Applications of MINMI and GBRM

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Load functions

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.2.1
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.2 --
## v ggplot2 3.3.6      v purrr   0.3.4
## v tibble  3.1.8      v dplyr   1.0.10
## v tidyr   1.2.1      v stringr 1.4.1
## v readr   2.1.2      v forcats 0.5.2
```

```
## Warning: package 'tibble' was built under R version 4.2.1
```

```
## Warning: package 'tidyr' was built under R version 4.2.1
```

```
## Warning: package 'readr' was built under R version 4.2.1
```

```
## Warning: package 'dplyr' was built under R version 4.2.1
```

```
## Warning: package 'stringr' was built under R version 4.2.1
```

```
## Warning: package 'forcats' was built under R version 4.2.1
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(readxl)
```

```
## Warning: package 'readxl' was built under R version 4.2.1
```

```
source("../src/garthwaite-robbins-munro-functions.R")
source("../src/minmi-functions.R")
```

```
##
## Attaching package: 'extraDistr'
##
## The following object is masked from 'package:purrr':
##
##     rdunif
```

```
# source("../src/GRIWM.R")
source("../src/simulated-inversion.R")
```

```
## Loading required package: nlme
##
## Attaching package: 'nlme'
##
## The following object is masked from 'package:dplyr':
##
##     collapse
##
## This is mgcv 1.8-40. For overview type 'help("mgcv-package")'.
```

```
theme_set(theme_bw())
```

```
alpha = 0.05
```

Import Data

```
cave_bear = read_excel(path='../data/fossildata.xlsx',
                       sheet="Ursus.spe.Eur.ext",
                       range="M3:N33",
                       col_names=c("age", "sd"),
                       col_types=c('numeric', 'numeric'))

mammoth = read_excel(path='../data/fossildata.xlsx',
                     sheet="Mammoths Eurasian",
                     range="M3:N205",
                     col_names=c("age", "sd"),
                     col_types=c('numeric', 'numeric'))

megaloceros = read_excel(path='../data/fossildata.xlsx',
                         sheet="Megaloceros",
                         range="M3:N48",
                         col_names=c("age", "sd"),
                         col_types=c('numeric', 'numeric'))

neanderthal = read_excel(path='../data/fossildata.xlsx',
                         sheet="NeandertalEur",
                         range="M3:N147",
                         col_names=c("age", "sd"),
                         col_types=c('numeric', 'numeric'))

bison = read_excel(path='../data/fossildata.xlsx',
```

```r
                          sheet="BisPriscus.ext",
                          range="M3:N15",
                          col_names=c("age", "sd"),
                          col_types=c('numeric', 'numeric'))

jelephant = read_excel(path='../data/fossildata.xlsx',
                          sheet="Paleolox.Japan",
                          range="M3:N13",
                          col_names=c("age", "sd"),
                          col_types=c('numeric', 'numeric'))

cave_hyena = read_excel(path='../data/fossildata.xlsx',
                          sheet="CrocCroc.Eur",
                          range="M3:N81",
                          col_names=c("age", "sd"),
                          col_types=c('numeric', 'numeric'))

tmp = rbind(data.frame(age=cave_bear$age, dataset="Cave Bear"),
            data.frame(age=bison$age, dataset="Steppe Bison"),
            data.frame(age=mammoth$age, dataset="Eurasian Mammoth"),
            data.frame(age=cave_hyena$age, dataset="Cave Hyena"))
```
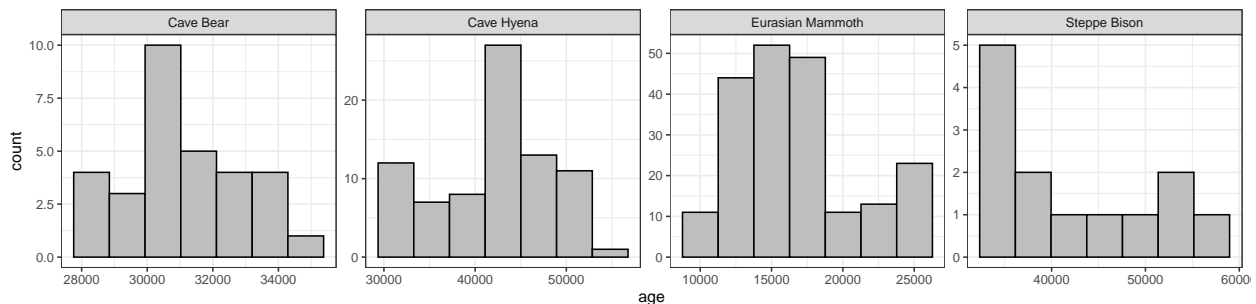
Histograms

```r
p = tmp %>% ggplot(aes(x=age)) +
  geom_histogram(position="identity", color="black", fill="grey", bins=7) +
  facet_wrap(dataset ~ ., scale="free", nrow=1)

p
```



```r
ggsave(file="../figures/applications-hists.svg", plot=p, width=12, height=3)
```

```r
estimate_extinction = function (dates, sd, K, theta.test_vec, alpha=0.05, label) {
  SIUGM.results = simulated_inversion(alpha=alpha, dates=dates, sd=sd, K=K, theta.test_vec = theta.test_
  SIUGM = list(lower = SIUGM.results$lower,
               point = SIUGM.results$point,
               upper = SIUGM.results$upper,
               method = "SI-UGM")

  MINMI = estimate_extinction.minmi(W = dates, sd=sd, level=1-alpha, K=K)
```

```
    MINMI$method = "MINMI"

    SIRM = estimate_CI.rm(W = dates, K=K, alpha=alpha, max_iter=3000, eps.mean=0, eps.sigma=mean(sd), .mod
    SIRM$method = "SI-RM"

    estimates = data.frame(
      method = factor(),
      lower = numeric(),
      upper = numeric(),
      point = numeric(),
      n = numeric(),
      sigma = numeric(),
      dataset = factor()
    )
    estimates = rbind(estimates, MINMI, SIUGM, SIRM)
    estimates$n = length(dates)
    estimates$sigma = mean(sd)
    estimates$dataset = paste0(label, " (n=", length(dates), ")")
    return(estimates)
}
```

Cave Bear

```
cave_bear.K = 34000
cave_bear = cave_bear[cave_bear$age < cave_bear.K, ]
cave_bear.thetas = seq(22000, 29000)

cave_bear.estimates = estimate_extinction(dates=cave_bear$age, sd=cave_bear$sd, K=cave_bear.K, theta.te
cave_bear.estimates
```

```
##      point    lower    upper method  n   sigma          dataset
## 1 27946.58 26909.00 29097.54  MINMI 30 672.775 Cave Bear (n=30)
## 2 28186.53 27066.01 29331.62 SI-UGM 30 672.775 Cave Bear (n=30)
## 3 27832.00 26334.41 28648.92  SI-RM 30 672.775 Cave Bear (n=30)
```
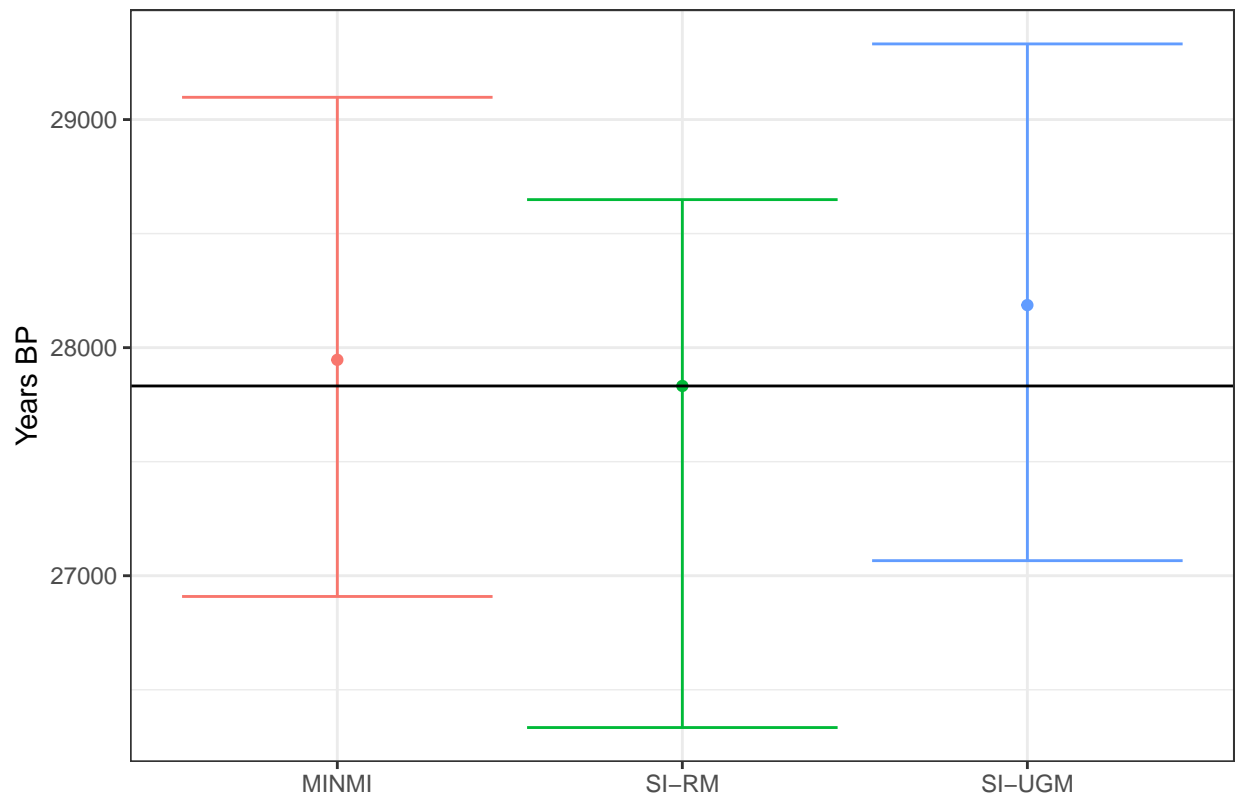
```
ggplot(data=cave_bear.estimates, aes(colour=method)) +
  geom_errorbar(aes(x=method, ymin=lower, ymax=upper)) +
  geom_point(aes(x=method, y=point)) +
  geom_hline(yintercept=min(cave_bear$age)) +
  guides(colour="none") +
  labs(x=NULL, y="Years BP", title="Cave Bear Extinction (Ursus.spe.Eur.ext)")
```

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Cave Bear Extinction (Ursus.spe.Eur.ext)


Eurasian Mammoth

```
mammoth.K = 25000
mammoth = mammoth[mammoth$age < mammoth.K, ]
mammoth.thetas = seq(4000, 14000)

mammoth.estimates = estimate_extinction(dates=mammoth$age, sd=mammoth$sd, K=mammoth.K, theta.test_vec =
mammoth.estimates
```

```
##      point    lower    upper method   n    sigma                      dataset
## 1 10949.15 10578.86 11408.49  MINMI 194 281.5696 Eurasian Mammoth (n=194)
## 2 11003.50 10580.02 11426.98 SI-UGM 194 281.5696 Eurasian Mammoth (n=194)
## 3 10832.00 10246.78 11033.88  SI-RM 194 281.5696 Eurasian Mammoth (n=194)
```

```
ggplot(data=mammoth.estimates, aes(colour=method)) +
  geom_errorbar(aes(x=method, ymin=lower, ymax=upper)) +
  geom_point(aes(x=method, y=point)) +
  guides(colour="none") +
  geom_hline(yintercept=min(mammoth$age)) +
  labs(x=NULL, y="Years BP", title="Mammoth Extinction (MammothPrimEBer)")
```

## Mammoth Extinction (MammothPrimEBer)
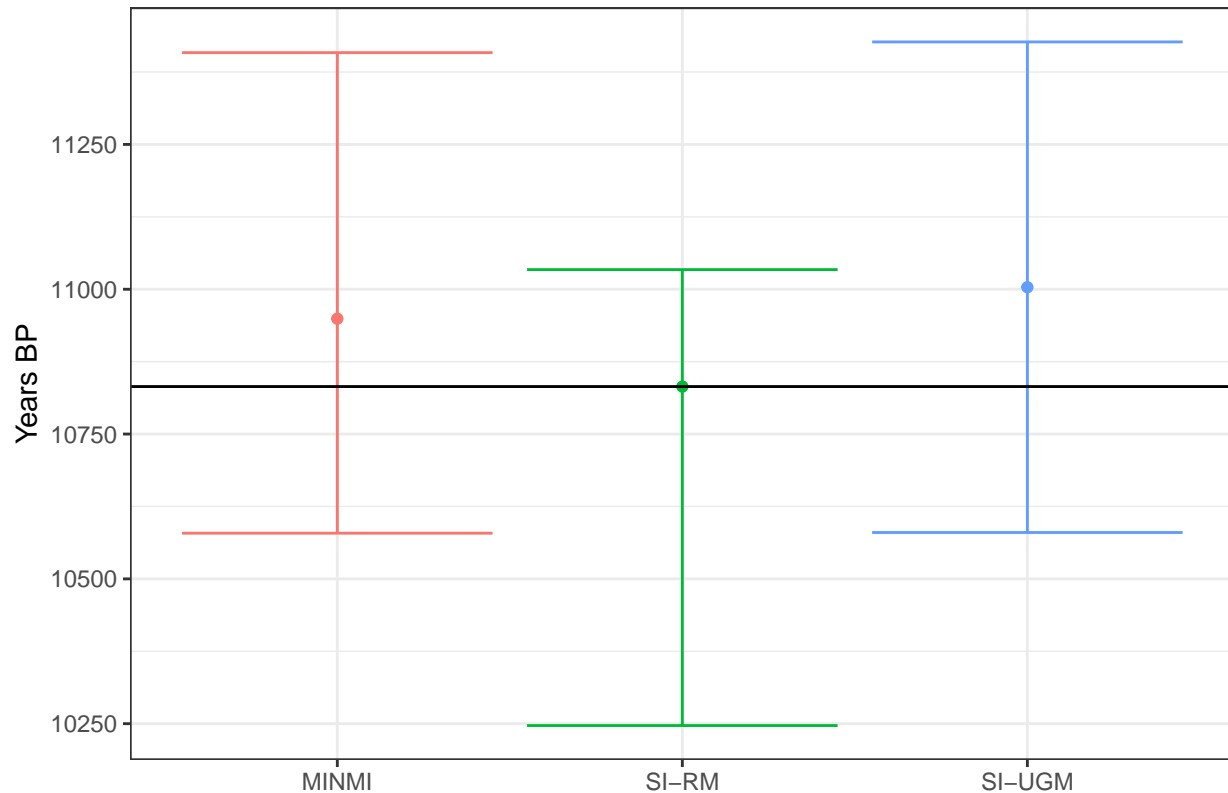
Giant Deer

```
megaloceros.K = 14000
megaloceros = megaloceros[megaloceros$age < megaloceros.K, ]
megaloceros.thetas = seq(8000, 13000)

megaloceros.estimates = estimate_extinction(dates=megaloceros$age, sd=megaloceros$sd, K=megaloceros.K,
megaloceros.estimates
```

```
##      point    lower    upper method  n  sigma          dataset
## 1 12401.21 12209.40 12586.89  MINMI 40 103.05 Giant Deer (n=40)
## 2 12466.58 12261.90 12582.28 SI-UGM 40 103.05 Giant Deer (n=40)
## 3 12402.00 12246.01 12532.00  SI-RM 40 103.05 Giant Deer (n=40)
```

```
ggplot(data=megaloceros.estimates, aes(colour=method)) +
  geom_errorbar(aes(x=method, ymin=lower, ymax=upper)) +
  geom_point(aes(x=method, y=point)) +
  guides(colour="none") +
  geom_hline(yintercept=min(megaloceros$age)) +
  labs(x=NULL, y="Years BP", title="Giant Deer Extinction (megaloceros)")
```

Giant Deer Extinction (megaloceros)
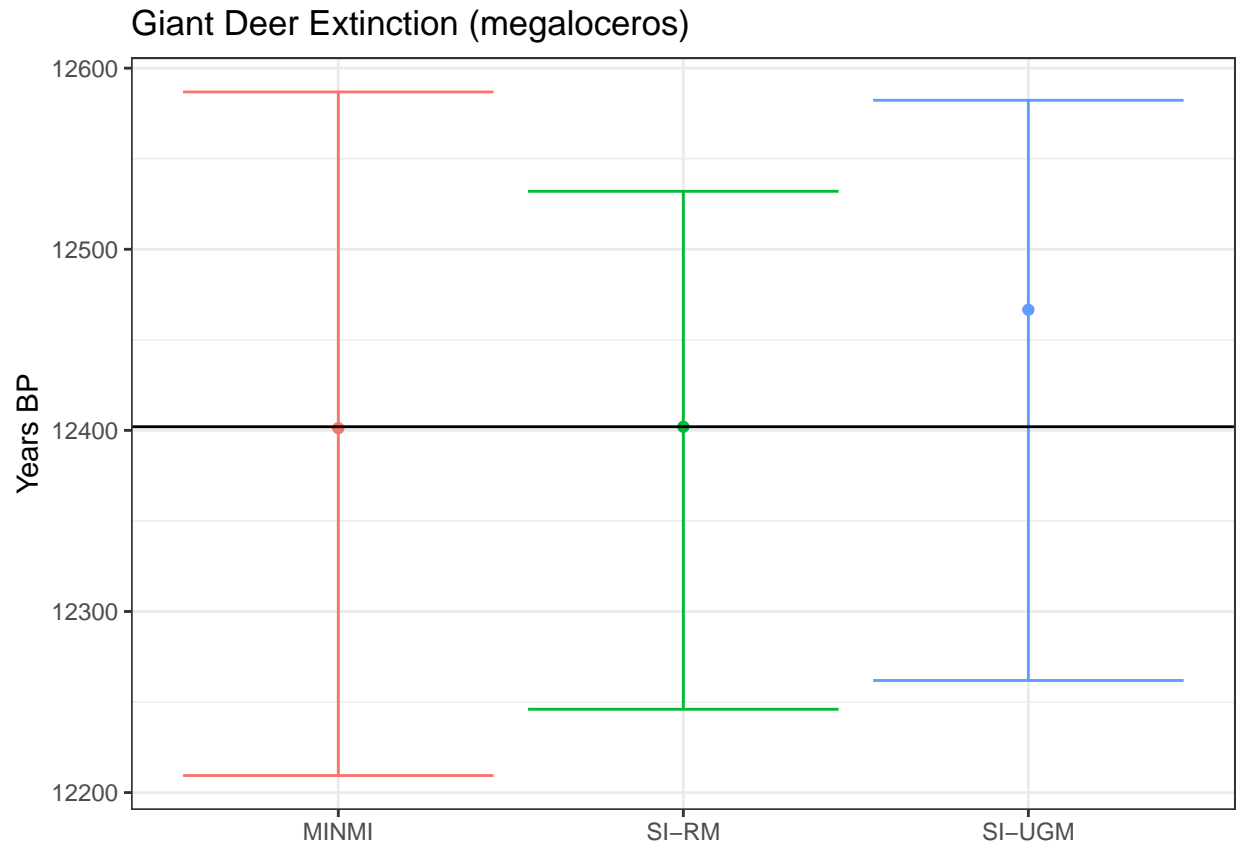
Neanderthal

```
neanderthal.K = 48000
neanderthal = neanderthal[neanderthal$age < neanderthal.K, ]
neanderthal.thetas = seq(38000, 44000)

neanderthal.estimates = estimate_extinction(dates=neanderthal$age, sd=neanderthal$sd, K=neanderthal.K,
neanderthal.estimates
```

```
##      point    lower    upper method   n    sigma            dataset
## 1 42078.54 41224.16 43228.89  MINMI 134 893.5634 Neanderthal (n=134)
## 2 42282.32 41534.67 43394.05 SI-UGM 134 893.5634 Neanderthal (n=134)
## 3 41015.00 38734.57 41414.30  SI-RM 134 893.5634 Neanderthal (n=134)
```

```
ggplot(data=neanderthal.estimates, aes(colour=method)) +
  geom_errorbar(aes(x=method, ymin=lower, ymax=upper)) +
  geom_point(aes(x=method, y=point)) +
  guides(colour="none") +
  geom_hline(yintercept=min(neanderthal$age)) +
  labs(x=NULL, y="Years BP", title="Neanderthal Extinction")
```

Neanderthal Extinction
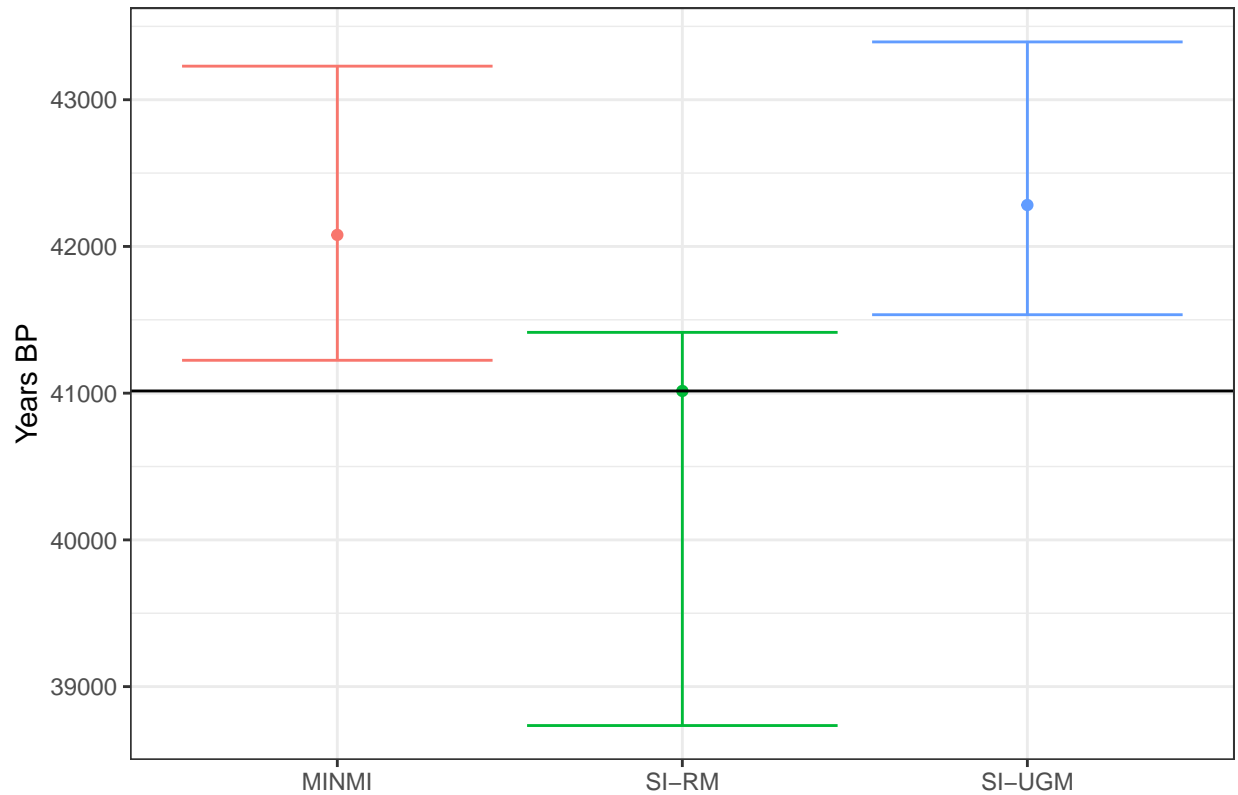
Steppe Bison

```
bison.K = 55000
bison = bison[bison$age < bison.K, ]
bison.thetas = seq(25000, 35000)

bison.estimates = estimate_extinction(dates=bison$age, sd=bison$sd, K=bison.K, theta.test_vec = bison.th
bison.estimates
```

```
##      point    lower    upper method  n    sigma            dataset
## 1 31063.08 24326.05 33808.48  MINMI 12 1123.417 Steppe Bison (n=12)
## 2 31238.77 24759.81 33911.07 SI-UGM 12 1123.417 Steppe Bison (n=12)
## 3 32489.00 30282.75 38382.76  SI-RM 12 1123.417 Steppe Bison (n=12)
```

```
ggplot(data=bison.estimates, aes(colour=method)) +
  geom_errorbar(aes(x=method, ymin=lower, ymax=upper)) +
  geom_point(aes(x=method, y=point)) +
  guides(colour="none") +
  geom_hline(yintercept=min(bison$age)) +
  labs(x=NULL, y="Years BP", title="Steppe Bison Extinction")
```

Steppe Bison Extinction
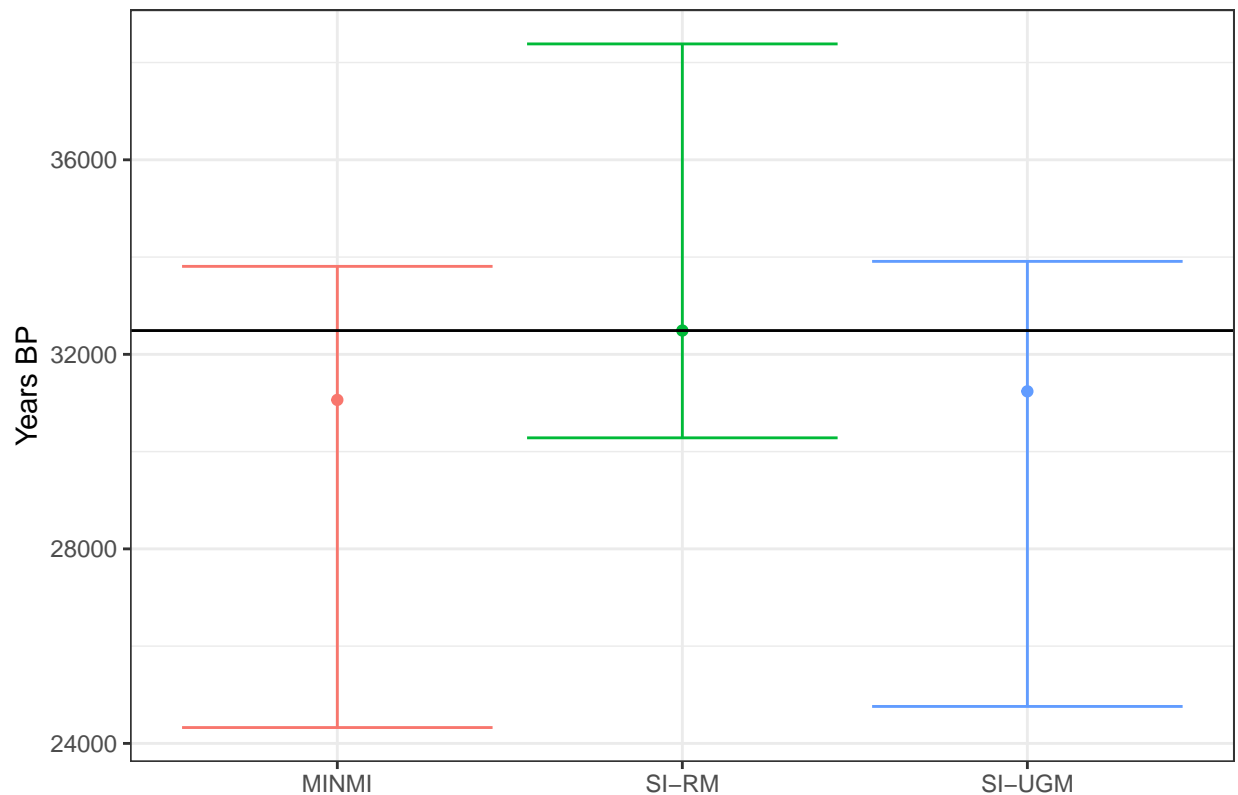
Japanese Elephant

```
jelephant.K = 40000
jelephant = jelephant[jelephant$age < jelephant.K, ]
jelephant.thetas = seq(25000, 35000)

jelephant.estimates = estimate_extinction(dates=jelephant$age, sd=jelephant$sd, K=jelephant.K, theta.te
jelephant.estimates
```

```
##      point    lower    upper method  n   sigma                       dataset
## 1 25877.79 20880.96 27704.02  MINMI 10 708.175 Japanese Elephant (n=10)
## 2 25846.92 21631.36 27509.73 SI-UGM 10 708.175 Japanese Elephant (n=10)
## 3 26745.50 26165.03 29797.52  SI-RM 10 708.175 Japanese Elephant (n=10)
```

```
ggplot(data=jelephant.estimates, aes(colour=method)) +
  geom_errorbar(aes(x=method, ymin=lower, ymax=upper)) +
  geom_point(aes(x=method, y=point)) +
  guides(colour="none") +
  geom_hline(yintercept=min(jelephant$age), linetype="dashed") +
  annotate(geom="text", label=paste("Obs. Min.", min(jelephant$age)), x=0, y=min(jelephant$age)+250, hj
  labs(x=NULL, y="Years BP", title="Japanese Elephant Extinction")
```

Japanese Elephant Extinction
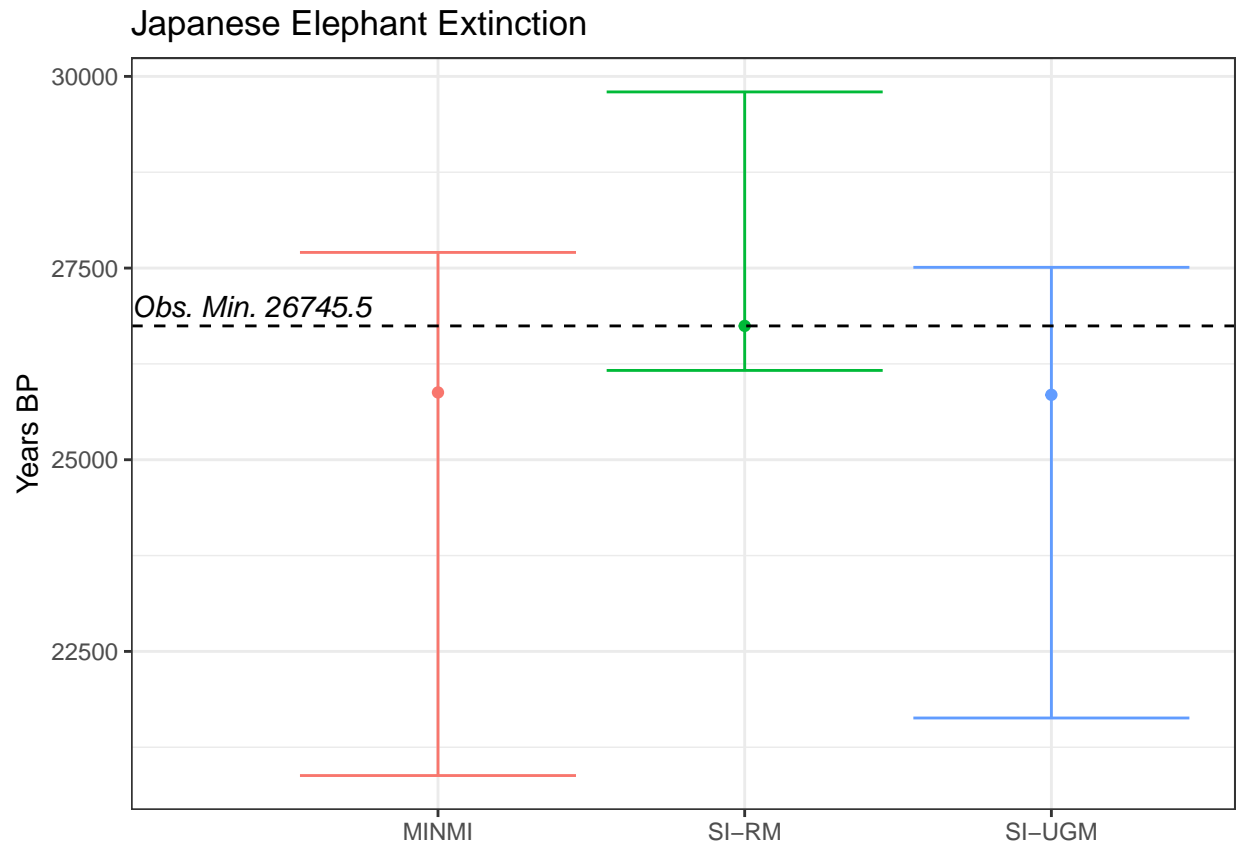
Cave Hyena

```
cave_hyena.K = 55000
cave_hyena = cave_hyena[cave_hyena$age < cave_hyena.K, ]
cave_hyena.thetas = seq(20000, 30000)

cave_hyena.estimates = estimate_extinction(dates=cave_hyena$age, sd=cave_hyena$sd, K=cave_hyena.K, theta
cave_hyena.estimates
```

```
##      point    lower    upper method  n    sigma           dataset
## 1 30098.38 28440.61 31812.23  MINMI 79 1117.924 Cave Hyena (n=79)
## 2 29995.93 28290.49 31701.79 SI-UGM 79 1117.924 Cave Hyena (n=79)
## 3 29465.50 28135.81 32051.25  SI-RM 79 1117.924 Cave Hyena (n=79)
```

```
ggplot(data=cave_hyena.estimates, aes(colour=method)) +
  geom_errorbar(aes(x=method, ymin=lower, ymax=upper)) +
  geom_point(aes(x=method, y=point)) +
  guides(colour="none") +
  geom_hline(yintercept=min(cave_hyena$age), linetype="dashed") +
  annotate(geom="text", label=paste("Obs. Min.", min(cave_hyena$age)), x=0, y=min(cave_hyena$age)+150, h
  labs(x=NULL, y="Years BP", title="Cave Hyena Extinction")
```

Cave Hyena Extinction
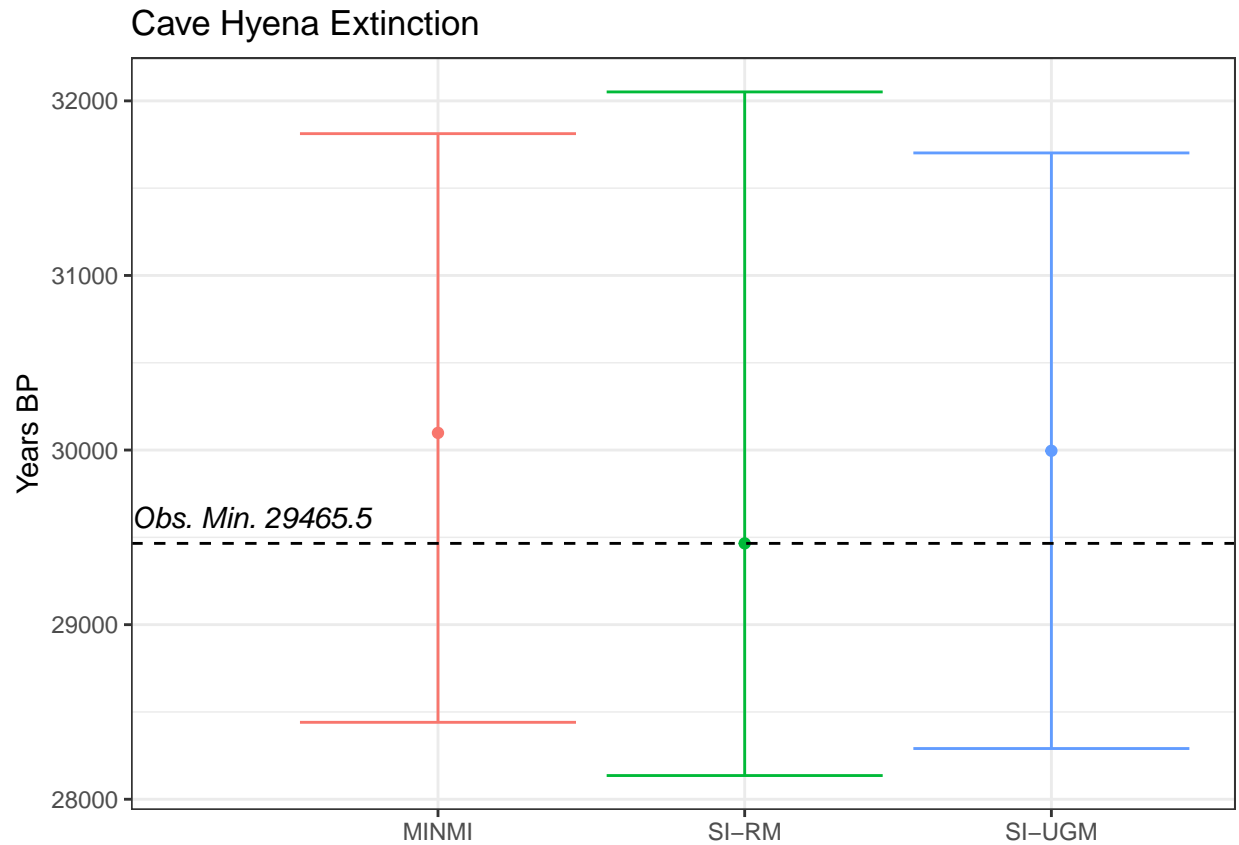
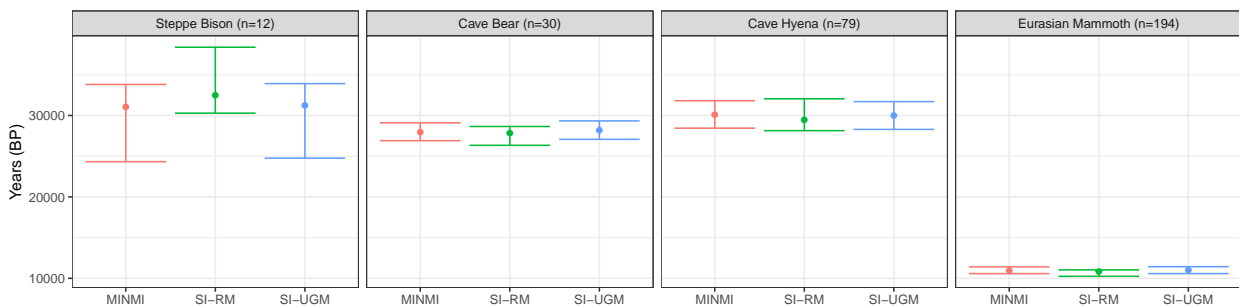**Combined**

```
all_results = rbind(cave_bear.estimates, mammoth.estimates, bison.estimates, cave_hyena.estimates)#, ma

p = all_results %>%
  ggplot(aes(colour=method)) +
  geom_errorbar(aes(x=method, ymin=lower, ymax=upper)) +
  geom_point(aes(x=method, y=point)) +
  guides(colour="none") +
  labs(x=NULL, y="Years (BP)") +
  facet_wrap(fct_reorder(dataset, n) ~ ., nrow=1, dir='v')

p
```

```
ggsave(file="../figures/applications.svg", plot=p, width=12, height=3)
```

```
library(knitr)
```

```
## Warning: package 'knitr' was built under R version 4.2.1
```

```
all_results %>%
  mutate(Extinction = paste0(scales::label_comma()(round(point, 1)), " (", scales::label_comma()(round(
          Method = method) %>%
  select(Method, dataset, Extinction) %>%
  pivot_wider(names_from=dataset, values_from=Extinction) %>%
  kable(booktabs=T, format="latex") %>%
  writeLines("../figures/table-applications-CIs.tex")
```