLAINS	31.828456-109.949686"	Hall and Steidl
Greenspan et al		Greenspan Greenspan 95K Female	8.28	14.869	7	Telemetry	95 Kernel	Kernel	NO	Female	T. carolina	tc.f	SOUTHEASTERN USA PLAINS	34.341686-106.973286"	Nieuwolt
Greenspan et al		Greenspan Greenspan MCP Female	8.33	15.028	7	Telemetry	95 MCP	MCP	NO	Female	T. carolina	tc.f	SOUTHEASTERN USA PLAINS	42.038584-89.962680"	Refsnider et al
Kaye, Walsh, and Ross		Kaye, Delia Kaye Female	2.6	3.500179	5	Telemetry	MCP	MCP	NO	Female	T. carolina	tc.f	MIXED WOOD PLAINS		
Lentz		Lentz, Jenn Lentz Female	5.92	7.49	20	other	MCP	MCP	NO	Female	T. carolina	tc.f	SOUTHEASTERN USA PLAINS		
Madden		Madden, R Madden 95 BN Female	8.75	5.48	13	Telemetry	95 Bivariate Normal	Ellipse	NO	Female	T. carolina	tc.f	MISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS		
Madden		Madden, R Madden Convex Polygon Female	2.77	1.93	13	Telemetry	Convex Polygon	MCP	NO	Female	T. carolina	tc.f	MISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS		
Quinn		Quinn, Der Quinn Female MCP	4	2.413124	7	Telemetry	MCP	MCP	NO	Female	T. carolina	tc.f	MIXED WOOD PLAINS		
Aall		Aall, Natha Aall Male MCP	0.205	0.4366	5	Telemetry	MCP	MCP	NO	Male	T. carolina	tc.m	OZARK/OUACHITA-APPALACHIAN FORESTS Baker	38.310454-82.343395"	
Baker		Baker, Jear Baker 95 K Male	4.5	1.594428	10	Telemetry	95 Kernel	Kernel	NO	Male	T. carolina	tc.m	SOUTHEASTERN USA PLAINS	40.122466-87.697554"	
Baker		Baker, Jear Baker MCP Male	3.5	2.051124	10	Telemetry	MCP	MCP	NO	Male	T. carolina	tc.m	SOUTHEASTERN USA PLAINS	40.122466-87.697554"	
Cook		Cook, Robt Cook 95 BN Male	7	5.68	15	Telemetry	95 Bivariate Normal	Ellipse	YES	Male	T. carolina	tc.m	MISSISSIPPI ALLUVIAL AND SOUTHEAST US Currylow et al	39.325851-86.419921"	
Cook		Cook, Robt Cook 95 HM Male	3.37	3.12	15	Telemetry	95 HM	HM	YES	Male	T. carolina	tc.m	MISSISSIPPI ALLUVIAL AND SOUTHEAST US Donaldson and Echternacht	35.732852-84.333811"	
Currylow et al		Currylow, / Currylow post 95 k male	18.66	45.745	7	Telemetry	95 Kernel	Kernel	NO	Male	T. carolina	tc.m	SOUTHEASTERN USA PLAINS	31.251275-84.372605"	Greenspan et al
Currylow et al		Currylow, / Currylow post MCP male	16.72	34.659	7	Telemetry	MCP	MCP	NO	Male	T. carolina	tc.m	SOUTHEASTERN USA PLAINS	35.500037-80.845197"	Hester et al
Greenspan et al		Greenspan Greenspan 95K Male	11.7	17.16	9	Telemetry	95 Kernel	Kernel	NO	Male	T. carolina	tc.m	SOUTHEASTERN USA PLAINS	41.308274-72.927883"	Quinn
Greenspan et al		Greenspan Greenspan MCP Male	11.7	17.25	9	Telemetry	95 MCP	MCP	NO	Male	T. carolina	tc.m	SOUTHEASTERN USA PLAINS	38.888604-91.909924"	Rittenhouse et al PF
Lentz		Lentz, Jenn Lentz Male	1.51	1.33	17	other	MCP	MCP	NO	Male	T. carolina	tc.m	SOUTHEASTERN USA PLAINS		
Madden		Madden, R Madden 95 BN Male	4.76	2.78	10	Telemetry	95 Bivariate Normal	Ellipse	NO	Male	T. carolina	tc.m	MISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS		
Madden		Madden, R Madden Convex Polygon Male	1.27	1.08	10	Telemetry	Convex Polygon	MCP	NO	Male	T. carolina	tc.m	MISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS		
Quinn		Quinn, Der Quinn Male MCP	5.649	5.738962	7	Telemetry	MCP	MCP	NO	Male	T. carolina	tc.m	MIXED WOOD PLAINS		
Bayless		Bayless, J. \ Bayless MA Mixed	1.2468	0.842016	5	other	MA	MCP	NO	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS	38.676241-77.264481"	Bayless
Davis		Davis, Mar Davis Mixed MCP	3.77	0.134748	4	Telemetry	MCP	MCP	YES	Mixed	T. carolina	tc.mix	OZARK/OUACHITA-APPALACHIAN FORESTS Holy	41.798734-99.397211"	
Donaldson and Echternacht		Donaldson Donaldson 95 K Mixed	2.26	0.76	6	other	95 Kernel	Kernel	NO	Mixed	T. carolina	tc.mix	OZARK/OUACHITA-APPALACHIAN FORESTS Kapfer et al elon and natural	36.011786-79.425628"	
Donaldson and Echternacht		Donaldson Donaldson MCP Mixed	1.88	0.49	6	other	MCP	MCP	NO	Mixed	T. carolina	tc.mix	OZARK/OUACHITA-APPALACHIAN FORESTS Kapfer et al zoo	35.744956-79.829674"	
Farnsworth and Seigel		Farnsworth Farnsworth on site Mixed MCP	5.61	2.64	20	Telemetry	MCP	MCP	YES	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS	41.967742-70.906877"	Kaye, Walsh, and Ross
Farnsworth and Seigel		Farnsworth Farnsworth off site Mixed MCP	14.71	2.64	14	Telemetry	MCP	MCP	YES	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS	38.784576-76.700784"	Lentz
Farnsworth and Seigel		Farnsworth Farnsworth Native Mixed MCP	4.31	2.64	18	Telemetry	MCP	MCP	NO	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS	40.804826-73.336230"	Madden
Hester et al		Hester, Joy Hester Not Relocated 95 K Mixed	2.8	2.21359	10	Telemetry	95 Kernel	Kernel	YES	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS	38.888604-91.909924"	Rittenhouse et al Baskett
Hester et al		Hester, Joy Hester Not Relocated MCP Mixed	6.45	4.427	10	Telemetry	MCP	MCP	YES	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS	32.345704-95.382582"	Samuelson
Hester et al		Hester, Joy Hester Relocated 95 K Mixed	18.26	12.445	8	Telemetry	95 Kernel	Kernel	YES	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS	33.577866-101.855166"	Sosa and Perry
Hester et al		Hester, Joy Hester Relocated MCP Mixed	18.02	11.3842	10	Telemetry	MCP	MCP	YES	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS	40.235396-100.529612"	Trail
Kapfer et al		Kapfer, Jos Kapfer Elon Mixed	1.106	1.185	5	Telemetry	MCP	MCP	NO	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS	41.588666-83.891053"	Wilson
Kapfer et al		Kapfer, Jos Kapfer Haw Mixed	2.48	0.87	4	Telemetry	MCP	MCP	NO	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS		
Kapfer et al		Kapfer, Jos Kapfer Zoo Mixed	7.017	9.212	2	Telemetry	MCP	MCP	NO	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS		
Rittenhouse et al		Rittenhouse Rittenhouse PF1 Mixed	9.44	2.58	19	Telemetry	95 Kernel	Kernel	NO	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS		
Rittenhouse et al		Rittenhouse Rittenhouse PF2 Mixed	3.73	3.73	19	Telemetry	95 Kernel	Kernel	YES	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS		
Rittenhouse et al		Rittenhouse Rittenhouse TB1 Mixed	6.48	2.58	16	Telemetry	95 Kernel	Kernel	NO	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS		
Rittenhouse et al		Rittenhouse Rittenhouse TB2 Mixed	28.37	11.37	16	Telemetry	95 Kernel	Kernel	YES	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS		
Samuelson		Samuelson Samuelson Resident	7.89	10.41	5	Telemetry	Blank	NA	NO	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS		
Samuelson		Samuelson Samuelson Translocated	14.22	8.134	5	Telemetry	Blank	NA	YES	Mixed	T. carolina	tc.mix	SOUTHEASTERN USA PLAINS		
Wilson		Wilson, Stc Wilson Mixed MCP	18.317	27.16599	5	Telemetry	MCP	MCP	NO	Mixed	T. carolina	tc.mix	CENTRAL USA PLAINS		
Bernstein and Richtsmeier		Bernstein, Bernstein 95K Female	0.825383	0.079552	5	Telemetry	95 Kernel	Kernel	NO	Female	T. ornata	to.f	TEMPERATE PRAIRIES	41.798066C-91.685788"	Bernstein and Richtsmeier
Bernstein and Richtsmeier		Bernstein, Bernstein MCP Female	3.0324	1.519646	5	Telemetry	MCP	MCP	NO	Female	T. ornata	to.f	TEMPERATE PRAIRIES	41.798066C-91.685788"	Bernstein and Richtsmeier
Holy		Holy, Lisa L Holy Female 1994	19.09714	10.78702	7	Telemetry	MA	MCP	NO	Female	T. ornata	to.f	WEST-CENTRAL SEMI-ARID PRAIRIES		
Nieuwolt		Nieuwolt, I Nieuwolt Female 95 Ellipse	3.6228	3.4038	8	Telemetry	95 Ellipse	Ellipse	NO	Female	T. ornata	to.f	COLD DESERTS		
Nieuwolt		Nieuwolt, I Nieuwolt Female 95 HM	1.0892	1.4009	8	Telemetry	95 HM	HM	NO	Female	T. ornata	to.f	COLD DESERTS		
Nieuwolt		Nieuwolt, I Nieuwolt Female Min Pol	1.3391	1.2082	8	Telemetry	Minimum Polygon	MCP	NO	Female	T. ornata	to.f	COLD DESERTS		
Refsnider et al		Refsnider, Refsnider Female 95K	2.4	0.8	14	Telemetry	95 Kernel	Kernel	NO	Female	T. ornata	to.f	CENTRAL USA PLAINS		
Refsnider et al		Refsnider, Refsnider Female MCP	4.3	5	14	Telemetry	MCP	MCP	NO	Female	T. ornata	to.f	CENTRAL USA PLAINS		
Sosa and Perry		Sosa, J. Sosa Female MCP Natural	3.13	2.44	9	Telemetry	MCP	MCP	NO	Female	T. ornata	to.f	SOUTH CENTRAL SEMI-ARID PRAIRIES		
Bernstein and Richtsmeier		Bernstein, Bernstein 95K Male	1.076367	0.192081	3	Telemetry	95 Kernel	Kernel	NO	Male	T. ornata	to.m	TEMPERATE PRAIRIES	41.798066C-91.685788"	Bernstein and Richtsmeier
Bernstein and Richtsmeier		Bernstein, Bernstein MCP Male	5.803	2.323728	3	Telemetry	MCP	MCP	NO	Male	T. ornata	to.m	TEMPERATE PRAIRIES	41.798066C-91.685788"	Bernstein and Richtsmeier
Holy		Holy, Lisa L Holy Male 1994	18.5335	11.26826	8	Telemetry	MA	MCP	NO	Male	T. ornata	to.m	WEST-CENTRAL SEMI-ARID PRAIRIES		
Nieuwolt		Nieuwolt, I Nieuwolt Male 95 Ellipse	7.144	5.6547	7	Telemetry	95 Ellipse	Ellipse	NO	Male	T. ornata	to.m	COLD DESERTS		
Nieuwolt		Nieuwolt, I Nieuwolt Male 95 HM	1.2804	1.4198	7	Telemetry	95 HM	HM	NO	Male	T. ornata	to.m	COLD DESERTS		
Nieuwolt		Nieuwolt, I Nieuwolt Male Min Pol	2.1067	1.4888	7	Telemetry	Minimum Polygon	MCP	NO	Male	T. ornata	to.m	COLD DESERTS		
Refsnider et al		Refsnider, Refsnider Male 95K	2.8	1	6	Telemetry	95 Kernel	Kernel	NO	Male	T. ornata	to.m	CENTRAL USA PLAINS		
Refsnider et al		Refsnider, Refsnider Male MCP	3.1	2	6	Telemetry	MCP	MCP	NO	Male	T. ornata	to.m	CENTRAL USA PLAINS		
Sosa and Perry		Sosa, J. Sosa Male MCP Natural	3.19	1.84	8	Telemetry	MCP	MCP	NO	Male	T. ornata	to.m	SOUTH CENTRAL SEMI-ARID PRAIRIES		
Trail		Trail, Trail	6.8	7.76	3	Telemetry	MCP	MCP	NO	Male	T. ornata	to.m	SOUTH CENTRAL SEMI-ARID PRAIRIES		
Hall and Steidl		Hall, David Hall 95K Mixed	6.4	1	24	Telemetry	95 Kernel	Kernel	NO	Mixed	T. ornata	to.mix	WESTERN SIERRA MADRE PIEDMONT		
Hall and Steidl		Hall, David Hall MCP Mixed	10	2.3	24	Telemetry	MCP	MCP	NO	Mixed	T. ornata	to.mix	WESTERN SIERRA MADRE PIEDMONT		
Sosa and Perry		Sosa, J. Sosa Mixed Urban	1.55	0.63	3	Telemetry	MCP	MCP	NO	Mixed	T. ornata	to.mix	SOUTH CENTRAL SEMI-ARID PRAIRIES		

Turtle_meta-analysis_code.R

habeck

Fri Aug 19 10:42:43 2016

```
# Meta-analysis: Box turtle home range size - Code authored by Chris Habeck, Kutztown University

# Load RData

load("C:/Users/habeck/Desktop/Dropbox/KU/Current Research/Miranda Meta-Analysis/Turtle meta-analysis/.RData")

# Load libraries

library(metafor)
```

```
## Loading required package: Matrix
```

```
## Loading 'metafor' package (version 1.9-8). For an overview
## and introduction to the package please type: help(metafor).
```

```
library(multcomp)
```

```
## Loading required package: mvtnorm
```

```
## Loading required package: survival
```

```
## Loading required package: TH.data
```

```
## Loading required package: MASS
```

```
##
## Attaching package: 'TH.data'
```

```
## The following object is masked from 'package:MASS':
##
##      geyser
```

```
#_____

# Create a few helpful functions

import = function() {read.table("clipboard", header = T, sep = "\t", quote = "\"")}
```

```
export = function(x) {write.table(x, "clipboard")}
st.err = function(x) sqrt(var(x)/length(x))

#_____

# Copy data from excel file to clipboard and run import function to create R data files

#dat.all = import()
#dat.to = import()
#dat.tc = import()

#_____

# Calculate effect sizes and sampling variance for each data set.
# Here, measure = "MN" tells escalc that our response variable is the raw mean.

ef.all = escalc(measure = "MN", mi= m, sdi= sd, ni= n, data=dat.all)
ef.to = escalc(measure = "MN", mi= m, sdi= sd, ni= n, data=dat.to)
ef.tc = escalc(measure = "MN", mi= m, sdi= sd, ni= n, data=dat.tc)

#_____

#Subset ef.all data set to include only T. ornata cases and exclude "Mixed" from sex column

ef.to.sex <- subset(ef.all, species=="T. ornata" & sex!="Mixed")
droplevels.factor(ef.to.sex$sex)
```

```
## [1] Female Male Female Male Female Male Female Male Female Male
## [11] Female Male Male Male Female Female Female Male Female Male
## [21] Female Male Male Male Female Male
## Levels: Female Male
```

```
droplevels.factor(ef.to.sex$species)
```

```
## [1] T. ornata T. ornata T. ornata T. ornata T. ornata T. ornata T. ornata
## [8] T. ornata T. ornata T. ornata T. ornata T. ornata T. ornata T. ornata
## [15] T. ornata T. ornata T. ornata T. ornata T. ornata T. ornata T. ornata
## [22] T. ornata T. ornata T. ornata T. ornata T. ornata
## Levels: T. ornata
```

```
droplevels.factor(ef.to.sex$Author)
```

```
## [1] Nieuwolt Nieuwolt
## [3] Nieuwolt Nieuwolt
## [5] Nieuwolt Nieuwolt
## [7] Bernstein and Richtsmeier Bernstein and Richtsmeier
## [9] Refsnider et al Refsnider et al
## [11] Sosa and Perry Sosa and Perry
## [13] Sosa and Perry Holy
## [15] Holy Holy
## [17] Bernstein and Richtsmeier Bernstein and Richtsmeier
```

```
## [19] Refsnider et al          Refsnider et al
## [21] Sosa and Perry           Sosa and Perry
## [23] Sosa and Perry           Trail
## [25] Nieuwolt                 Nieuwolt
## 6 Levels: Bernstein and Richtsmeier Holy Nieuwolt ... Trail
```

```
#
# Estimate T.ornata home range size using all cases, no moderators

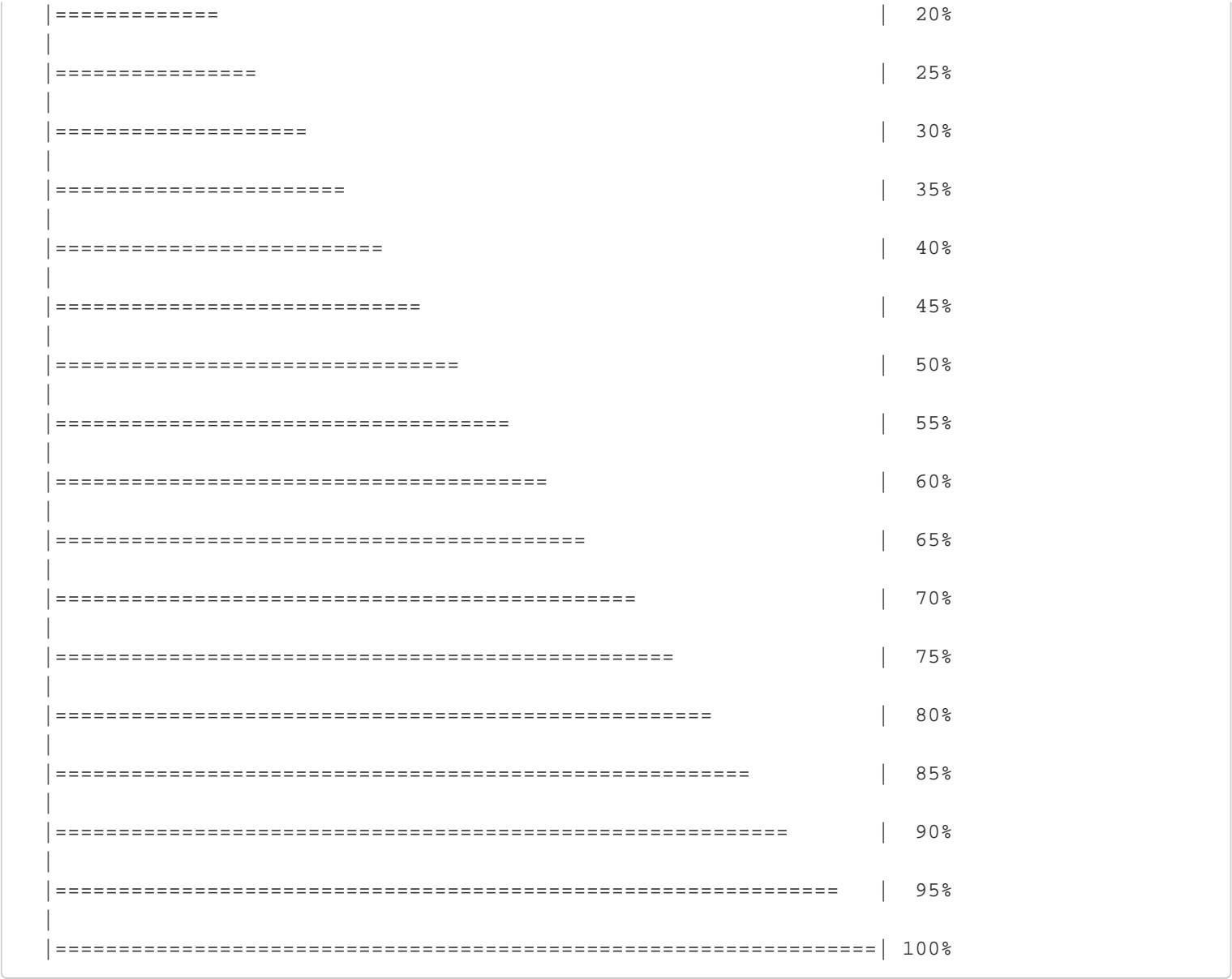
mod.to.int = rma.mv(yi,vi,random = ~1|Author, data = ef.to)
summary(mod.to.int)
```

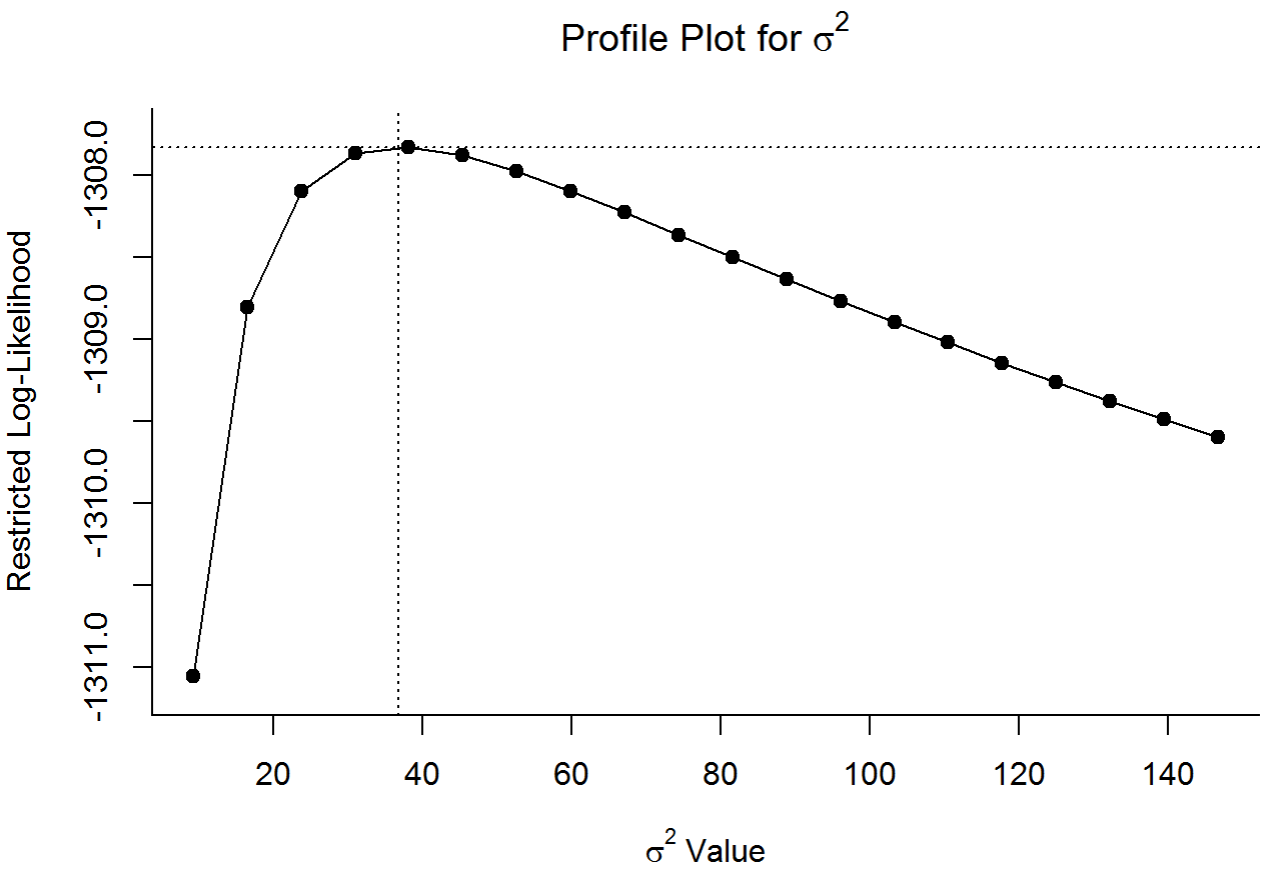
```
##
## Multivariate Meta-Analysis Model (k = 34; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -1307.8281    2615.6563    2619.6563    2622.6493    2620.0563
##
## Variance Components:
##
##              estim      sqrt  nlvls  fixed  factor
## sigma^2      36.6887   6.0571      7     no  Author
##
## Test for Heterogeneity:
## Q(df = 33) = 3790.9213, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##   5.3918    2.3672    2.2777    0.0227    0.7521   10.0315      *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot. If the log-likelihood does not peak and then quickly drop at the mode
l estimate
# (dotted vertical), then the model is overparameterized

profile(mod.to.int, sigma2=1)
```

```
##
|
|
|
|====| 0%
|
|=====| 5%
|
|=====| 10%
|
|=====| 15%
|
```





```
# Eggar's test for bias in the data. Since our effect response is the raw mean, I think this
# test has low utility, but at least we can say we did it, and let the reviewers decide for th
# emselves.

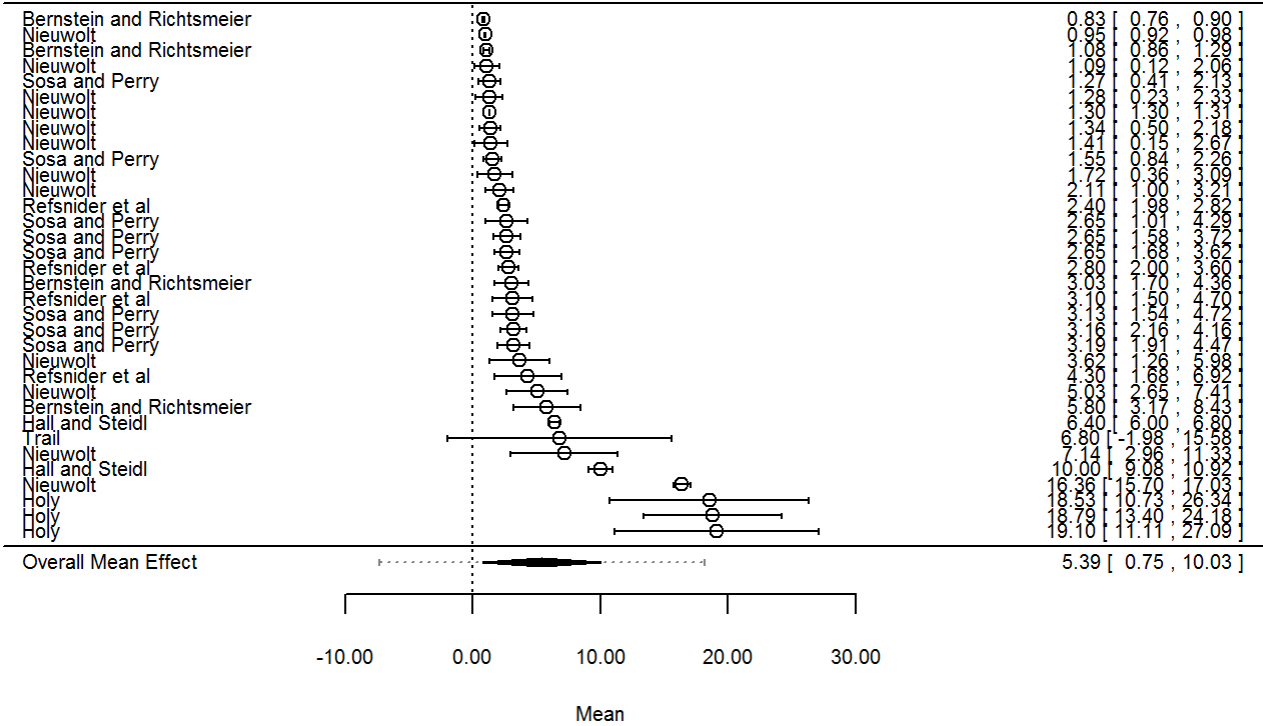
mod.to.int.bias = rma.mv(yi,vi,mod = ~sqrt(vi), random = ~1|Author, data = ef.to)
summary(mod.to.int.bias)
```

```
##
## Multivariate Meta-Analysis Model (k = 34; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -1212.2824    2424.5648    2430.5648    2434.9620    2431.4219
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed  factor
## sigma^2    8.9501  2.9917     7     no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 32) = 3359.2850, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 194.9555, p-val < .0001
##
## Model Results:
```

```
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      2.0487  1.2385   1.6542  0.0981  -0.3786   4.4761      .
## sqrt(vi)     3.4792  0.2492  13.9626  <.0001   2.9908   3.9676    ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

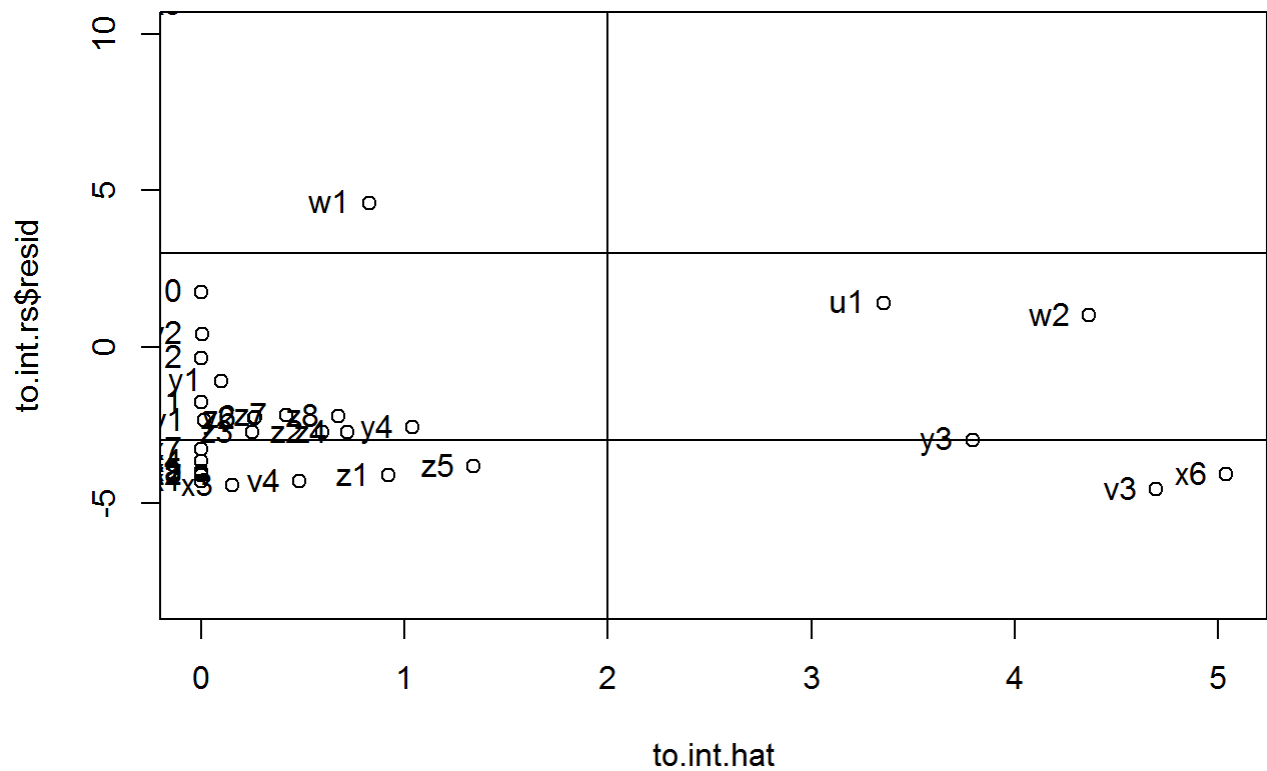
```
# Create forest plot for the model

forest(mod.to.int, slab = ef.to$Author, psize = 1.5, pch = 21,
       mlab = "Overall Mean Effect", addcred = TRUE, order = "obs")
```



```
# Identify influential outliers using ID column

to.int.rs = rstandard(mod.to.int)
to.int.hat = hatvalues(mod.to.int)/mean(hatvalues(mod.to.int))
plot(to.int.hat, to.int.rs$resid, ylim = c(-8.0,10))
text(to.int.hat, to.int.rs$resid, labels = ef.to$ID, cex= 1, pos = 2)
abline(h = -3)
abline(h = 3)
abline( v = 2)
```



```
# Removing influntial outliers by ID: v3, x6, y3

ef.to.infout = ef.to[!(ef.to$ID %in% c("v3", "x6", "y3")),]

# Test for home range size estimate: no moderators, no influential outliers
# These results are not sig different from the original model, so I suggest we retain all data
.

mod.to.int.infout = rma.mv(yi,vi,random = ~1|Author, data = ef.to.infout)
summary(mod.to.int.infout)
```

```
##
## Multivariate Meta-Analysis Model (k = 31; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -1132.5390    2265.0781    2269.0781    2271.8805    2269.5225
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed  factor
## sigma^2    36.2921  6.0243     7     no  Author
##
## Test for Heterogeneity:
## Q(df = 30) = 3359.3385, p-val < .0001
##
```

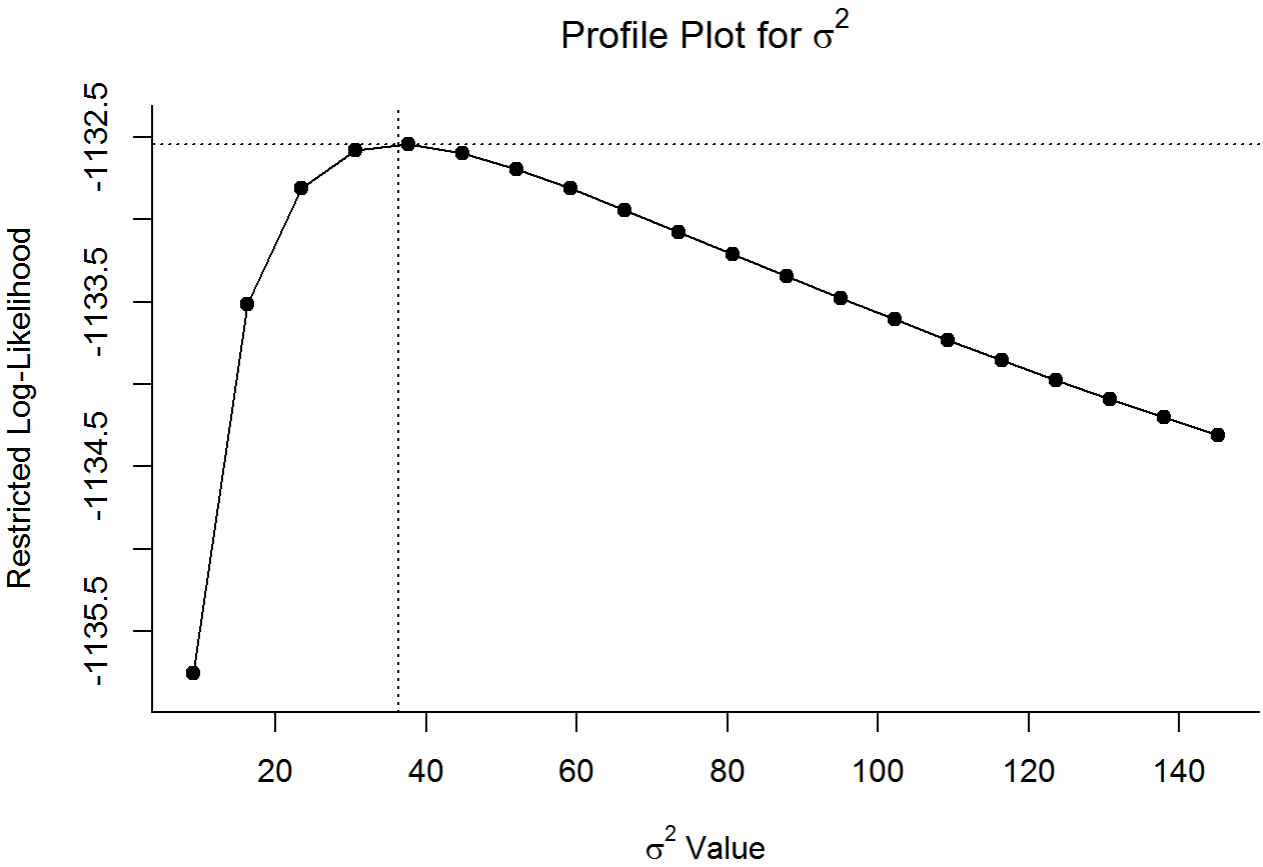
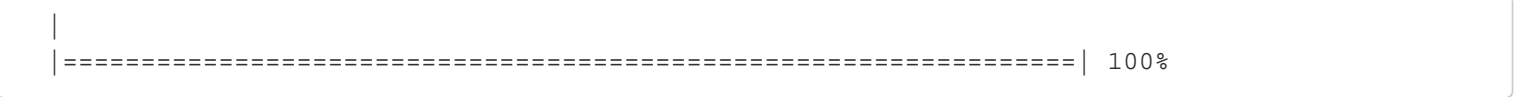


```
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    5.4530    2.3555    2.3150    0.0206    0.8362   10.0697      *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot

profile(mod.to.int.infout, sigma2=1)
```





```
# Delta AICc against int-only model: basically, tests whether the infout model
# is a better fit than the int-only model. Delta AICc >2 suggest a better fit.

AIC(mod.to.int.infout, mod.to.int, correct = TRUE)

##                df      AICc
## mod.to.int.infout  2 2269.523
## mod.to.int         2 2620.056

AIC(mod.to.int, correct = TRUE) - AIC(mod.to.int.infout,correct = TRUE)

## [1] 350.5338

# The infout model is more parsimoniuos , but the estimate and CIs are almost identical.
# So I suggest we retain all data for further analysis, rather than exclude these three points
.

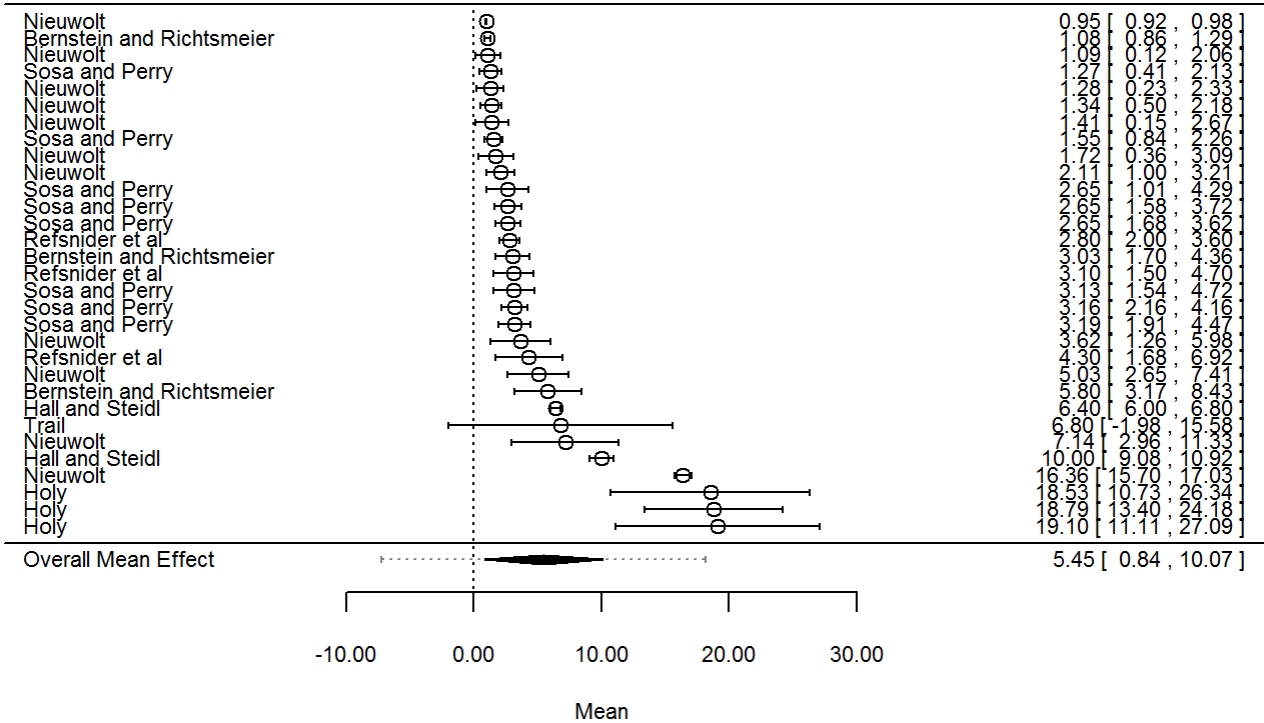
# Calculate McFadden's pseudo R2: basically, represents increase of predictive power above tha
t of the int-omly model.
#
```

```
1-(logLik(mod.to.int.infout)/logLik(mod.to.int))

## 'log Lik.' 0.1340307 (df=2)

# Create forest plot for the model

forest(mod.to.int.infout, slab = ef.to.infout$Author, psize = 1.5, pch = 21,
        mlab = "Overall Mean Effect", addcred = TRUE, order = "obs")
```



```
#

# Test: Effect of sex on T. ornata hr size

mod.to.sex.int = rma.mv(yi,vi,random = ~1|Author, data = ef.to.sex)
summary(mod.to.sex.int)

##
## Multivariate Meta-Analysis Model (k = 26; method: REML)
##
##   logLik  Deviance      AIC      BIC     AICc
## -59.5494  119.0988  123.0988  125.5366  123.6443
##
## Variance Components:
##
```

```
##          estim      sqrt  nlvls  fixed  factor
## sigma^2    44.3126  6.6568      6     no  Author
##
## Test for Heterogeneity:
## Q(df = 25) = 255.5660, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##   5.1655    2.8120   1.8370   0.0662   -0.3459   10.6768      .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Testing main effect to display level-specific estimates

mod.to.sex.d = rma.mv(yi,vi,mods = ~ sex-1, random = ~1|Author, data = ef.to.sex)
```

```
## Warning in rma.mv(yi, vi, mods = ~sex - 1, random = ~1 | Author, data =
## ef.to.sex): Redundant predictors dropped from the model.
```

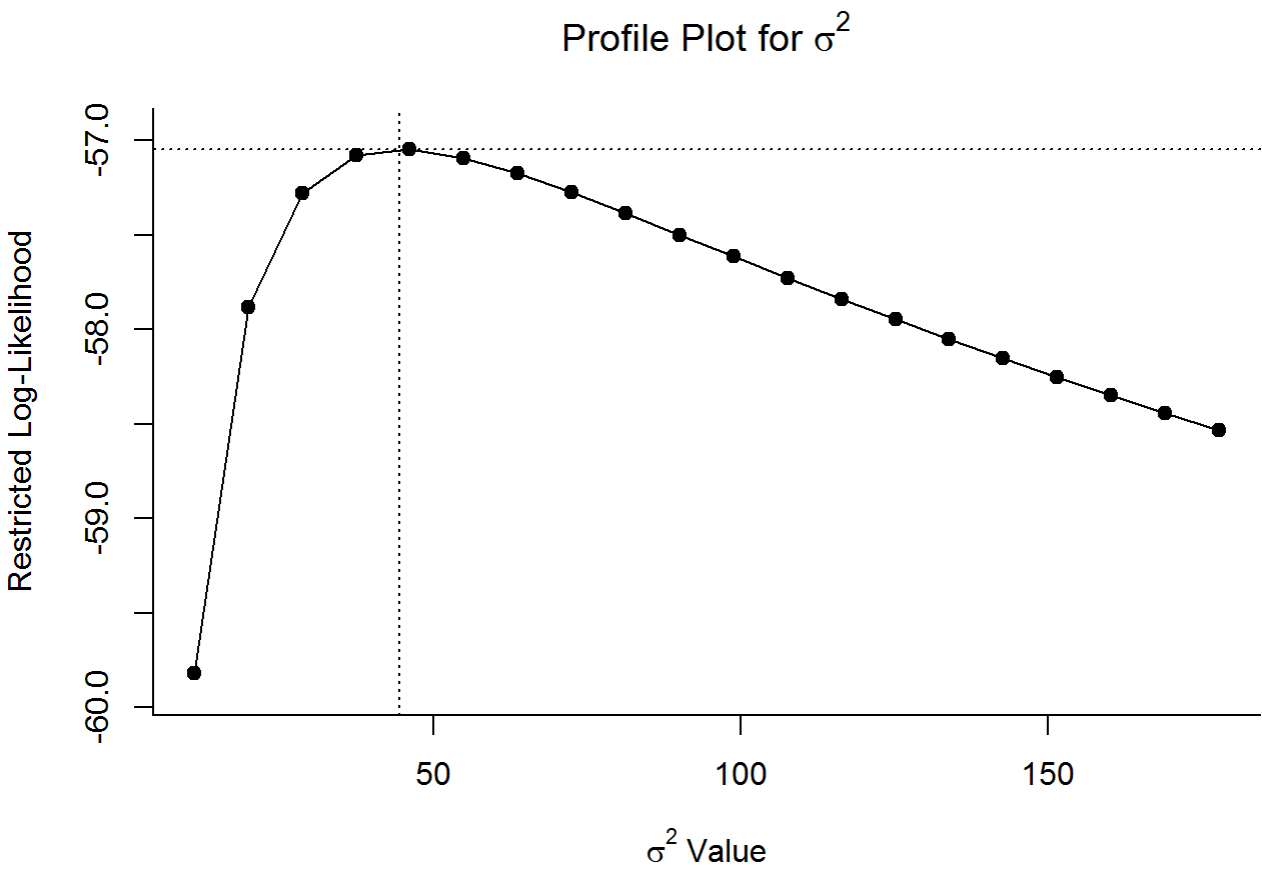
```
summary(mod.to.sex.d)
```

```
##
## Multivariate Meta-Analysis Model (k = 26; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -57.0453  114.0907  120.0907  123.6249  121.2907
##
## Variance Components:
##
##          estim      sqrt  nlvls  fixed  factor
## sigma^2    44.4588  6.6677      6     no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 24) = 228.5094, p-val < .0001
##
## Test of Moderators (coefficient(s) 1,2):
## QM(df = 2) = 9.1427, p-val = 0.0103
##
## Model Results:
##
##          estimate      se      zval      pval      ci.lb      ci.ub
## sexFemale    5.0507  2.8168   1.7931   0.0730   -0.4701   10.5714      .
## sexMale      5.3074  2.8170   1.8841   0.0596   -0.2137   10.8285      .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot
```

```
profile(mod.to.sex, sigma2=1)
```





```
# Delta AICc against int-only model
AIC(mod.to.sex, mod.to.sex.int, correct = TRUE)
```

```
##           df      AICc
## mod.to.sex      3 121.2907
## mod.to.sex.int  2 123.6443
```

```
AIC(mod.to.sex.int, correct = TRUE) - AIC(mod.to.sex,correct = TRUE)
```

```
## [1] 2.353572
```

```
# Calculate McFadden's pseudo R2
1-(logLik(mod.to.sex)/logLik(mod.to.sex.int))
```

```
## 'log Lik.' 0.0420501 (df=3)
```

```
# Test: Effect of hr_estimator on T. ornata hr size

mod.to.hr = rma.mv(yi,vi,mods = ~ hr_estimator, random = ~1|Author, data = ef.to)
summary(mod.to.hr)
```

```
##
## Multivariate Meta-Analysis Model (k = 34; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -742.8435    1485.6870    1495.6870    1502.6930    1498.1870
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed  factor
## sigma^2      27.6779  5.2610      7      no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 30) = 2871.9707, p-val < .0001
##
## Test of Moderators (coefficient(s) 2,3,4):
## QM(df = 3) = 1126.1612, p-val < .0001
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          3.3715  2.2321    1.5105    0.1309   -1.0033    7.7462
## hr_estimatorHM    -3.4179  0.7936   -4.3071   <.0001   -4.9732   -1.8626
## hr_estimatorKernel  1.5811  0.8970    1.7626    0.0780   -0.1770    3.3392
## hr_estimatorMCP     4.3260  0.8289    5.2187   <.0001    2.7013    5.9506
##
## intrcpt
## hr_estimatorHM      ***
## hr_estimatorKernel      .
## hr_estimatorMCP      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Testing main effect to display level-specific estimates

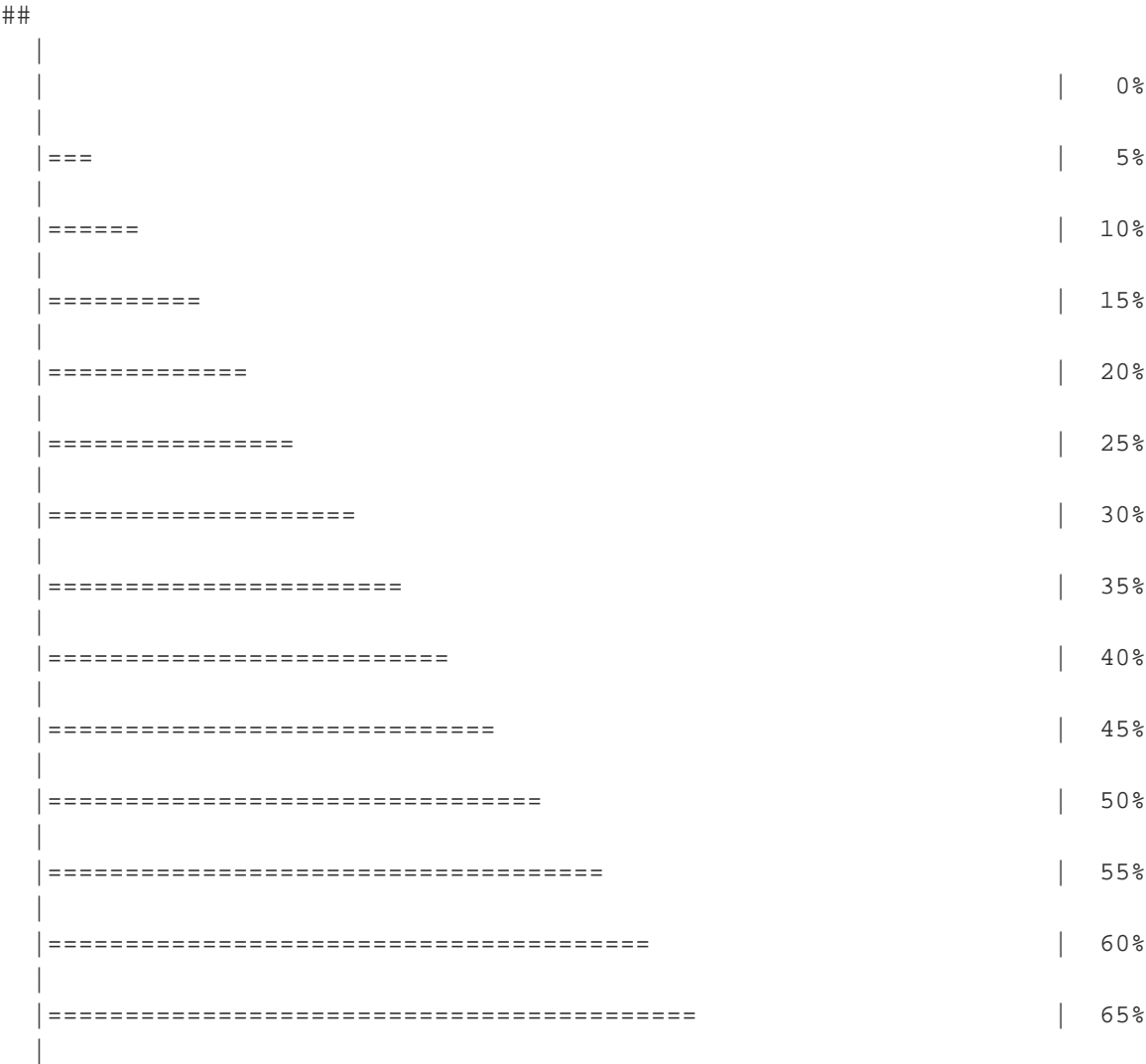
mod.to.hr.d = rma.mv(yi,vi,mods = ~ hr_estimator-1, random = ~1|Author, data = ef.to)
summary(mod.to.hr.d)
```

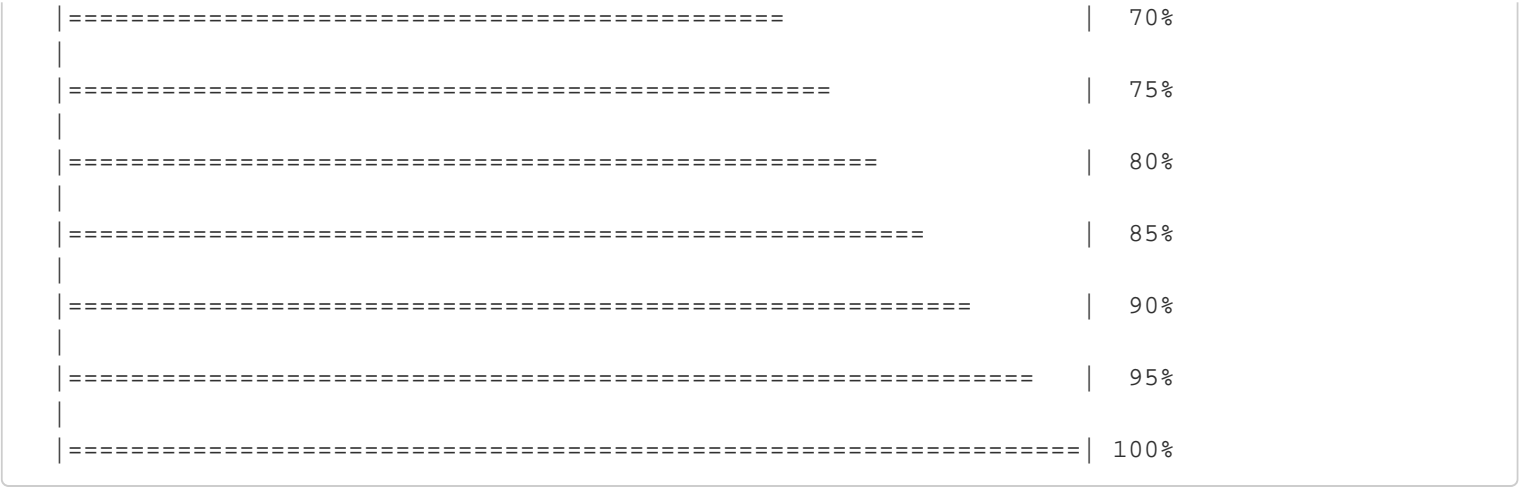
```
##
## Multivariate Meta-Analysis Model (k = 34; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -742.8435    1485.6870    1495.6870    1502.6930    1498.1870
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed  factor
## sigma^2      27.6774  5.2609      7      no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 30) = 2871.9707, p-val < .0001
##
## Test of Moderators (coefficient(s) 1,2,3,4):
```

```
## QM(df = 4) = 1132.7595, p-val < .0001
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## hr_estimatorEllipse    3.3715  2.2321   1.5105  0.1309   -1.0033   7.7462
## hr_estimatorHM         -0.0464  2.0862  -0.0223  0.9822   -4.1354   4.0425
## hr_estimatorKernel     4.9526  2.0808   2.3802  0.0173    0.8744   9.0308
## hr_estimatorMCP         7.6974  2.0767   3.7065  0.0002    3.6271  11.7677
##
## hr_estimatorEllipse
## hr_estimatorHM
## hr_estimatorKernel      *
## hr_estimatorMCP         ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

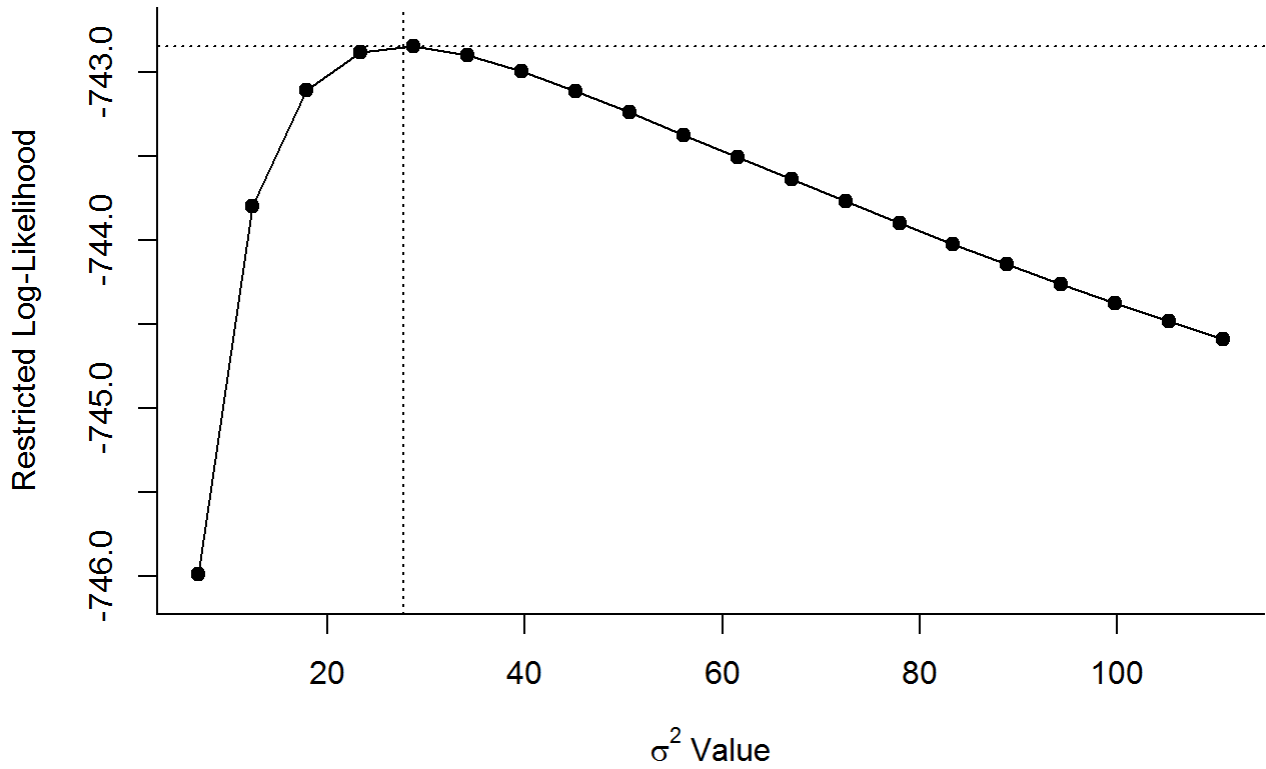
```
# Profile liklihood plot

profile(mod.to.hr, sigma2=1)
```





Profile Plot for σ^2



```
# Delta AICc against int-only model
AIC(mod.to.hr, mod.to.int, correct = TRUE)
```

```
##           df      AICc
## mod.to.hr    5 1498.187
## mod.to.int    2 2620.056
```

```
AIC(mod.to.int, correct = TRUE) - AIC(mod.to.hr,correct = TRUE)
```

```
## [1] 1121.869
```

```
# Calculate McFadden's pseudo R2
1-(logLik(mod.to.hr)/logLik(mod.to.int))
```

```
## 'log Lik.' 0.4320022 (df=5)
```

```
#Multiple comparisons using Holm-Bonferroni method
summary(glht(mod.to.hr, linfct=cbind(contrMat(c("Ellipse"=1,"HM"=1,"Kernel"=1,"MCP"=1),
type="Tukey"))), test=adjusted("holm"))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: rma.mv(yi = yi, V = vi, mods = ~hr_estimator, random = ~1 | Author,
## data = ef.to)
##
## Linear Hypotheses:
## Estimate Std. Error z value Pr(>|z|)
## HM - Ellipse == 0 -6.7893 2.6213 -2.590 0.0288 *
## Kernel - Ellipse == 0 -1.7904 2.6914 -0.665 1.0000
## MCP - Ellipse == 0 0.9545 2.6506 0.360 1.0000
## Kernel - HM == 0 4.9990 0.4182 11.953 < 2e-16 ***
## MCP - HM == 0 7.7438 0.2396 32.315 < 2e-16 ***
## MCP - Kernel == 0 2.7449 0.3431 8.001 5.33e-15 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- holm method)
```

```
## Test: Effect of sample size on T. ornata hr size

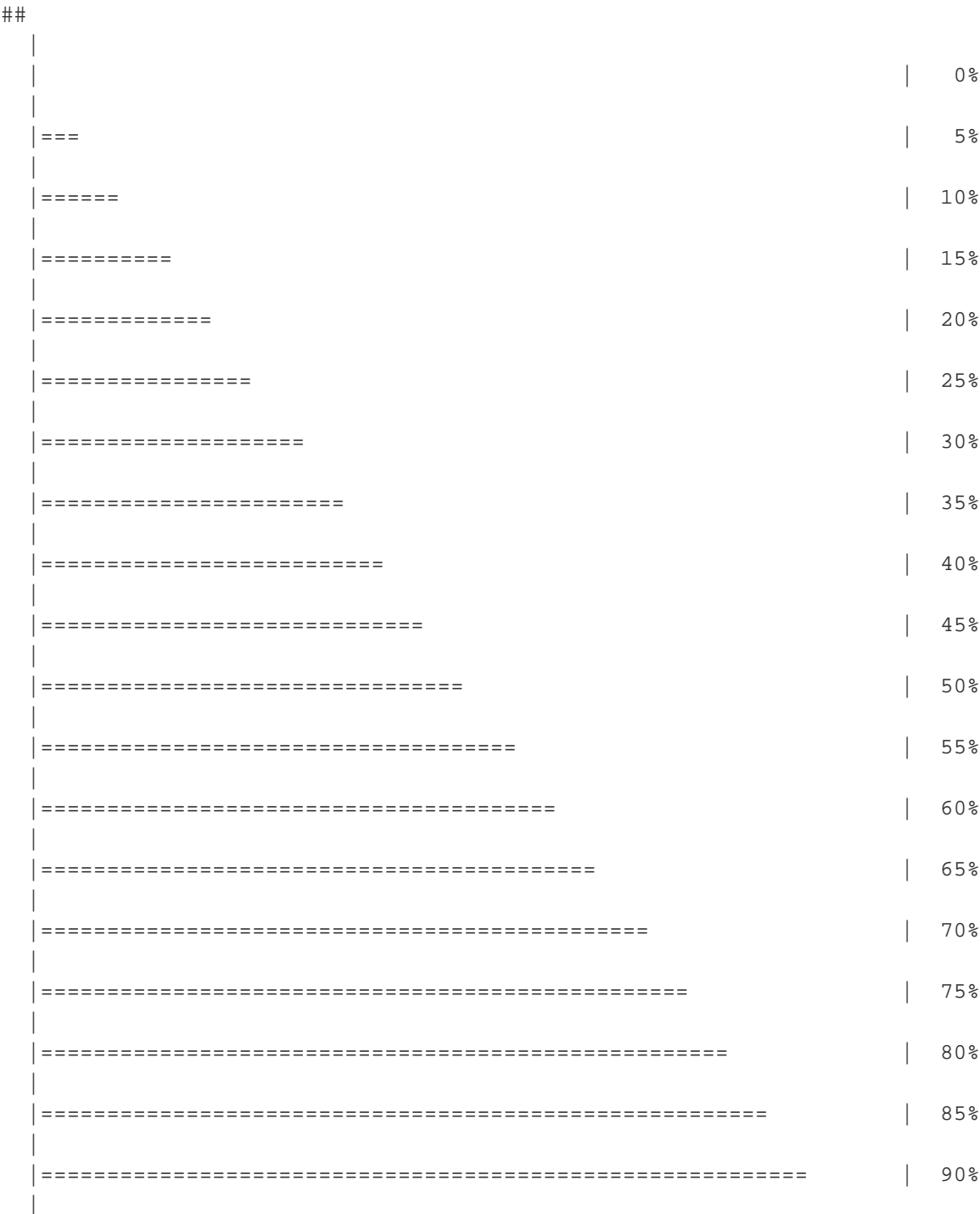
mod.to.n = rma.mv(yi,vi,mods = ~ n, random = ~1|Author, data = ef.to)
summary(mod.to.n)
```

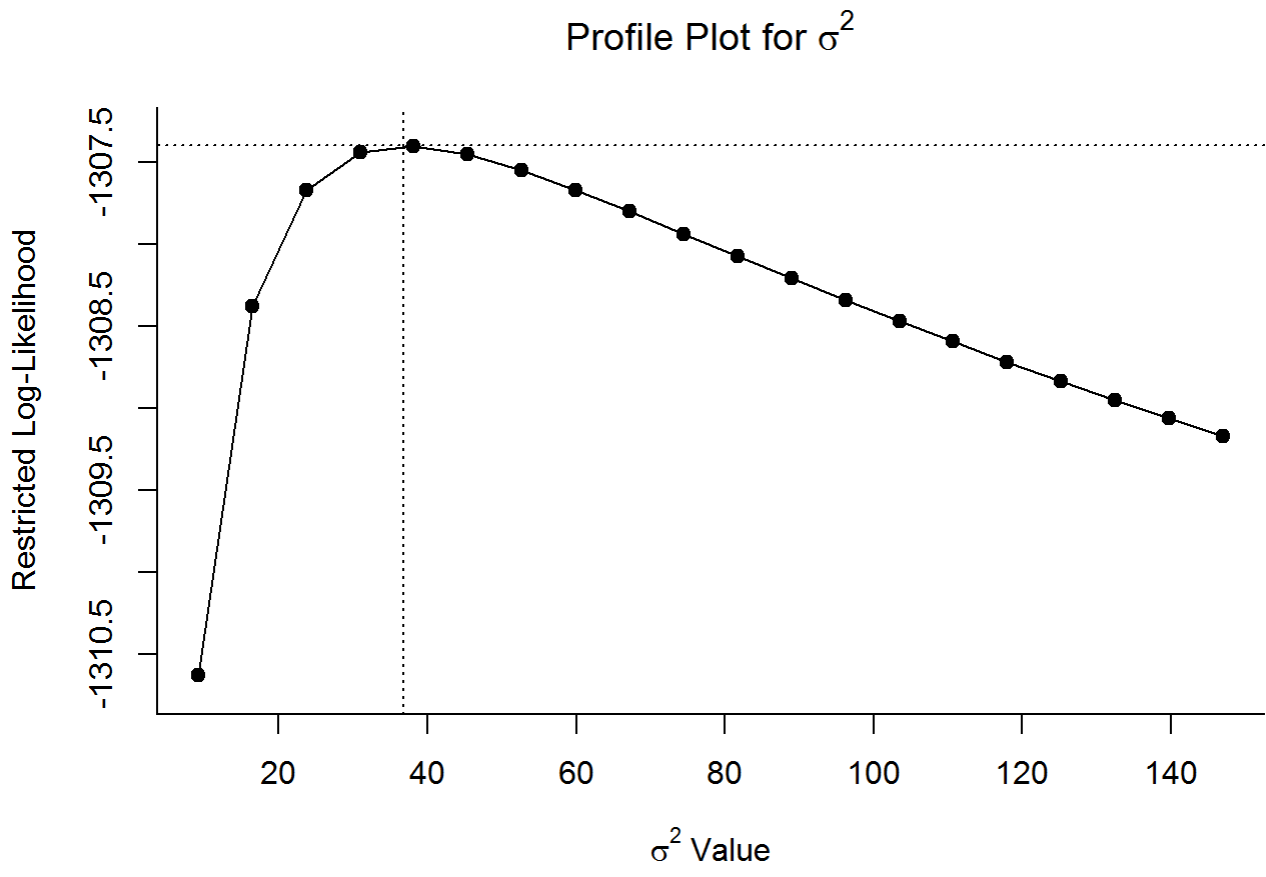
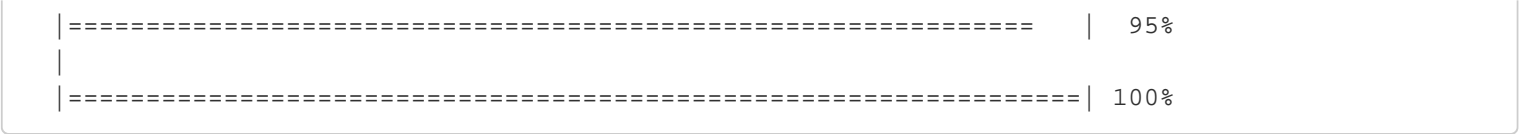
```
##
## Multivariate Meta-Analysis Model (k = 34; method: REML)
##
## logLik Deviance AIC BIC AICc
## -1307.3974 2614.7948 2620.7948 2625.1920 2621.6519
##
## Variance Components:
##
## estim sqrt nlvls fixed factor
## sigma^2 36.7421 6.0615 7 no Author
##
## Test for Residual Heterogeneity:
## QE(df = 32) = 3532.5251, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 0.0125, p-val = 0.9108
##
```

```
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      5.4167  2.3790   2.2768  0.0228   0.7539  10.0796  *
## n           -0.0021  0.0189  -0.1120  0.9108  -0.0391   0.0348
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot

profile(mod.to.n, sigma2=1)
```





```
# Delta AICc against int-only model
AIC(mod.to.n, mod.to.int, correct = TRUE)
```

```
##           df      AICc
## mod.to.n    3 2621.652
## mod.to.int  2 2620.056
```

```
AIC(mod.to.int, correct = TRUE) - AIC(mod.to.n,correct = TRUE)
```

```
## [1] -1.595635
```

```
# Calculate McFadden's pseudo R2
1-(logLik(mod.to.n)/logLik(mod.to.int))
```

```
## 'log Lik.' 0.000329366 (df=3)
```

```
## Test: Effect of ecoregion on T. ornata hr size
```

```
mod.to.eco = rma.mv(yi,vi,mods = ~ ecoregion, random = ~1|Author, data = ef.to)
summary(mod.to.eco)
```

```
##
## Multivariate Meta-Analysis Model (k = 34; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -1287.3519    2574.7038    2588.7038    2598.0292    2594.3038
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed  factor
## sigma^2    0.2697  0.5193      7     no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 28) = 2551.4472, p-val < .0001
##
## Test of Moderators (coefficient(s) 2,3,4,5,6):
## QM(df = 5) = 141.3000, p-val < .0001
##
## Model Results:
##
##                                     estimate      se      zval
## intrcpt                        2.5508    0.5505    4.6333
## ecoregionCOLD DESERTS          -1.2578    0.7568   -1.6619
## ecoregionSOUTH CENTRAL SEMI-ARID PRAIRIES -0.2276    0.7762   -0.2933
## ecoregionTEMPERATE PRAIRIES    -1.6934    0.7576   -2.2354
## ecoregionWEST-CENTRAL SEMI-ARID PRAIRIES  16.2486    2.1186    7.6696
## ecoregionWESTERN SIERRA MADRE PIEDMONT    4.4215    0.7796    5.6714
##                                     pval      ci.lb      ci.ub
## intrcpt                        <.0001    1.4718    3.6298    ***
## ecoregionCOLD DESERTS          0.0965   -2.7411    0.2256      .
## ecoregionSOUTH CENTRAL SEMI-ARID PRAIRIES 0.7693   -1.7489    1.2936
## ecoregionTEMPERATE PRAIRIES    0.0254   -3.1782   -0.2086      *
## ecoregionWEST-CENTRAL SEMI-ARID PRAIRIES <.0001   12.0963   20.4010    ***
## ecoregionWESTERN SIERRA MADRE PIEDMONT <.0001    2.8935    5.9496    ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Testing main effect to display level-specific estimates

mod.to.eco.d = rma.mv(yi,vi,mods = ~ ecoregion-1, random = ~1|Author, data = ef.to)
summary(mod.to.eco.d)
```

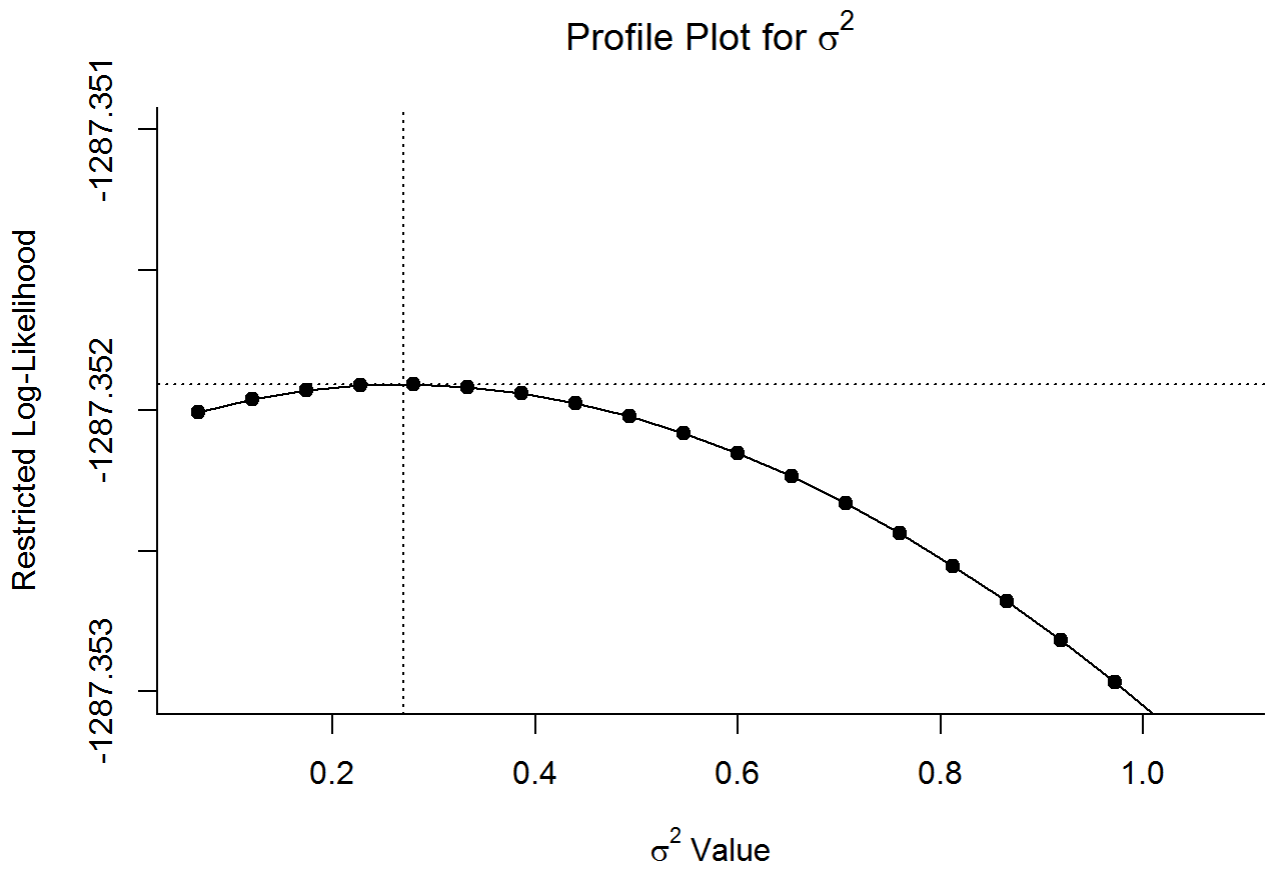
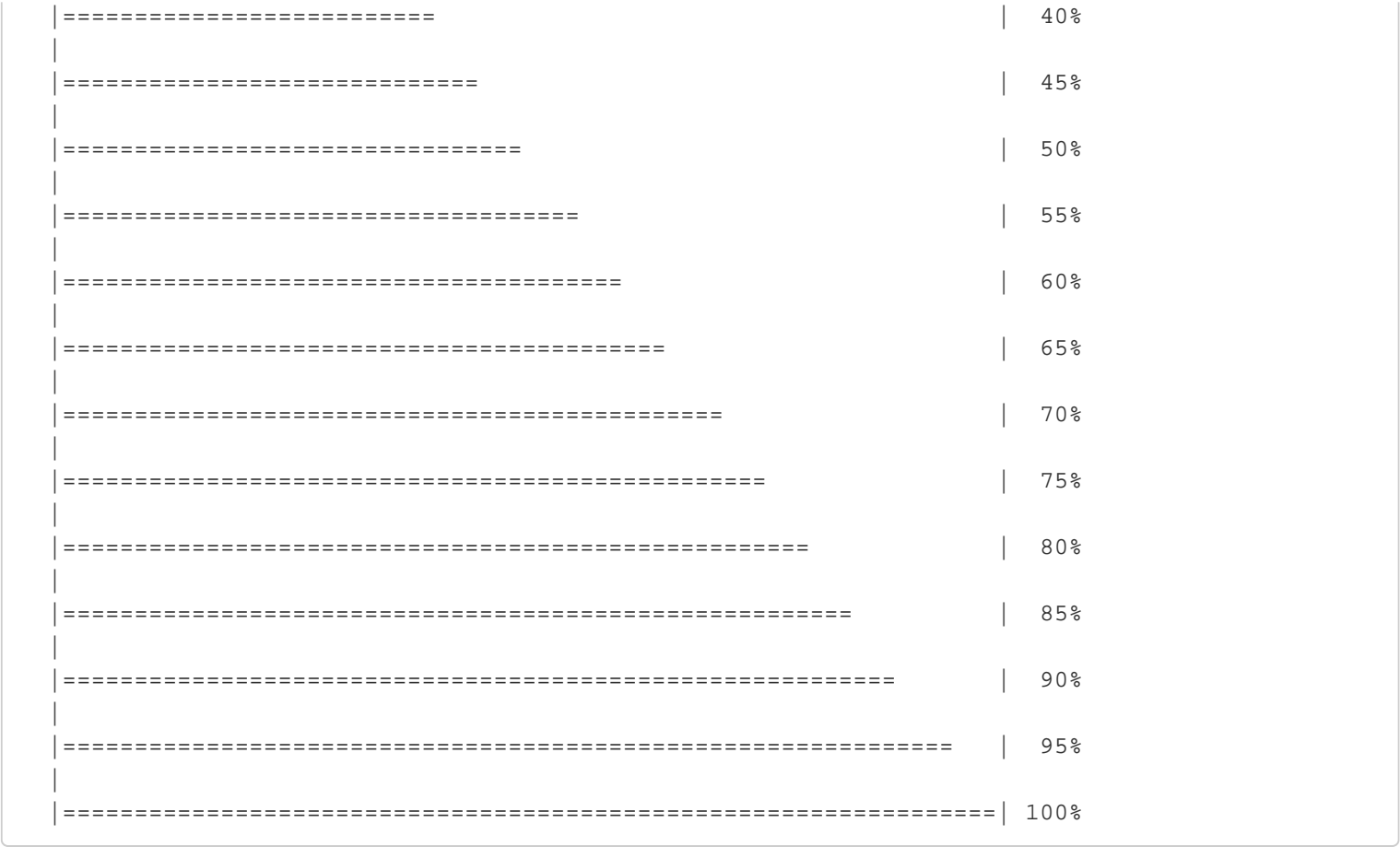
```
##
## Multivariate Meta-Analysis Model (k = 34; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -1287.3519    2574.7038    2588.7038    2598.0292    2594.3038
##
## Variance Components:
```

```
##
##          estim    sqrt  nlvls  fixed  factor
## sigma^2    0.2696  0.5193      7     no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 28) = 2551.4472, p-val < .0001
##
## Test of Moderators (coefficient(s) 1,2,3,4,5,6):
## QM(df = 6) = 292.4102, p-val < .0001
##
## Model Results:
##
##                                     estimate      se      zval
## ecoregionCENTRAL USA PLAINS          2.5508  0.5505  4.6336
## ecoregionCOLD DESERTS                1.2930  0.5193  2.4900
## ecoregionSOUTH CENTRAL SEMI-ARID PRAIRIES  2.3231  0.5471  4.2463
## ecoregionTEMPERATE PRAIRIES           0.8574  0.5204  1.6476
## ecoregionWEST-CENTRAL SEMI-ARID PRAIRIES  18.7994  2.0458  9.1893
## ecoregionWESTERN SIERRA MADRE PIEDMONT    6.9723  0.5520 12.6313
##                                     pval      ci.lb      ci.ub
## ecoregionCENTRAL USA PLAINS          <.0001  1.4718  3.6298  ***
## ecoregionCOLD DESERTS                0.0128  0.2753  2.3108   *
## ecoregionSOUTH CENTRAL SEMI-ARID PRAIRIES <.0001  1.2508  3.3954  ***
## ecoregionTEMPERATE PRAIRIES           0.0994 -0.1626  1.8773   .
## ecoregionWEST-CENTRAL SEMI-ARID PRAIRIES <.0001 14.7897 22.8091  ***
## ecoregionWESTERN SIERRA MADRE PIEDMONT <.0001  5.8905  8.0542  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot

profile(mod.to.eco, sigma2=1, ylim=c(-1287.353,-1287.351))
```





```
# Delta AICc against int-only model
AIC(mod.to.eco, mod.to.int, correct = TRUE)
```

```
##           df      AICc
## mod.to.eco   7 2594.304
## mod.to.int   2 2620.056
```

```
AIC(mod.to.int, correct = TRUE) - AIC(mod.to.eco,correct = TRUE)
```

```
## [1] 25.75247
```

```
# Calculate McFadden's pseudo R2
1-(logLik(mod.to.eco)/logLik(mod.to.int))
```

```
## 'log Lik.' 0.01565667 (df=7)
```

```
#Multiple comparisons usung Holm-Bonferroni method
summary(glht(mod.to.eco, linfct=cbind(contrMat(c("CENTRAL USA PLAINS"=1, "COLD DESERTS"=1,"SOUTH CENTRAL SEMI-ARID PRAIRIES"=1,
                                           "TEMPERATE PRAIRIES"=1,"WEST-CENTRAL SEMI-ARID PRAIRIES"=1,"WESTERN SIERRA MADRE PIEDMONT"=1)),
                                           type="Tukey"))), test=adjusted("holm"))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: rma.mv(yi = yi, V = vi, mods = ~ecoregion, random = ~1 | Author,
## data = ef.to)
##
## Linear Hypotheses:
##
## COLD DESERTS - CENTRAL USA PLAINS == 0 Estimate -3.8085
## SOUTH CENTRAL SEMI-ARID PRAIRIES - CENTRAL USA PLAINS == 0 -2.7784
## TEMPERATE PRAIRIES - CENTRAL USA PLAINS == 0 -4.2442
## WEST-CENTRAL SEMI-ARID PRAIRIES - CENTRAL USA PLAINS == 0 13.6978
## WESTERN SIERRA MADRE PIEDMONT - CENTRAL USA PLAINS == 0 1.8708
## SOUTH CENTRAL SEMI-ARID PRAIRIES - COLD DESERTS == 0 1.0301
## TEMPERATE PRAIRIES - COLD DESERTS == 0 -0.4357
## WEST-CENTRAL SEMI-ARID PRAIRIES - COLD DESERTS == 0 17.5064
## WESTERN SIERRA MADRE PIEDMONT - COLD DESERTS == 0 5.6793
## TEMPERATE PRAIRIES - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0 -1.4658
## WEST-CENTRAL SEMI-ARID PRAIRIES - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0 16.4763
## WESTERN SIERRA MADRE PIEDMONT - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0 4.6492
## WEST-CENTRAL SEMI-ARID PRAIRIES - TEMPERATE PRAIRIES == 0 17.9421
## WESTERN SIERRA MADRE PIEDMONT - TEMPERATE PRAIRIES == 0 6.1150
## WESTERN SIERRA MADRE PIEDMONT - WEST-CENTRAL SEMI-ARID PRAIRIES == 0 -11.8271
## Std. Error
## COLD DESERTS - CENTRAL USA PLAINS == 0 1.2174
## SOUTH CENTRAL SEMI-ARID PRAIRIES - CENTRAL USA PLAINS == 0 1.2295
```


## TEMPERATE PRAIRIES - CENTRAL USA PLAINS == 0	1.2178
## WEST-CENTRAL SEMI-ARID PRAIRIES - CENTRAL USA PLAINS == 0	2.3233
## WESTERN SIERRA MADRE PIEDMONT - CENTRAL USA PLAINS == 0	1.2317
## SOUTH CENTRAL SEMI-ARID PRAIRIES - COLD DESERTS == 0	0.7543
## TEMPERATE PRAIRIES - COLD DESERTS == 0	0.7352
## WEST-CENTRAL SEMI-ARID PRAIRIES - COLD DESERTS == 0	2.1107
## WESTERN SIERRA MADRE PIEDMONT - COLD DESERTS == 0	0.7579
## TEMPERATE PRAIRIES - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0	0.7551
## WEST-CENTRAL SEMI-ARID PRAIRIES - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0	2.1177
## WESTERN SIERRA MADRE PIEDMONT - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0	0.7772
## WEST-CENTRAL SEMI-ARID PRAIRIES - TEMPERATE PRAIRIES == 0	2.1109
## WESTERN SIERRA MADRE PIEDMONT - TEMPERATE PRAIRIES == 0	0.7586
## WESTERN SIERRA MADRE PIEDMONT - WEST-CENTRAL SEMI-ARID PRAIRIES == 0	2.1190
##	z value
## COLD DESERTS - CENTRAL USA PLAINS == 0	-3.128
## SOUTH CENTRAL SEMI-ARID PRAIRIES - CENTRAL USA PLAINS == 0	-2.260
## TEMPERATE PRAIRIES - CENTRAL USA PLAINS == 0	-3.485
## WEST-CENTRAL SEMI-ARID PRAIRIES - CENTRAL USA PLAINS == 0	5.896
## WESTERN SIERRA MADRE PIEDMONT - CENTRAL USA PLAINS == 0	1.519
## SOUTH CENTRAL SEMI-ARID PRAIRIES - COLD DESERTS == 0	1.366
## TEMPERATE PRAIRIES - COLD DESERTS == 0	-0.593
## WEST-CENTRAL SEMI-ARID PRAIRIES - COLD DESERTS == 0	8.294
## WESTERN SIERRA MADRE PIEDMONT - COLD DESERTS == 0	7.494
## TEMPERATE PRAIRIES - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0	-1.941
## WEST-CENTRAL SEMI-ARID PRAIRIES - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0	7.780
## WESTERN SIERRA MADRE PIEDMONT - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0	5.982
## WEST-CENTRAL SEMI-ARID PRAIRIES - TEMPERATE PRAIRIES == 0	8.500
## WESTERN SIERRA MADRE PIEDMONT - TEMPERATE PRAIRIES == 0	8.060
## WESTERN SIERRA MADRE PIEDMONT - WEST-CENTRAL SEMI-ARID PRAIRIES == 0	-5.582
##	Pr(> z)
## COLD DESERTS - CENTRAL USA PLAINS == 0	0.01054
## SOUTH CENTRAL SEMI-ARID PRAIRIES - CENTRAL USA PLAINS == 0	0.11916
## TEMPERATE PRAIRIES - CENTRAL USA PLAINS == 0	0.00344
## WEST-CENTRAL SEMI-ARID PRAIRIES - CENTRAL USA PLAINS == 0	3.35e-08
## WESTERN SIERRA MADRE PIEDMONT - CENTRAL USA PLAINS == 0	0.38640
## SOUTH CENTRAL SEMI-ARID PRAIRIES - COLD DESERTS == 0	0.38640
## TEMPERATE PRAIRIES - COLD DESERTS == 0	0.55344
## WEST-CENTRAL SEMI-ARID PRAIRIES - COLD DESERTS == 0	< 2e-16
## WESTERN SIERRA MADRE PIEDMONT - COLD DESERTS == 0	7.38e-13
## TEMPERATE PRAIRIES - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0	0.20894
## WEST-CENTRAL SEMI-ARID PRAIRIES - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0	8.79e-14
## WESTERN SIERRA MADRE PIEDMONT - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0	2.21e-08
## WEST-CENTRAL SEMI-ARID PRAIRIES - TEMPERATE PRAIRIES == 0	< 2e-16
## WESTERN SIERRA MADRE PIEDMONT - TEMPERATE PRAIRIES == 0	8.66e-15
## WESTERN SIERRA MADRE PIEDMONT - WEST-CENTRAL SEMI-ARID PRAIRIES == 0	1.91e-07
##	
## COLD DESERTS - CENTRAL USA PLAINS == 0	*
## SOUTH CENTRAL SEMI-ARID PRAIRIES - CENTRAL USA PLAINS == 0	
## TEMPERATE PRAIRIES - CENTRAL USA PLAINS == 0	**
## WEST-CENTRAL SEMI-ARID PRAIRIES - CENTRAL USA PLAINS == 0	***
## WESTERN SIERRA MADRE PIEDMONT - CENTRAL USA PLAINS == 0	
## SOUTH CENTRAL SEMI-ARID PRAIRIES - COLD DESERTS == 0	
## TEMPERATE PRAIRIES - COLD DESERTS == 0	
## WEST-CENTRAL SEMI-ARID PRAIRIES - COLD DESERTS == 0	***

```
## WESTERN SIERRA MADRE PIEDMONT - COLD DESERTS == 0 ***
## TEMPERATE PRAIRIES - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0
## WEST-CENTRAL SEMI-ARID PRAIRIES - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0 ***
## WESTERN SIERRA MADRE PIEDMONT - SOUTH CENTRAL SEMI-ARID PRAIRIES == 0 ***
## WEST-CENTRAL SEMI-ARID PRAIRIES - TEMPERATE PRAIRIES == 0 ***
## WESTERN SIERRA MADRE PIEDMONT - TEMPERATE PRAIRIES == 0 ***
## WESTERN SIERRA MADRE PIEDMONT - WEST-CENTRAL SEMI-ARID PRAIRIES == 0 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- holm method)
```

```
#####Tests not possible for gravid and relocated T. ornata , given lack of data#####

#
#

#Subset ef.all data set to include only T. carolina cases and exclude "Mixed" from sex column

ef.tc.sex <- subset(ef.all, species=="T. carolina"& sex!="Mixed")
droplevels.factor(ef.tc.sex$sex)
```

```
## [1] Female Female Female Male Female Male Female Female Female Male
## [11] Female Female Female Male Female Male Male Male Female Female
## [21] Female Female Male Female Male Female Male Female Male Female
## [31] Female Female Male Female Female Male Female Male Female Male
## [41] Female Male
## Levels: Female Male
```

```
droplevels.factor(ef.tc.sex$species)
```

```
## [1] T. carolina T. carolina T. carolina T. carolina T. carolina
## [6] T. carolina T. carolina T. carolina T. carolina T. carolina
## [11] T. carolina T. carolina T. carolina T. carolina T. carolina
## [16] T. carolina T. carolina T. carolina T. carolina T. carolina
## [21] T. carolina T. carolina T. carolina T. carolina T. carolina
## [26] T. carolina T. carolina T. carolina T. carolina T. carolina
## [31] T. carolina T. carolina T. carolina T. carolina T. carolina
## [36] T. carolina T. carolina T. carolina T. carolina T. carolina
## [41] T. carolina T. carolina
## Levels: T. carolina
```

```
droplevels.factor(ef.tc.sex$Author)
```

```
## [1] Cook Cook Cook
## [4] Cook Madden Madden
## [7] Cook Cook Cook
## [10] Cook Baker Baker
## [13] Baker Baker Capitano
## [16] Currylow et al Currylow et al Currylow et al
```

```
## [19] Currylow et al      Currylow et al      Currylow et al
## [22] Greenspan et al     Greenspan et al     Greenspan et al
## [25] Greenspan et al     Madden              Madden
## [28] Aall                Aall                Baker
## [31] Baker              Baker              Baker
## [34] Capitano            Kaye, Walsh, and Ross Kaye, Walsh, and Ross
## [37] Lentz              Lentz              Quinn
## [40] Quinn              Madden              Madden
## 10 Levels: Aall Baker Capitano Cook Currylow et al ... Quinn
```

```
#_____

# Estimate T.carolina home range size using all cases, no moderators

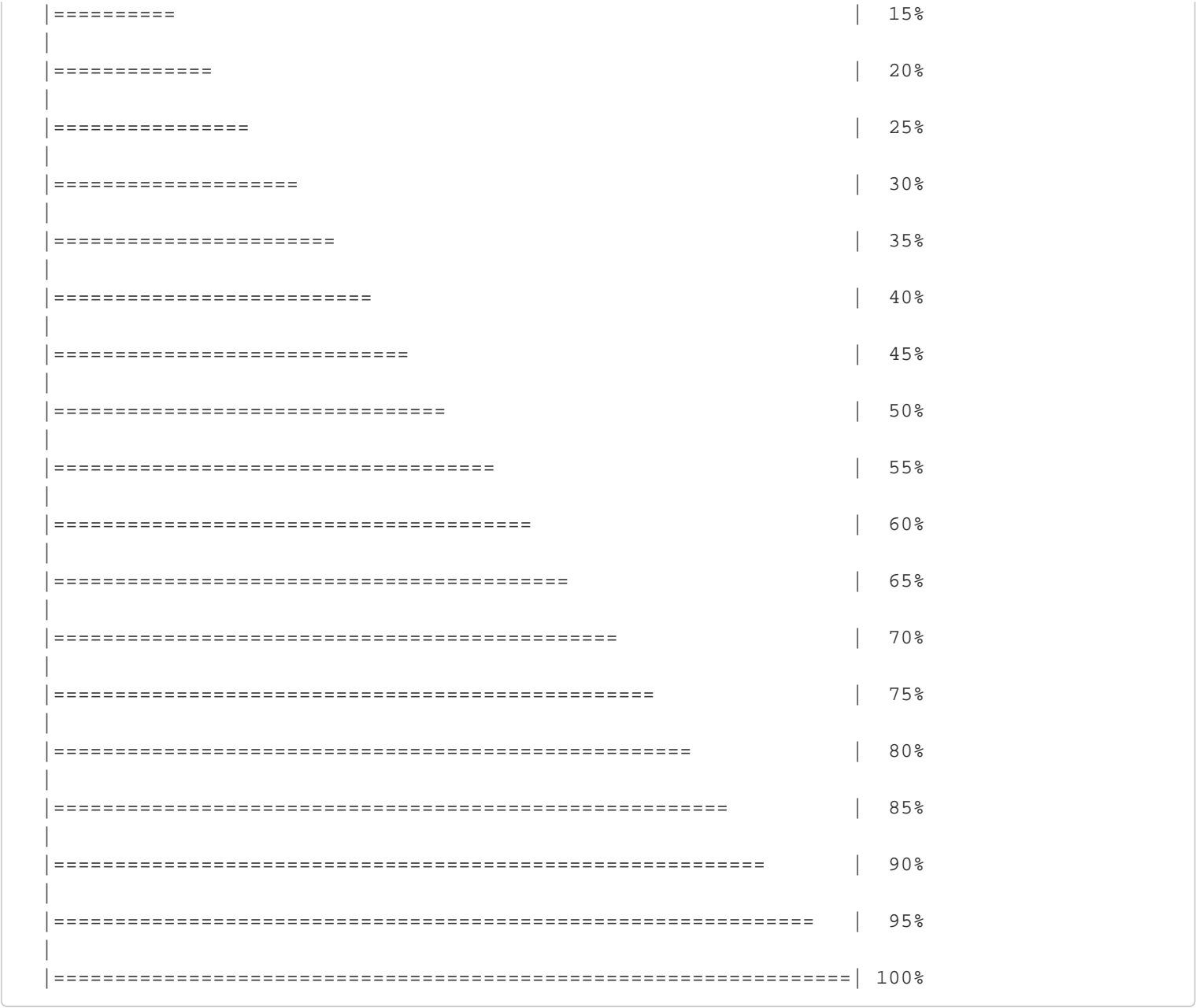
mod.tc.int = rma.mv(yi,vi,random = ~1|Author, data = ef.tc)
summary(mod.tc.int)
```

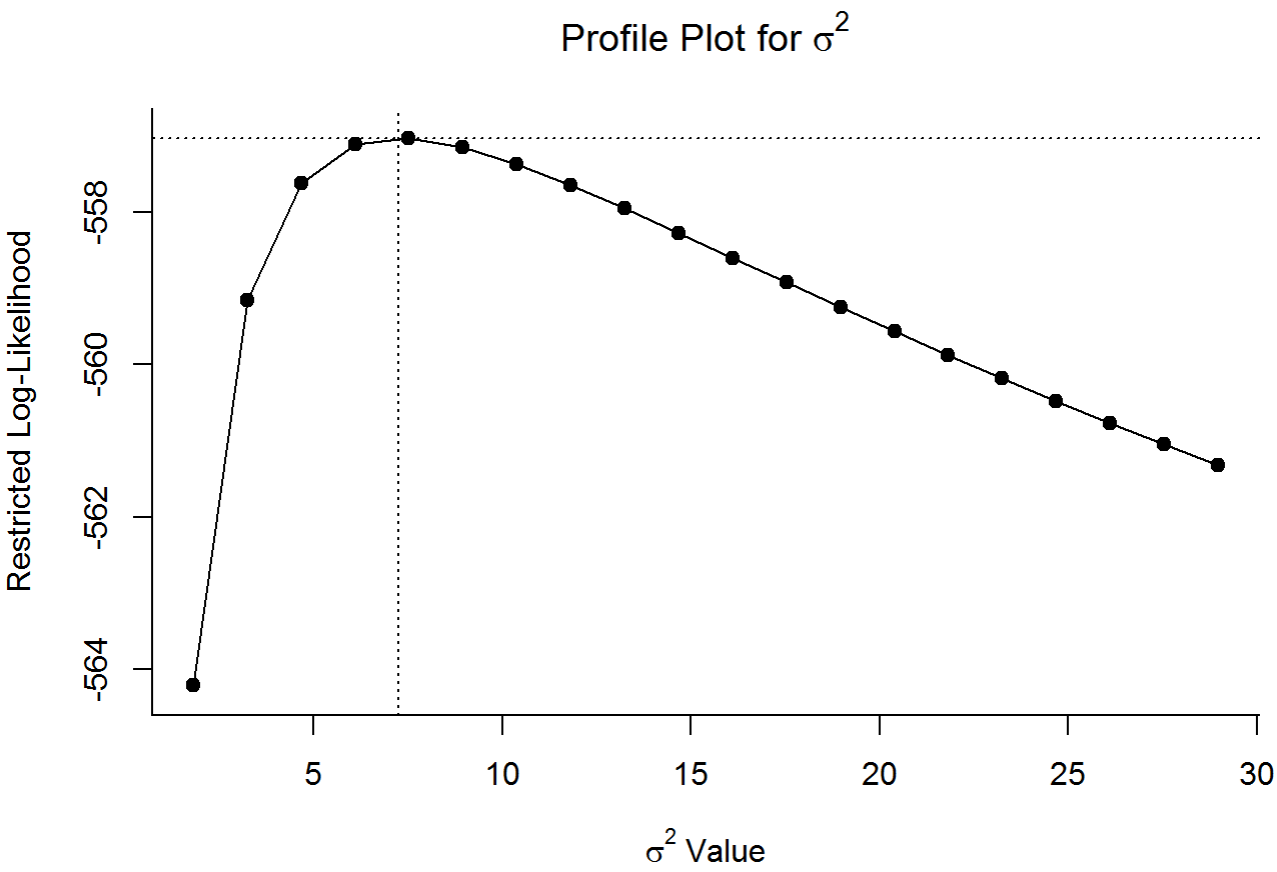
```
##
## Multivariate Meta-Analysis Model (k = 72; method: REML)
##
##      logLik    Deviance      AIC      BIC      AICc
## -557.0208  1114.0415  1118.0415  1122.5669  1118.2180
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed  factor
## sigma^2    7.2426  2.6912    19    no  Author
##
## Test for Heterogeneity:
## Q(df = 71) = 1928.1765, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub      ***
##  4.6097    0.6717    6.8632    <.0001    3.2933    5.9261
##
## ---
## Signif. codes:  0 '****' 0.001 '***' 0.01 '**' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot

profile(mod.tc.int, sigma2=1)
```

```
##
|
|
|
|====| 0%
|
|=====| 5%
|
|=====| 10%
|
```





```
# Eggar's test for bias in the data

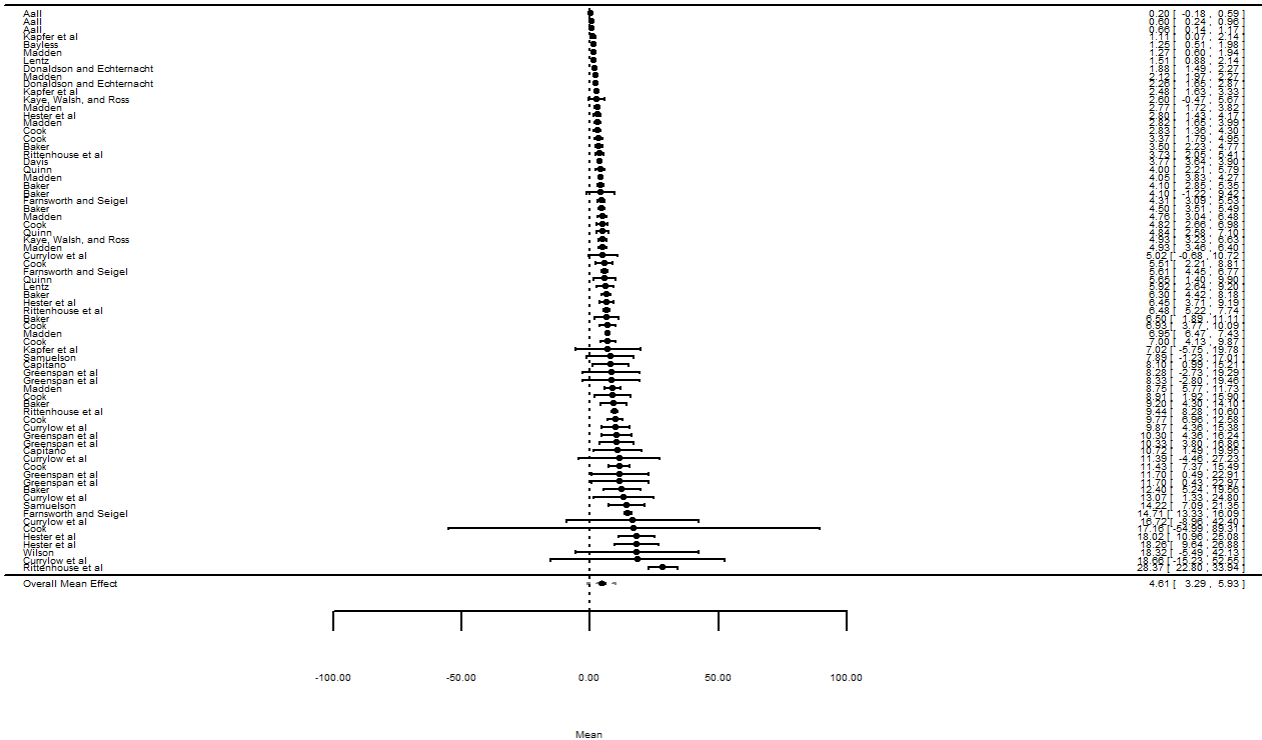
mod.tc.int.bias = rma.mv(yi,vi,mod = ~sqrt(vi), random = ~1|Author, data = ef.tc)
summary(mod.tc.int.bias)
```

```
##
## Multivariate Meta-Analysis Model (k = 72; method: REML)
##
##      logLik    Deviance      AIC      BIC      AICc
## -484.7326    969.4651    975.4651    982.2106    975.8288
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed  factor
## sigma^2     3.3643  1.8342     19     no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 70) = 1754.3916, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 142.1462, p-val < .0001
##
## Model Results:
##
##           estimate      se    zval    pval   ci.lb   ci.ub
```

```
## intrcpt      1.9191  0.5155   3.7228  0.0002  0.9088  2.9295  ***
## sqrt(vi)     2.5398  0.2130  11.9225  <.0001  2.1223  2.9573  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

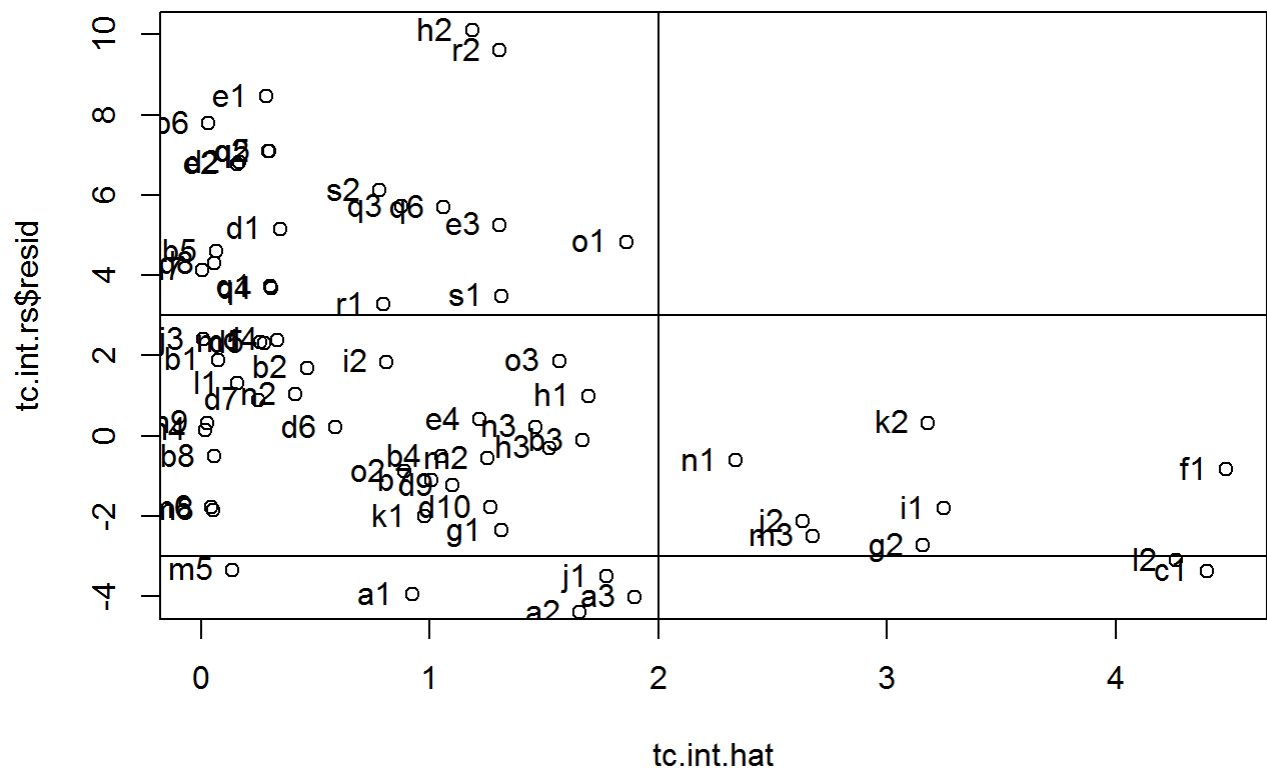
```
# Create forest plot for the model

forest(mod.tc.int, slab = ef.tc$Author, psize = 1.5, pch = 21,
       mlab = "Overall Mean Effect", addcred = TRUE, order = "obs")
```



```
# Identify influential outliers using ID column

tc.int.rs = rstandard(mod.tc.int)
tc.int.hat = hatvalues(mod.tc.int)/mean(hatvalues(mod.tc.int))
plot(tc.int.hat, tc.int.rs$resid, ylim = c(-4.0,10))
text(tc.int.hat, tc.int.rs$resid, labels = ef.tc$ID, cex= 1, pos = 2)
abline(h = -3)
abline(h = 3)
abline( v = 2)
```



```
# Removing influntial outliers by ID: c1, l2

ef.tc.infout = ef.tc[!(ef.tc$ID %in% c("c1", "l2")),]

# Test for home range size estimate: no moderators, no influential outliers

mod.tc.int.infout = rma.mv(yi,vi,random = ~1|Author, data = ef.tc.infout)
summary(mod.tc.int.infout)
```

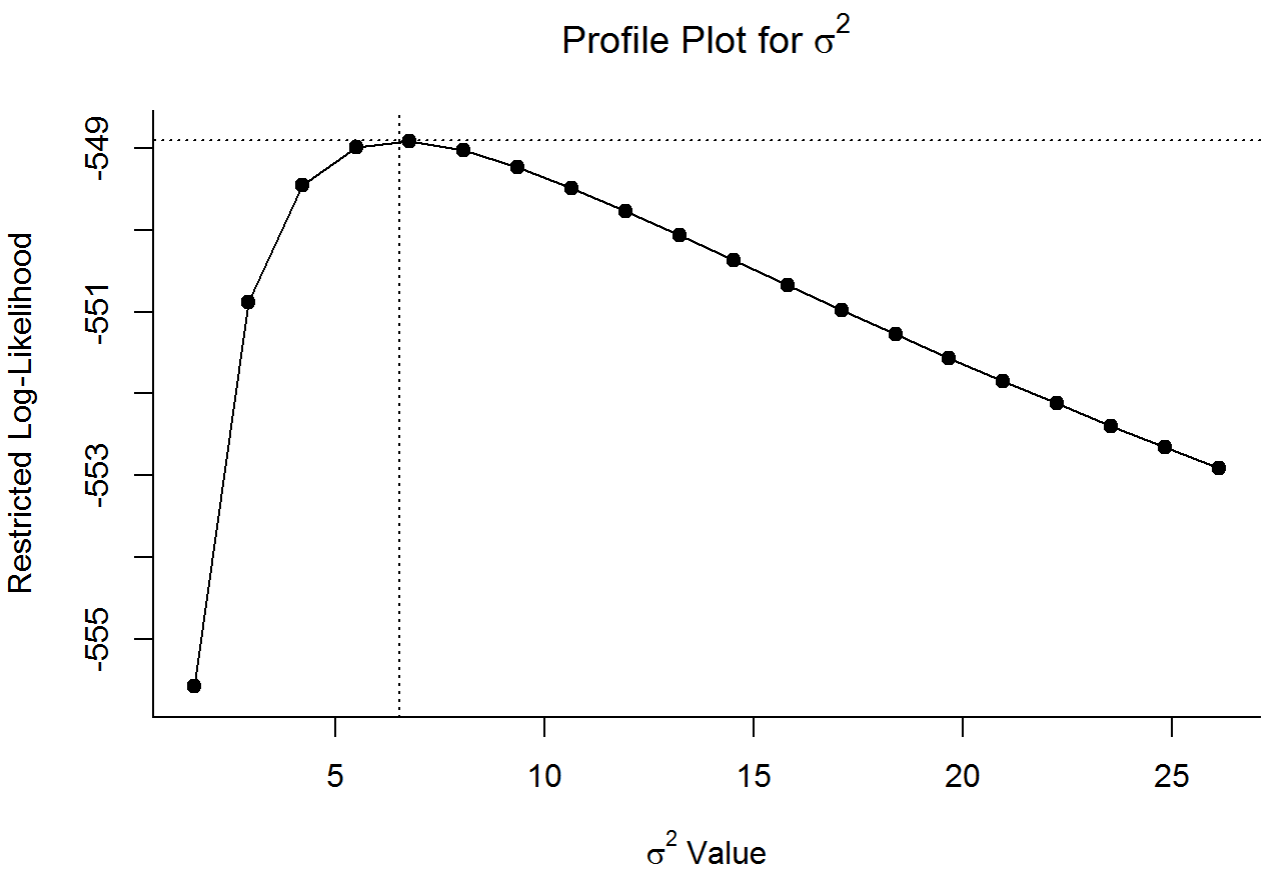
```
##
## Multivariate Meta-Analysis Model (k = 70; method: REML)
##
##      logLik    Deviance      AIC      BIC      AICc
## -548.9018  1097.8035  1101.8035  1106.2717  1101.9853
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed  factor
## sigma^2    6.5302  2.5554    18    no  Author
##
## Test for Heterogeneity:
## Q(df = 69) = 1882.5390, p-val < .0001
##
## Model Results:
##
```

```
## estimate      se      zval      pval      ci.lb      ci.ub
##    5.0560    0.6675    7.5748    <.0001    3.7478    6.3642      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot

profile(mod.tc.int.infout, sigma2=1)
```





```
# Delta AICc against int-only model
AIC(mod.tc.int.infout, mod.tc.int, correct = TRUE)
```

```
##           df      AICc
## mod.tc.int.infout  2 1101.985
## mod.tc.int         2 1118.218
```

```
AIC(mod.tc.int, correct = TRUE) - AIC(mod.tc.int.infout,correct = TRUE)
```

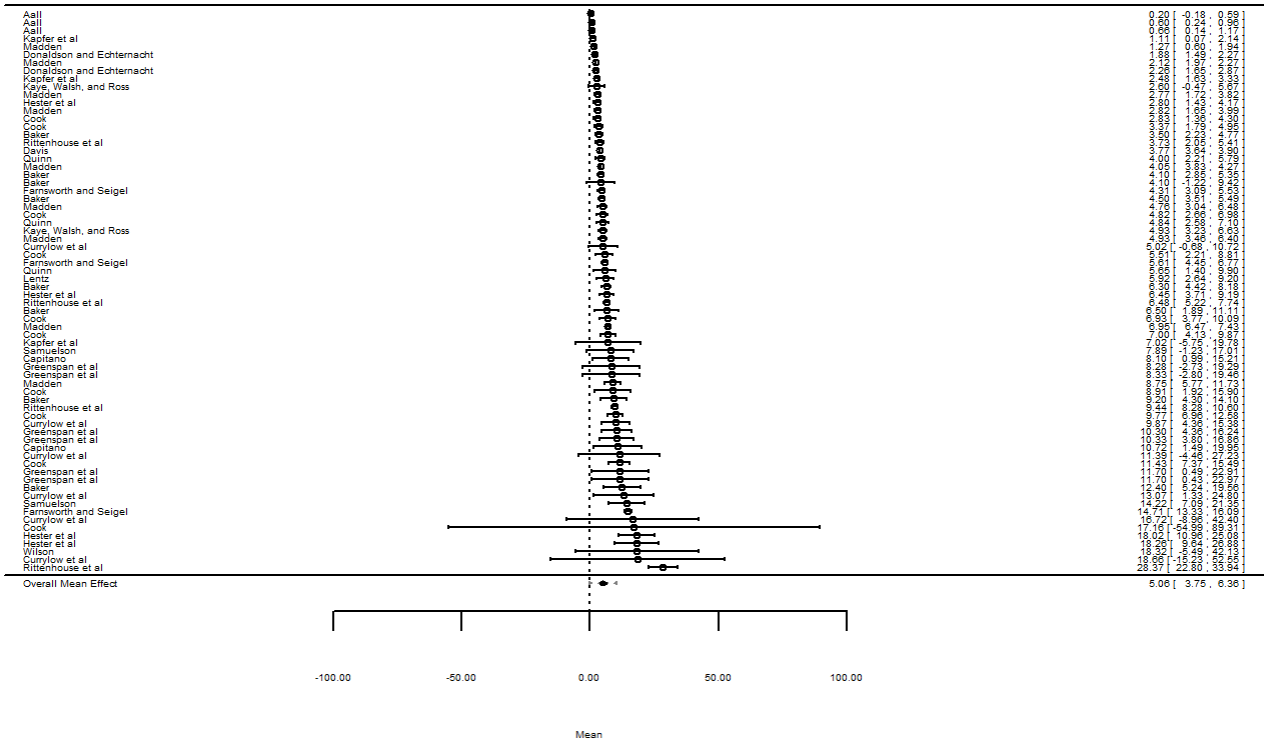
```
## [1] 16.23267
```

```
# Calculate McFadden's pseudo R2
1-(logLik(mod.tc.int.infout)/logLik(mod.tc.int))
```

```
## 'log Lik.' 0.01457578 (df=2)
```

```
# Create forest plot for the model

forest(mod.tc.int.infout, slab = ef.tc.infout$Author, psize = 1.5, pch = 21,
       mlab = "Overall Mean Effect", addcred = TRUE, order = "obs")
```



```
# Test: Effect of sex on T. carolina hr size

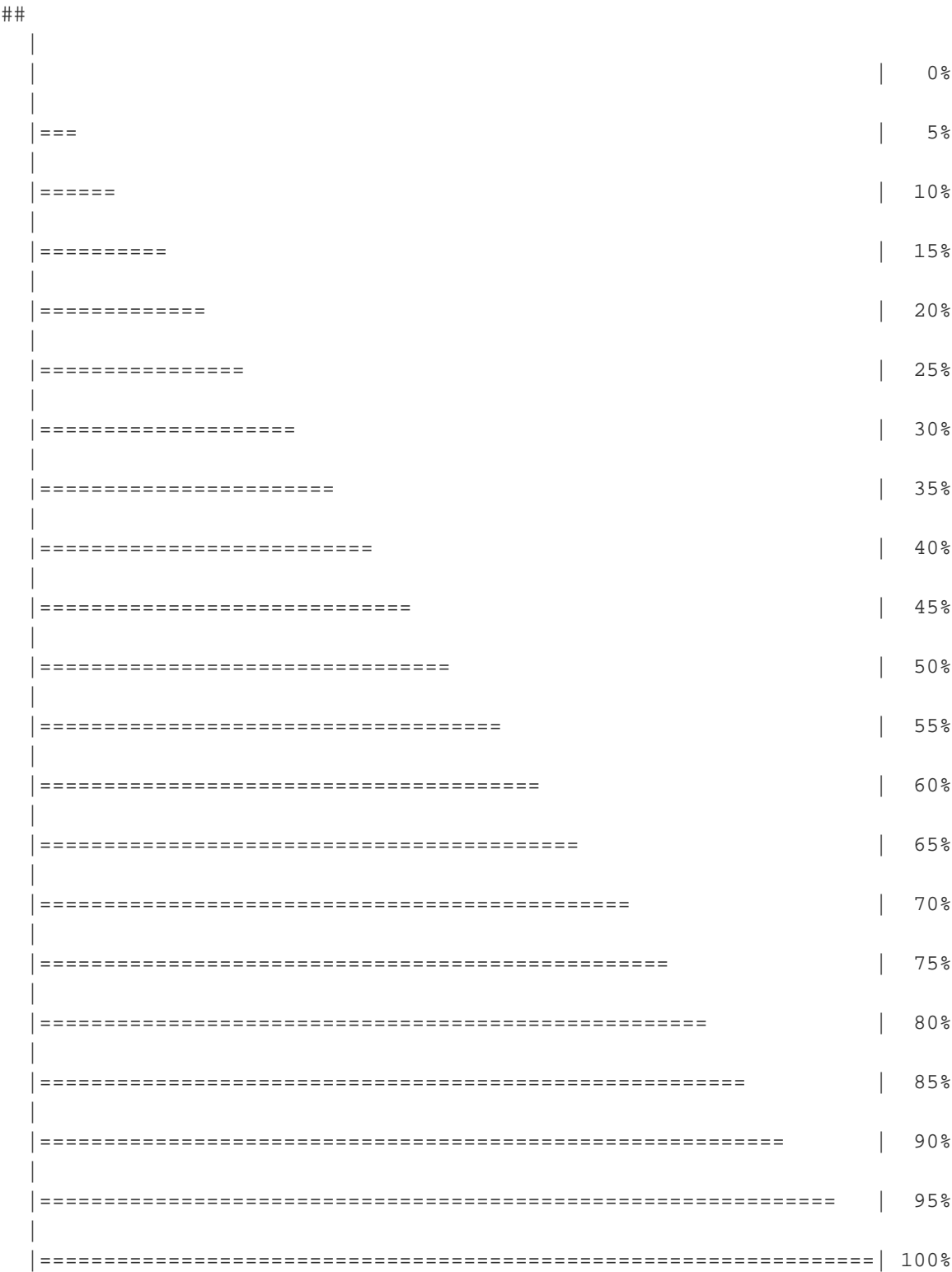
mod.tc.sex.int = rma.mv(yi,vi,random = ~1|Author, data = ef.tc.sex)
summary(mod.tc.sex.int)
```

```
##
## Multivariate Meta-Analysis Model (k = 42; method: REML)
##
##      logLik    Deviance      AIC      BIC      AICc
## -131.8368    263.6736    267.6736    271.1008    267.9894
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed  factor
## sigma^2    5.5129  2.3480     10     no  Author
##
## Test for Heterogeneity:
## Q(df = 41) = 356.1405, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub      ***
## 4.1796      0.8233    5.0764    <.0001    2.5659    5.7933
##
## ---
```

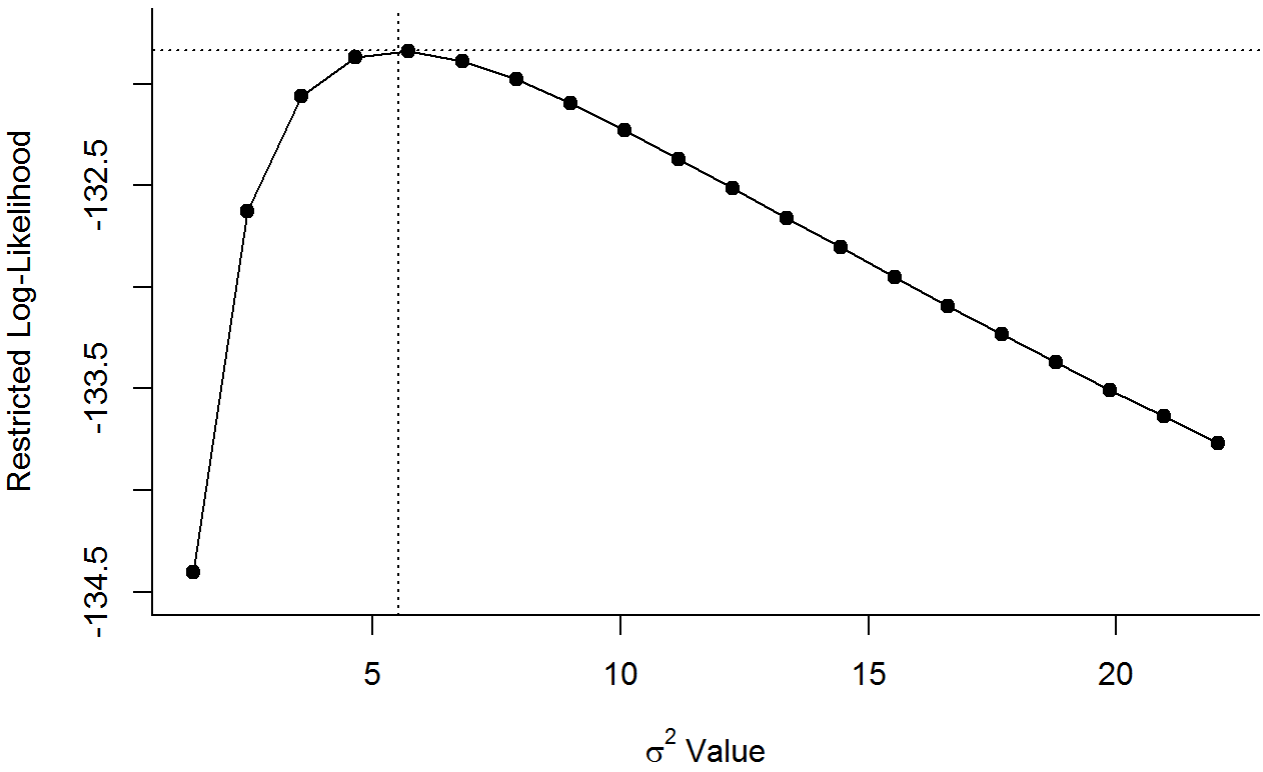
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot
```

```
profile(mod.tc.sex.int, sigma2=1)
```



Profile Plot for σ^2



```
mod.tc.sex = rma.mv(yi,vi,mods = ~ sex, random = ~1|Author, data = ef.tc.sex)
```

```
## Warning in rma.mv(yi, vi, mods = ~sex, random = ~1 | Author, data =  
## ef.tc.sex): Redundant predictors dropped from the model.
```

```
summary(mod.tc.sex)
```

```
##  
## Multivariate Meta-Analysis Model (k = 42; method: REML)  
##  
##      logLik    Deviance      AIC      BIC      AICc  
## -124.0125    248.0251    254.0251    259.0917    254.6917  
##  
## Variance Components:  
##  
##           estim    sqrt  nlvls  fixed  factor  
## sigma^2      4.7444  2.1782     10     no  Author  
##  
## Test for Residual Heterogeneity:  
## QE(df = 40) = 332.3100, p-val < .0001  
##  
## Test of Moderators (coefficient(s) 2):  
## QM(df = 1) = 14.4611, p-val = 0.0001  
##
```

```
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      4.6204  0.7824   5.9054 <.0001   3.0869   6.1538   ***
## sexMale     -0.8957  0.2355  -3.8028  0.0001  -1.3573  -0.4340   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Testing main effect to display level-specific estimates

mod.tc.sex.d = rma.mv(yi,vi,mods = ~ sex-1, random = ~1|Author, data = ef.tc.sex)
```

```
## Warning in rma.mv(yi, vi, mods = ~sex - 1, random = ~1 | Author, data =
## ef.tc.sex): Redundant predictors dropped from the model.
```

```
summary(mod.tc.sex.d)
```

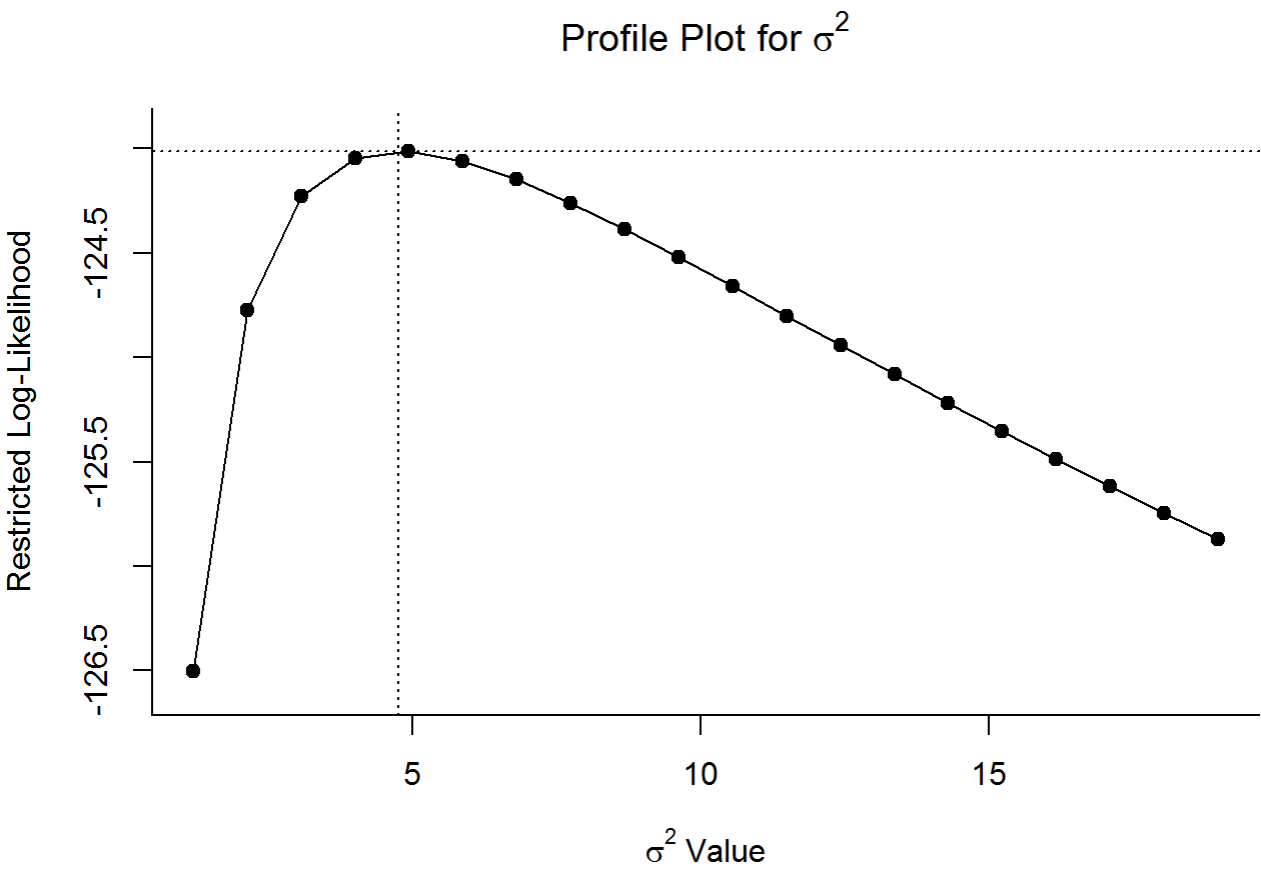
```
##
## Multivariate Meta-Analysis Model (k = 42; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
## -124.0125    248.0251    254.0251    259.0917    254.6917
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2    4.7444   2.1782     10     no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 40) = 332.3100, p-val < .0001
##
## Test of Moderators (coefficient(s) 1,2):
## QM(df = 2) = 42.9251, p-val < .0001
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## sexFemale      4.6204  0.7824   5.9054 <.0001   3.0869   6.1538   ***
## sexMale        3.7247  0.7777   4.7895 <.0001   2.2005   5.2489   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot

profile(mod.tc.sex, sigma2=1)
```

```
##
|
```





```
# Delta AICc against int-only model
AIC(mod.tc.sex, mod.tc.sex.int, correct = TRUE)
```

```
##           df      AICc
## mod.tc.sex      3 254.6917
## mod.tc.sex.int  2 267.9894
```

```
AIC(mod.tc.sex.int, correct = TRUE) - AIC(mod.tc.sex,correct = TRUE)
```

```
## [1] 13.29769
```

```
# Calculate McFadden's pseudo R2
1-(logLik(mod.tc.sex)/logLik(mod.tc.sex.int))
```

```
## 'log Lik.' 0.05934825 (df=3)
```

```
# Test: Effect of hr_estimator on T. carolina hr size

mod.tc.hr = rma.mv(yi,vi,mods = ~ hr_estimator, random = ~1|Author, data = ef.tc)
```

```
## Warning in rma.mv(yi, vi, mods = ~hr_estimator, random = ~1 | Author, data
```

```
## = ef.tc): Rows with NAs omitted from model fitting.
```

```
summary(mod.tc.hr)
```

```
##
## Multivariate Meta-Analysis Model (k = 70; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -387.9664    775.9329    785.9329    796.8812    786.9329
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed  factor
## sigma^2    6.0848  2.4667    18     no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 66) = 1531.4110, p-val < .0001
##
## Test of Moderators (coefficient(s) 2,3,4):
## QM(df = 3) = 317.2603, p-val < .0001
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          8.3510  0.6740   12.3896 <.0001    7.0299    9.6721
## hr_estimatorHM   -4.8045  0.8945   -5.3713 <.0001   -6.5577   -3.0513
## hr_estimatorKernel -3.8237  0.3943   -9.6979 <.0001   -4.5965   -3.0509
## hr_estimatorMCP   -4.1321  0.2419  -17.0785 <.0001   -4.6063   -3.6579
##
## intrcpt          ***
## hr_estimatorHM    ***
## hr_estimatorKernel ***
## hr_estimatorMCP    ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Testing main effect to display level-specific estimates

mod.tc.hr.d = rma.mv(yi,vi,mods = ~ hr_estimator-1, random = ~1|Author, data = ef.tc)
```

```
## Warning in rma.mv(yi, vi, mods = ~hr_estimator - 1, random = ~1 | Author, :
## Rows with NAs omitted from model fitting.
```

```
summary(mod.tc.hr.d)
```

```
##
## Multivariate Meta-Analysis Model (k = 70; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
```

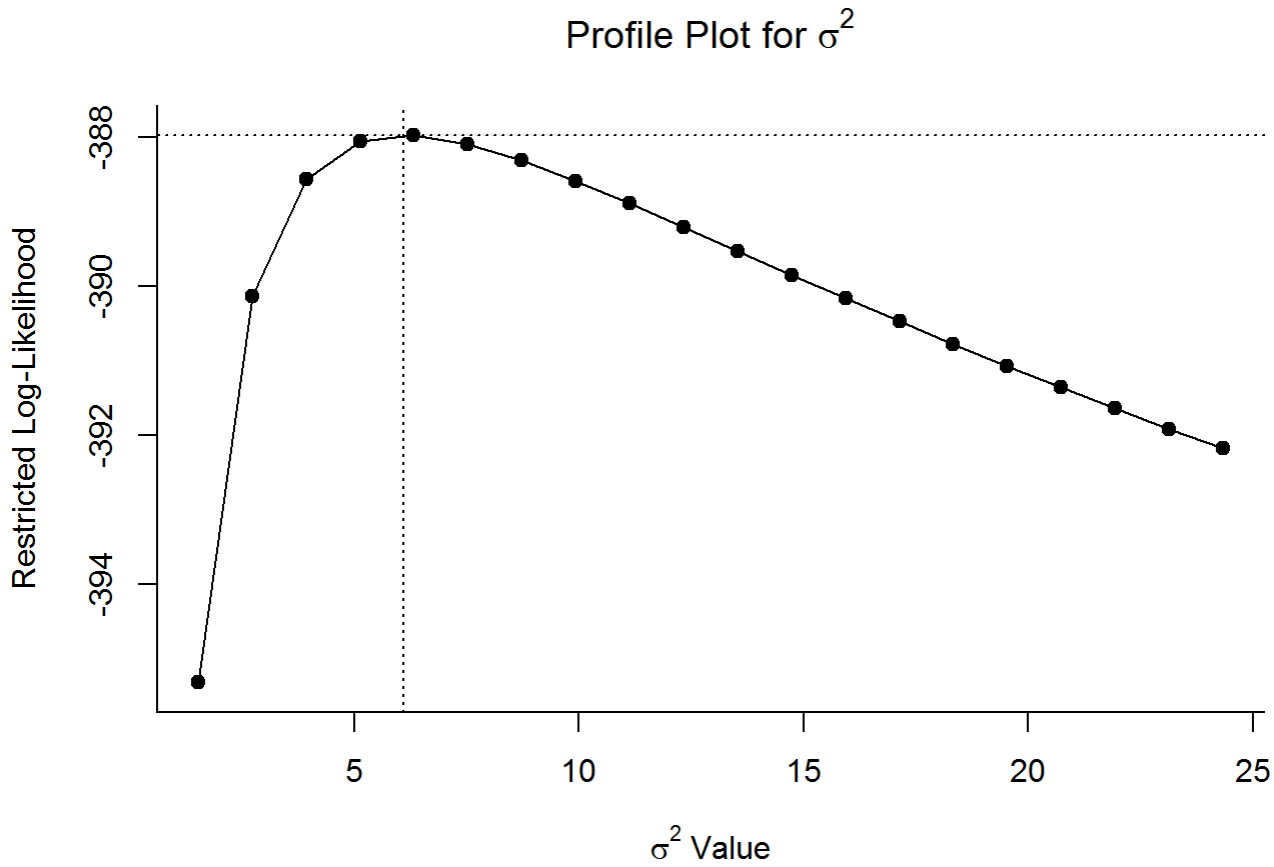
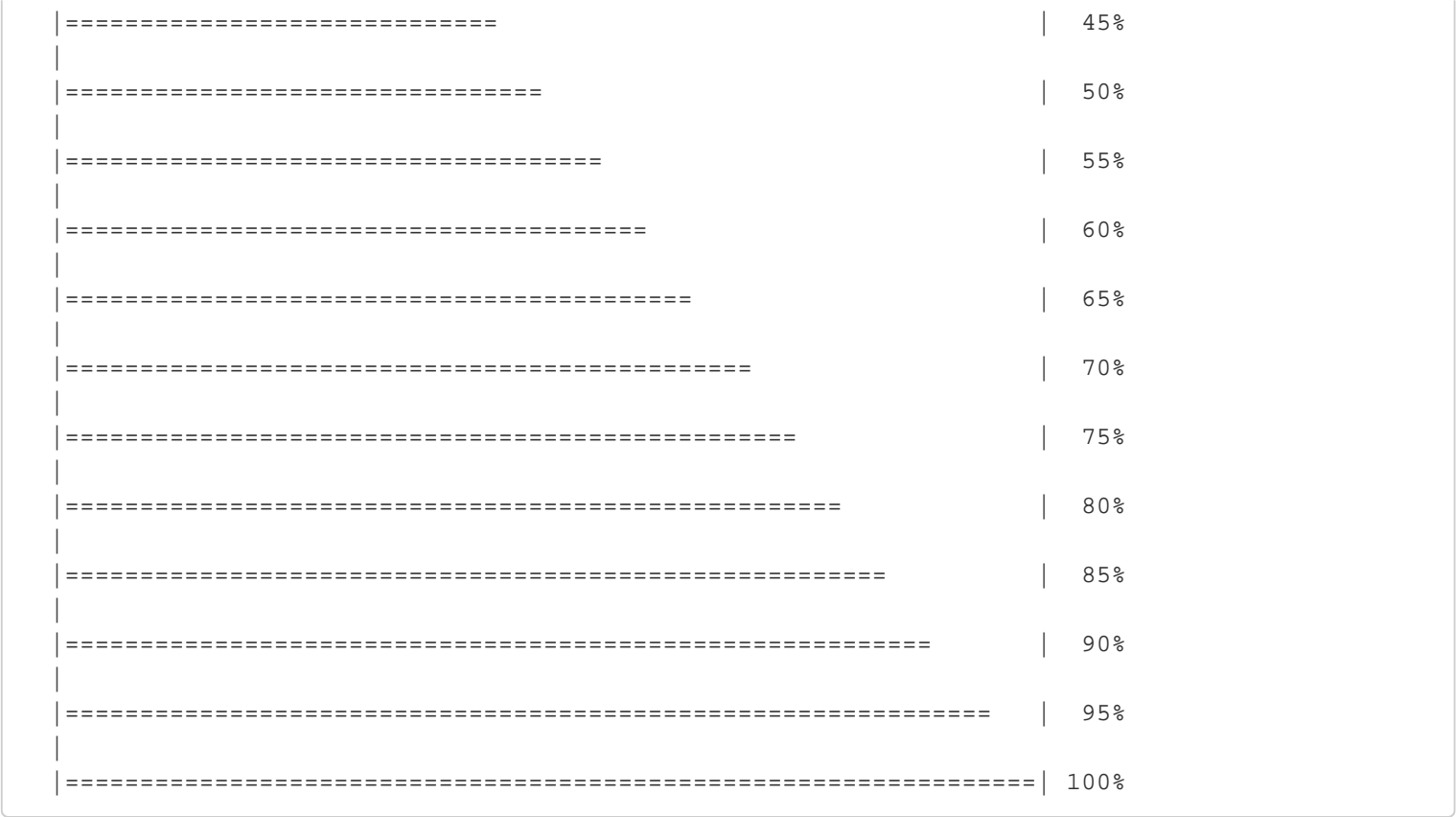


```
## -387.9664    775.9329    785.9329    796.8812    786.9329
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2    6.0848   2.4667     18     no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 66) = 1531.4110, p-val < .0001
##
## Test of Moderators (coefficient(s) 1,2,3,4):
## QM(df = 4) = 365.1382, p-val < .0001
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## hr_estimatorEllipse    8.3510  0.6740  12.3896 <.0001    7.0299    9.6721
## hr_estimatorHM          3.5465  1.0809   3.2812  0.0010    1.4280    5.6649
## hr_estimatorKernel      4.5273  0.6718   6.7389 <.0001    3.2106    5.8440
## hr_estimatorMCP         4.2189  0.6351   6.6433 <.0001    2.9742    5.4636
##
## hr_estimatorEllipse ***
## hr_estimatorHM      **
## hr_estimatorKernel  ***
## hr_estimatorMCP     ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot

profile(mod.tc.hr, sigma2=1)
```





```
# Delta AICc against int-only model
AIC(mod.tc.hr, mod.tc.int, correct = TRUE)
```

```
##           df      AICc
## mod.tc.hr    5  786.9329
## mod.tc.int   2 1118.2180
```

```
AIC(mod.tc.int, correct = TRUE) - AIC(mod.tc.hr,correct = TRUE)
```

```
## [1] 331.2851
```

```
# Calculate McFadden's pseudo R2
1-(logLik(mod.tc.hr)/logLik(mod.tc.int))
```

```
## 'log Lik.' 0.3034973 (df=5)
```

```
#Multiple comparisons using Holm-Bonferroni method
summary(glht(mod.tc.hr, linct=cbind(contrMat(c("Ellipse"=1,"HM"=1,"Kernel"=1,"MCP"=1),
type="Tukey"))), test=adjusted("holm"))
```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: rma.mv(yi = yi, V = vi, mods = ~hr_estimator, random = ~1 | Author,
## data = ef.tc)
##
## Linear Hypotheses:
##           Estimate Std. Error z value Pr(>|z|)
## HM - Ellipse == 0    -13.1555     1.1578 -11.362  <2e-16 ***
## Kernel - Ellipse == 0 -12.1747     0.8765 -13.890  <2e-16 ***
## MCP - Ellipse == 0   -12.4831     0.7889 -15.823  <2e-16 ***
## Kernel - HM == 0      0.9808     0.9698  1.011    0.936
## MCP - HM == 0         0.6724     0.9210  0.730    0.936
## MCP - Kernel == 0    -0.3084     0.3121 -0.988    0.936
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- holm method)
```

```
## Test: Effect of sample size on T. carolina hr size

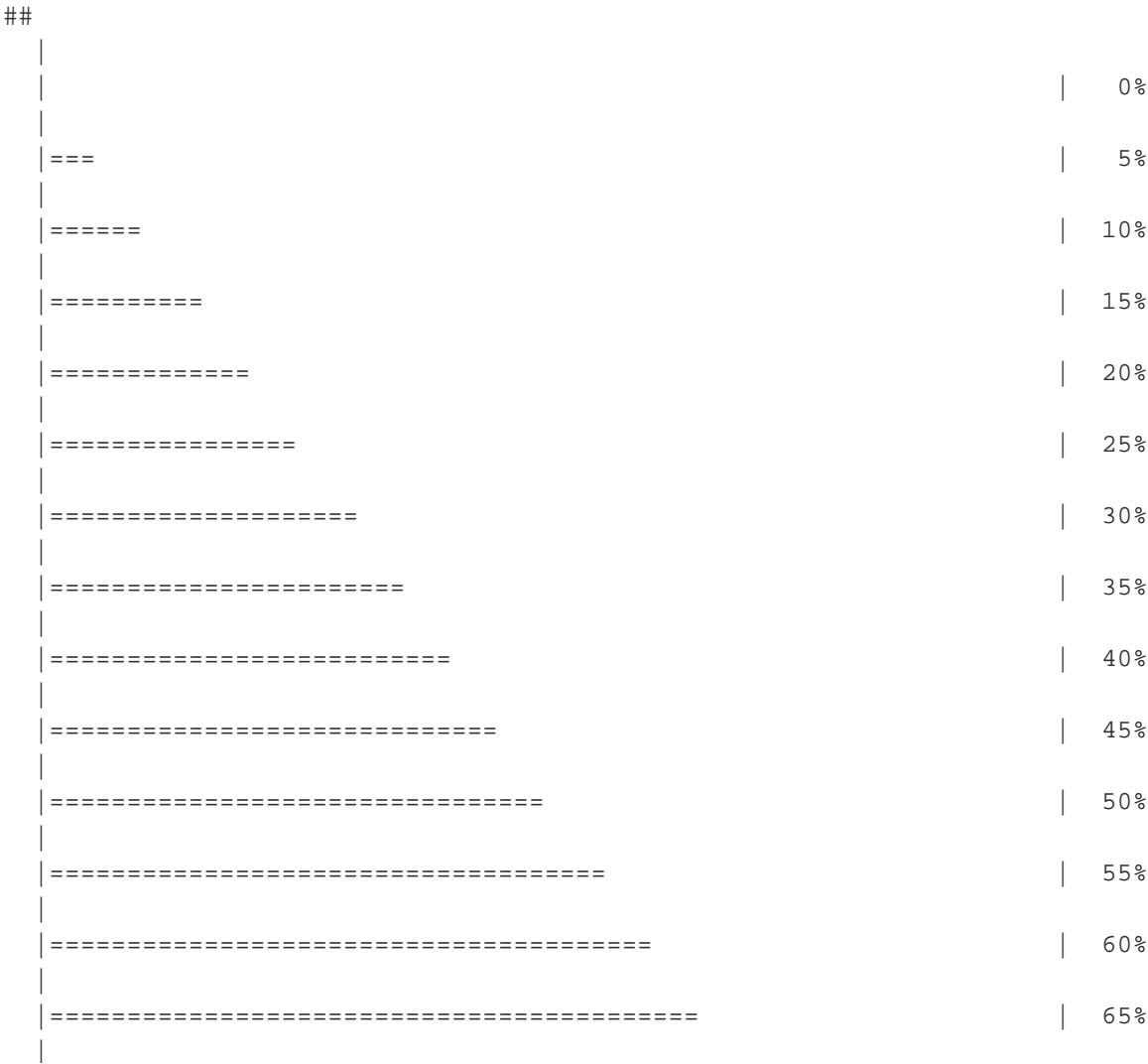
mod.tc.n = rma.mv(yi,vi,mods = ~ n, random = ~1|Author, data = ef.tc)
summary(mod.tc.n)
```

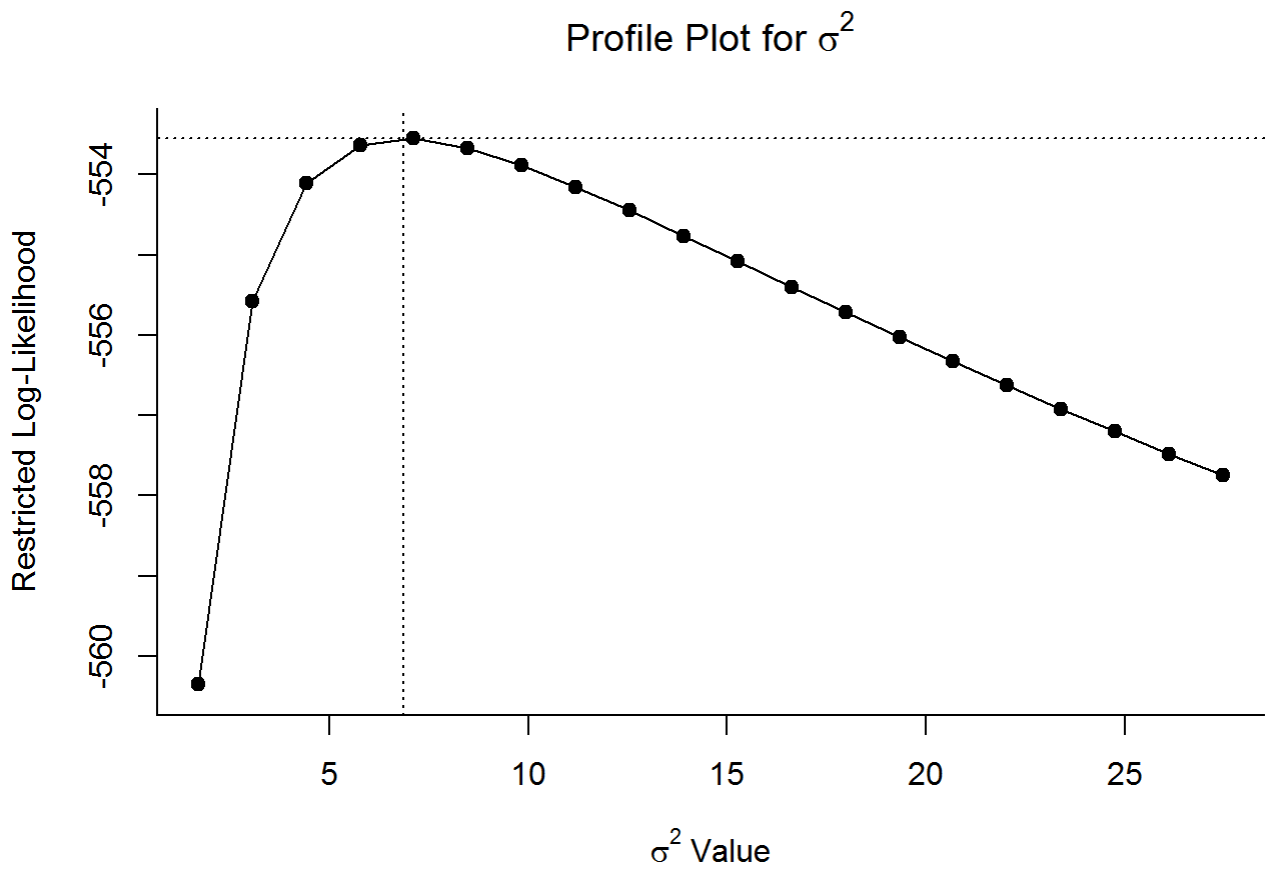
```
##
## Multivariate Meta-Analysis Model (k = 72; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
## -553.5489  1107.0978  1113.0978  1119.8432  1113.4614
##
## Variance Components:
```

```
##
##          estim      sqrt  nlvls  fixed  factor
## sigma^2    6.8630   2.6197    19     no   Author
##
## Test for Residual Heterogeneity:
## QE(df = 70) = 1926.0398, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 5.0351, p-val = 0.0248
##
## Model Results:
##
##          estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt    4.2067   0.6773   6.2111  <.0001   2.8792   5.5341   ***
## n          0.0362   0.0161   2.2439   0.0248   0.0046   0.0678    *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot

profile(mod.tc.n, sigma2=1)
```





```
# Delta AICc against int-only model
AIC(mod.tc.n, mod.tc.int, correct = TRUE)
```

##	df	AICc
## mod.tc.n	3	1113.461
## mod.tc.int	2	1118.218

```
AIC(mod.tc.int, correct = TRUE) - AIC(mod.tc.n,correct = TRUE)
```

```
## [1] 4.756617
```

```
# Calculate McFadden's pseudo R2
1-(logLik(mod.tc.n)/logLik(mod.tc.int))
```

```
## 'log Lik.' 0.006232966 (df=3)
```

```
## Test: Effect of ecoregion on T. carolina hr size

mod.tc.eco = rma.mv(yi,vi,mods = ~ ecoregion, random = ~1|Author, data = ef.tc)
summary(mod.tc.eco)
```

```
##
## Multivariate Meta-Analysis Model (k = 72; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -543.6427   1087.2854   1099.2854   1112.5135   1100.6854
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2      7.4243   2.7248     19     no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 67) = 1857.7924, p-val < .0001
##
## Test of Moderators (coefficient(s) 2,3,4,5):
## QM(df = 4) = 4.5245, p-val = 0.3396
##
## Model Results:
##
##                                     estimate
## intrcpt                                18.3170
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS -13.3918
## ecoregionMIXED WOOD PLAINS                                -13.8995
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS                -16.2407
## ecoregionSOUTHEASTERN USA PLAINS                           -12.9451
##                                     se
## intrcpt                                12.4508
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS 12.5718
## ecoregionMIXED WOOD PLAINS                                12.6093
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS                12.5500
## ecoregionSOUTHEASTERN USA PLAINS                           12.4849
##                                     zval
## intrcpt                                1.4711
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS -1.0652
## ecoregionMIXED WOOD PLAINS                                -1.1023
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS                -1.2941
## ecoregionSOUTHEASTERN USA PLAINS                           -1.0369
##                                     pval
## intrcpt                                0.1413
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS 0.2868
```

```
## ecoregionMIXED WOOD PLAINS 0.2703
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS 0.1956
## ecoregionSOUTHEASTERN USA PLAINS 0.2998
## ci.lb
## intrcpt -6.0861
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS -38.0322
## ecoregionMIXED WOOD PLAINS -38.6132
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS -40.8382
## ecoregionSOUTHEASTERN USA PLAINS -37.4151
## ci.ub
## intrcpt 42.7201
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS 11.2485
## ecoregionMIXED WOOD PLAINS 10.8143
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS 8.3569
## ecoregionSOUTHEASTERN USA PLAINS 11.5250
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Testing main effect to display level-specific estimates

mod.tc.eco.d = rma.mv(yi,vi,mods = ~ ecoregion-1, random = ~1|Author, data = ef.tc)
summary(mod.tc.eco.d)
```

```
##
## Multivariate Meta-Analysis Model (k = 72; method: REML)
##
##      logLik    Deviance      AIC      BIC      AICc
## -543.6427  1087.2854  1099.2854  1112.5135  1100.6854
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed  factor
## sigma^2    7.4243  2.7248    19    no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 67) = 1857.7924, p-val < .0001
##
## Test of Moderators (coefficient(s) 1,2,3,4,5):
## QM(df = 5) = 50.7325, p-val < .0001
##
## Model Results:
##
##                                     estimate
## ecoregionCENTRAL USA PLAINS          18.3170
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS    4.9252
## ecoregionMIXED WOOD PLAINS           4.4175
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS      2.0763
## ecoregionSOUTHEASTERN USA PLAINS          5.3719
## se
## ecoregionCENTRAL USA PLAINS          12.4508
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS    1.7403
## ecoregionMIXED WOOD PLAINS           1.9928
```

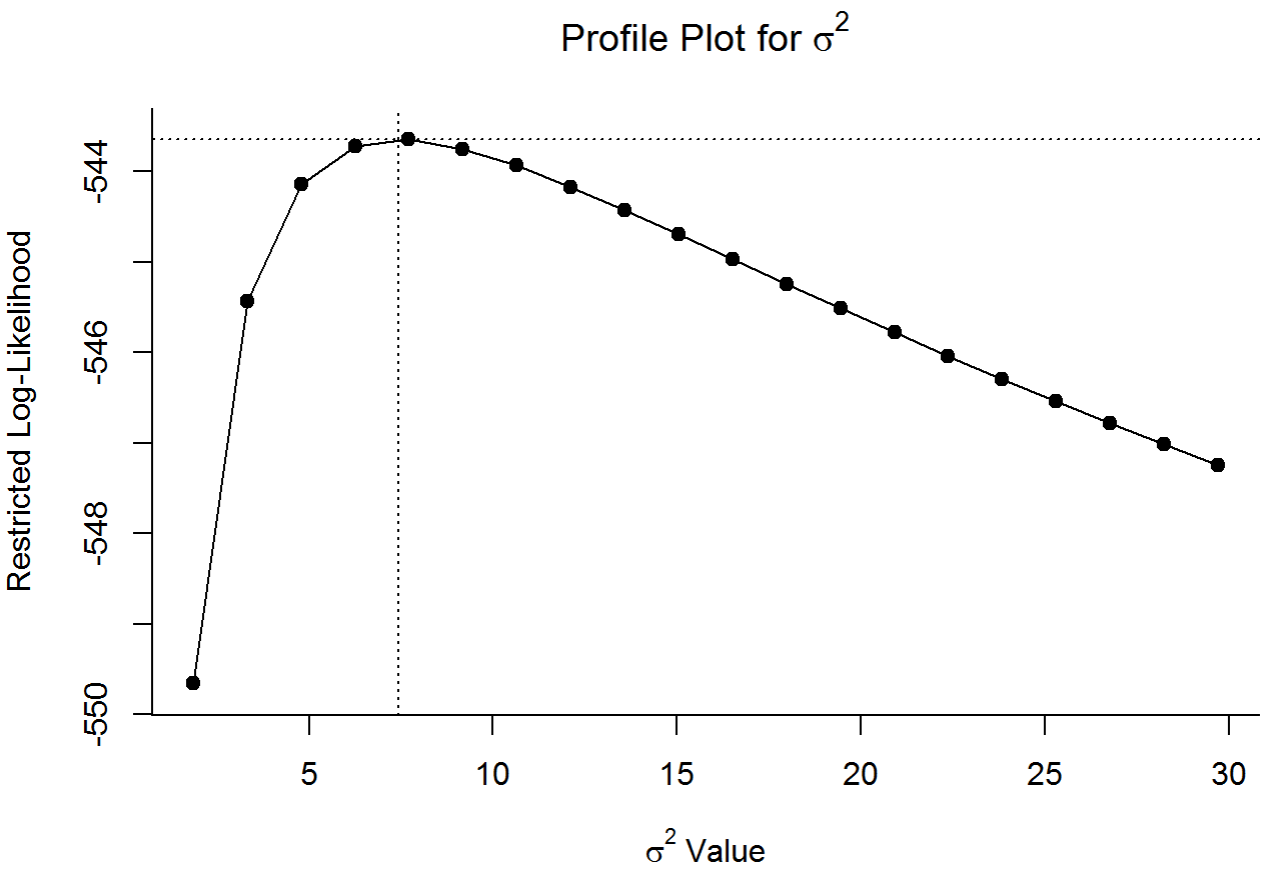
```
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS 1.5748
## ecoregionSOUTHEASTERN USA PLAINS 0.9225
## zval
## ecoregionCENTRAL USA PLAINS 1.4711
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS 2.8301
## ecoregionMIXED WOOD PLAINS 2.2168
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS 1.3185
## ecoregionSOUTHEASTERN USA PLAINS 5.8229
## pval
## ecoregionCENTRAL USA PLAINS 0.1413
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS 0.0047
## ecoregionMIXED WOOD PLAINS 0.0266
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS 0.1873
## ecoregionSOUTHEASTERN USA PLAINS <.0001
## ci.lb
## ecoregionCENTRAL USA PLAINS -6.0861
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS 1.5142
## ecoregionMIXED WOOD PLAINS 0.5117
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS -1.0102
## ecoregionSOUTHEASTERN USA PLAINS 3.5638
## ci.ub
## ecoregionCENTRAL USA PLAINS 42.7201
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS 8.3361
## ecoregionMIXED WOOD PLAINS 8.3234
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS 5.1629
## ecoregionSOUTHEASTERN USA PLAINS 7.1801
##
## ecoregionCENTRAL USA PLAINS
## ecoregionMISSISSIPPI ALLUVIAL AND SOUTHEAST USA COASTAL PLAINS **
## ecoregionMIXED WOOD PLAINS *
## ecoregionOZARK/OUACHITA-APPALACHIAN FORESTS
## ecoregionSOUTHEASTERN USA PLAINS ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot

profile(mod.tc.eco, sigma2=1)
```







```
# Delta AICc against int-only model
AIC(mod.tc.eco, mod.tc.int, correct = TRUE)
```

```
##           df      AICc
## mod.tc.eco  6 1100.685
## mod.tc.int  2 1118.218
```

```
AIC(mod.tc.int, correct = TRUE) - AIC(mod.tc.eco,correct = TRUE)
```

```
## [1] 17.53263
```

```
# Calculate McFadden's pseudo R2
1-(logLik(mod.tc.eco)/logLik(mod.tc.int))
```

```
## 'log Lik.' 0.0240172 (df=6)
```

```
## Test: Effect of relocation on T. carolina hr size

mod.tc.relo = rma.mv(yi,vi,mods = ~ relocated, random = ~1|Author, data = ef.tc)
summary(mod.tc.relo)
```

```
##
## Multivariate Meta-Analysis Model (k = 72; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -548.7080    1097.4159    1103.4159    1110.1614    1103.7795
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2      6.7258   2.5934     19     no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 70) = 1628.5440, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 13.3288, p-val = 0.0003
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt           4.0696   0.6643   6.1261   <.0001   2.7676   5.3717   ***
## relocatedYES       2.0238   0.5543   3.6509   0.0003   0.9373   3.1103   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Testing main effect to display level-specific estimates

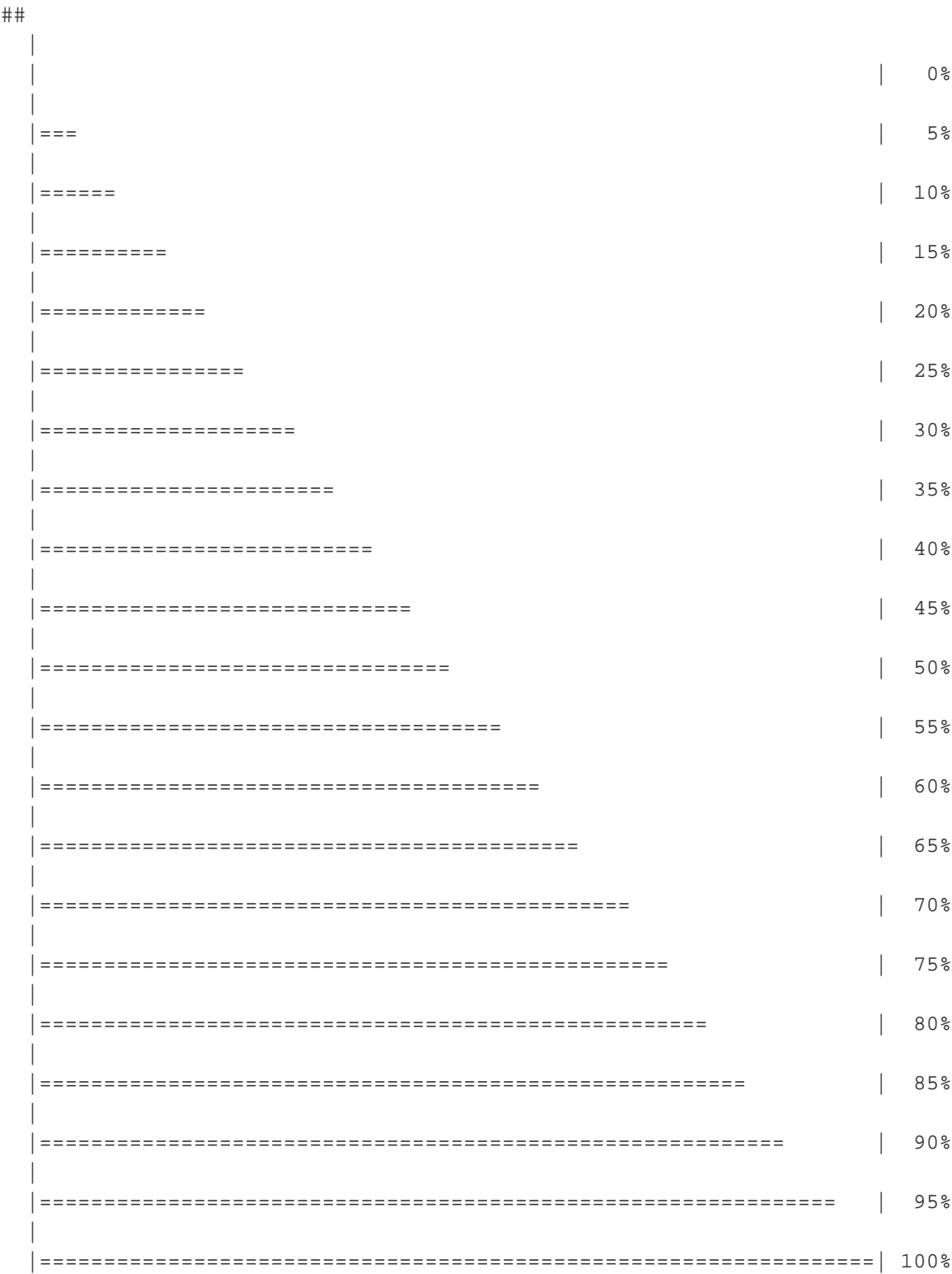
mod.tc.relo.d = rma.mv(yi,vi,mods = ~ relocated, random = ~1|Author, data = ef.tc)
summary(mod.tc.relo.d)
```

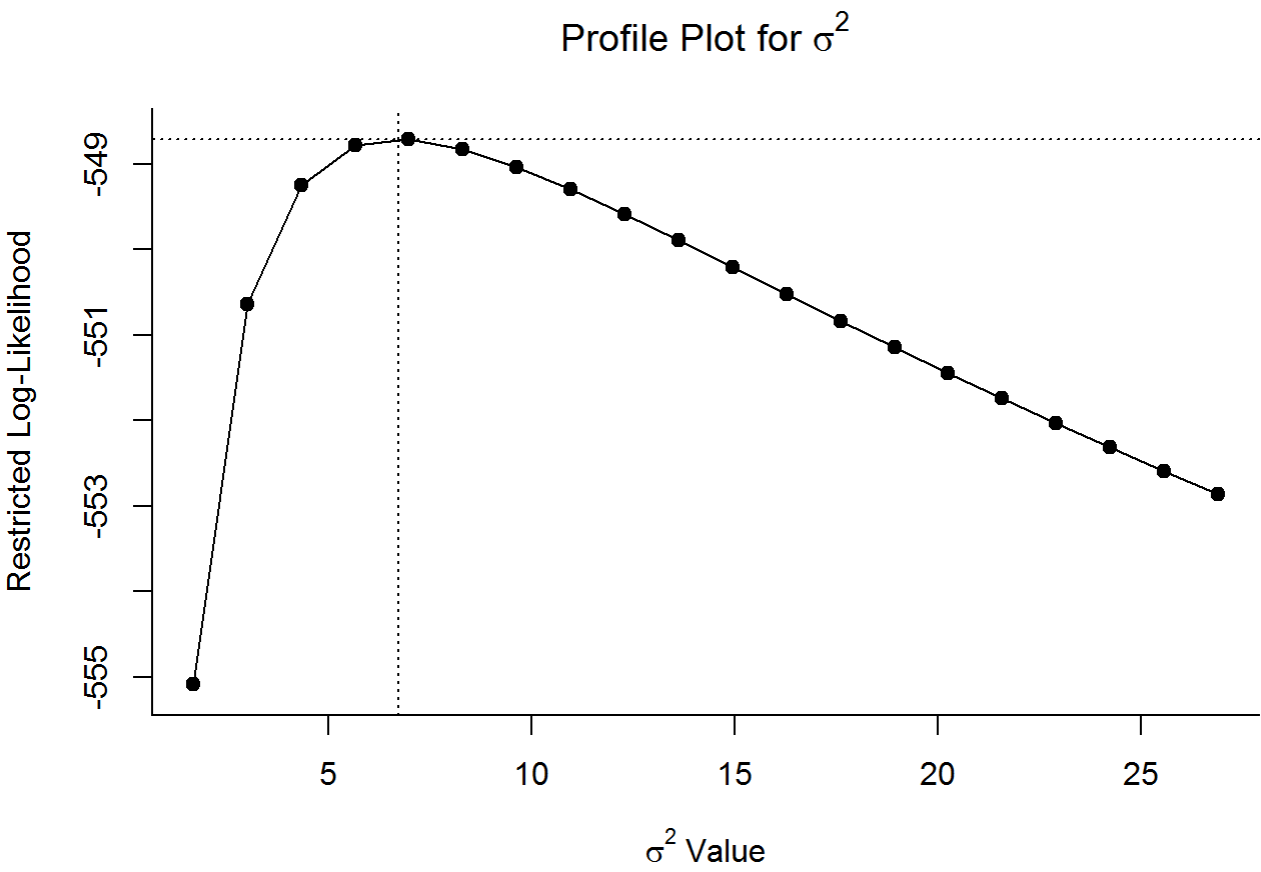
```
##
## Multivariate Meta-Analysis Model (k = 72; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -548.7080    1097.4159    1103.4159    1110.1614    1103.7795
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2      6.7258   2.5934     19     no  Author
##
## Test for Residual Heterogeneity:
## QE(df = 70) = 1628.5440, p-val < .0001
##
## Test of Moderators (coefficient(s) 2):
## QM(df = 1) = 13.3288, p-val = 0.0003
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt           4.0696   0.6643   6.1261   <.0001   2.7676   5.3717   ***
## relocatedYES       2.0238   0.5543   3.6509   0.0003   0.9373   3.1103   ***
```

```
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Profile liklihood plot

profile(mod.tc.relo, sigma2=1)
```





```
# Delta AICc against int-only model
AIC(mod.tc.relo, mod.tc.int, correct = TRUE)
```

```
##           df      AICc
## mod.tc.relo  3 1103.780
## mod.tc.int   2 1118.218
```

```
AIC(mod.tc.int, correct = TRUE) - AIC(mod.tc.relo,correct = TRUE)
```

```
## [1] 14.43848
```

```
# Calculate McFadden's pseudo R2
1-(logLik(mod.tc.relo)/logLik(mod.tc.int))
```

```
## 'log Lik.' 0.01492372 (df=3)
```

```
#Subset ef.tc.sex data set to include only T. carolina cases for female turtles

ef.tc.fg <- subset(ef.tc.sex, species=="T. carolina"& sex!="Male" & gravid == c("Gravid", "Not
gravid"))
droplevels.factor(ef.tc.f$sex)
```

```
## [1] Female Female Female Female Female Female Female Female Female Female Female
## [11] Female Female Female Female Female Female Female Female Female Female Female
## [21] Female Female Female Female Female Female
## Levels: Female
```

```
droplevels.factor(ef.tc.f$gravid)
```

```
## [1] Unknown Unknown Gravid Unknown Unknown Unknown Gravid
## [8] Unknown Gravid Notgravid Unknown Unknown Male Mixed
## [15] Unknown Unknown Unknown Unknown Unknown Gravid Notgravid
## [22] Unknown Unknown Unknown Unknown Unknown
## Levels: Gravid Male Mixed Notgravid Unknown Unknown
```

```
## Test: Effect of gravid on T. carolina hr size not possible: lack of sample size
```