Supplementary Material for Sluis et al. 2022

Contents

R Session info:

```
session <- sessionInfo()
print(session, locale = FALSE)
```

```
## R version 4.2.0 (2022-04-22)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Pop!_OS 22.04 LTS
##
## Matrix products: default
## BLAS:   /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblasp-r0.3.20.so
##
## attached base packages:
## [1] stats     graphics  grDevices datasets  utils     methods   base
##
## other attached packages:
##  [1] equatiomatic_0.3.1 MASS_7.3-57        corrplot_0.92       ggfortify_0.4.14
##  [5] broom_1.0.1        forcats_0.5.1       stringr_1.4.1       dplyr_1.0.10
##  [9] purrr_0.3.4        readr_2.1.2         tidyr_1.2.1         tibble_3.1.8
## [13] ggplot2_3.3.6      tidyverse_1.3.1     here_1.0.1
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.8.3      lubridate_1.8.0   assertthat_0.2.1 rprojroot_2.0.3
##  [5] digest_0.6.29     utf8_1.2.2        mime_0.12         R6_2.5.1
##  [9] cellranger_1.1.0  backports_1.4.1   reprex_2.0.1      evaluate_0.16
## [13] httr_1.4.3        pillar_1.8.1      rlang_1.0.6       readxl_1.4.0
## [17] rstudioapi_0.13   rmarkdown_2.16    bit_4.0.4         munsell_0.5.0
## [21] shiny_1.7.1       httpuv_1.6.5      compiler_4.2.0    modelr_0.1.8
## [25] xfun_0.33         pkgconfig_2.0.3   htmltools_0.5.3   tidyselect_1.1.2
## [29] gridExtra_2.3     bookdown_0.29     fansi_1.0.3       later_1.3.0
```

```
## [33] crayon_1.5.1     tzdb_0.3.0      dbplyr_2.2.0     withr_2.5.0
## [37] grid_4.2.0       xtable_1.8-4    jsonlite_1.8.0   gtable_0.3.1
## [41] lifecycle_1.0.2  DBI_1.1.2       magrittr_2.0.3   scales_1.2.1
## [45] cli_3.4.1        stringi_1.7.8   vroom_1.5.7      renv_0.15.5
## [49] promises_1.2.0.1 fs_1.5.2        xml2_1.3.3       ellipsis_0.3.2
## [53] generics_0.1.3   vctrs_0.4.1     tools_4.2.0      bit64_4.0.5
## [57] glue_1.6.2       hms_1.1.2       parallel_4.2.0   fastmap_1.1.0
## [61] yaml_2.3.5       colorspace_2.0-3 rvest_1.0.2     knitr_1.40
## [65] haven_2.5.0
```

Age group definitions:

Age category	Age range
1	$0 - 19$
2	$20 - 29$
3	$30 - 39$
4	$40 - 49$
5	$50 - 59$
6	$60 - 69$
7	$70 - 79$
8	$80 - 89$

1 Summary statistics

1.1 Age-at-death within the sample

```
# Age
  # descriptive statistics for whole sample
age_summ_tot <- region_means_all %>%
  filter(region == "all",
         method == "snodgrass") %>%
  count(id, known_age) %>%
  summarise(n = n(),
            mean = mean(known_age, na.rm = T),
            sd = sd(known_age, na.rm = T),
            range = paste(range(known_age, na.rm = T), collapse = "--")) %>%
  mutate(sex = "Both", .before = mean)
  # descriptive statistics by age category and sex
age_group_summ <- region_means_all %>%
  group_by(age_group, sex) %>%
  count(id, known_age) %>%
  summarise(n = n(),
            mean = mean(known_age, na.rm = T), # mean age within each age cat
            sd = sd(known_age, na.rm = T))

age_sex_summ <- region_means_all %>%
  group_by(sex) %>%
  count(id, known_age) %>%
  summarise(n = n(),
            mean = mean(known_age, na.rm = T),
            sd = sd(known_age, na.rm = T),
            range = paste(range(known_age, na.rm = T), collapse = "--")) %>%
  add_row(age_summ_tot)
```

Table 2: Summary statistics for age-at-death.

sex	n	mean	sd	range
F	48	46.89583	17.51017	20–80
M	40	52.27500	21.02012	19–84
Both	88	49.34091	19.26040	19–84

Table 3: Summary statistics for grouped ages-at-death.

age__group	sex	n	mean	sd
1	M	1	19.00000	NA
2	F	12	25.50000	3.554766
2	M	7	23.14286	2.410295
3	F	6	32.33333	3.444803
3	M	6	34.33333	3.141125
4	F	8	45.75000	2.434866
4	M	3	44.33333	2.081666
5	F	10	54.90000	2.685351
5	M	6	56.66667	1.751190
6	F	7	65.00000	2.828427
6	M	6	63.83333	3.868678
7	F	4	75.25000	3.403430
7	M	7	74.28571	2.138090
8	F	1	80.00000	NA
8	M	4	82.00000	1.825742

```
females <- age_sex_summ %>%
  filter(sex == "F")
males <- age_sex_summ %>%
  filter(sex == "M")
```

The age distribution between males and females is very similar in mean and shape. The mean age of males is 52.3 ± 21, with a range of 19–84. The mean age of females is 46.9 ± 17.5, with a range of 20–80.

```
raw_data %>%
  filter(vertebral_position == "Superior") %>%
  ggplot(aes(x = known_age, fill = sex)) +
    geom_density(alpha = 0.5) +
    scale_fill_viridis_d() +
  theme_bw()
```

1.2 Osteophyte scores

A comparison of osteophyte scores between methods.

```
region_means_all %>%
  ggplot(aes(x = sex, y = region_mean, fill = sex)) +
    geom_violin(alpha = 0.8) +
    geom_boxplot(width = 0.2, fill = "white") +
    facet_wrap(~ method + region) +
    coord_flip() +
    scale_fill_viridis_d() +
```
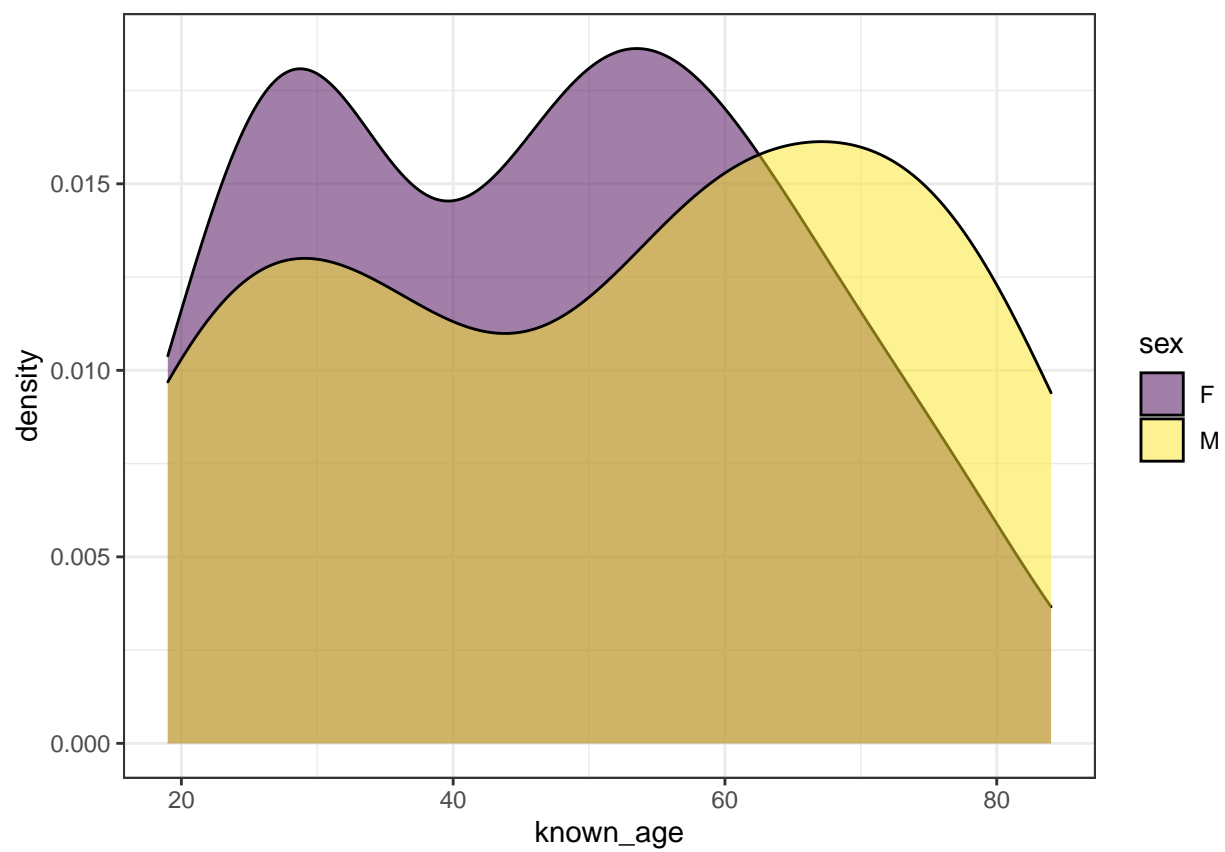
Figure 1: Age distribution for each sex. F = Female, M = Male.

```
  theme_bw() +
  theme(legend.position = "none")
```
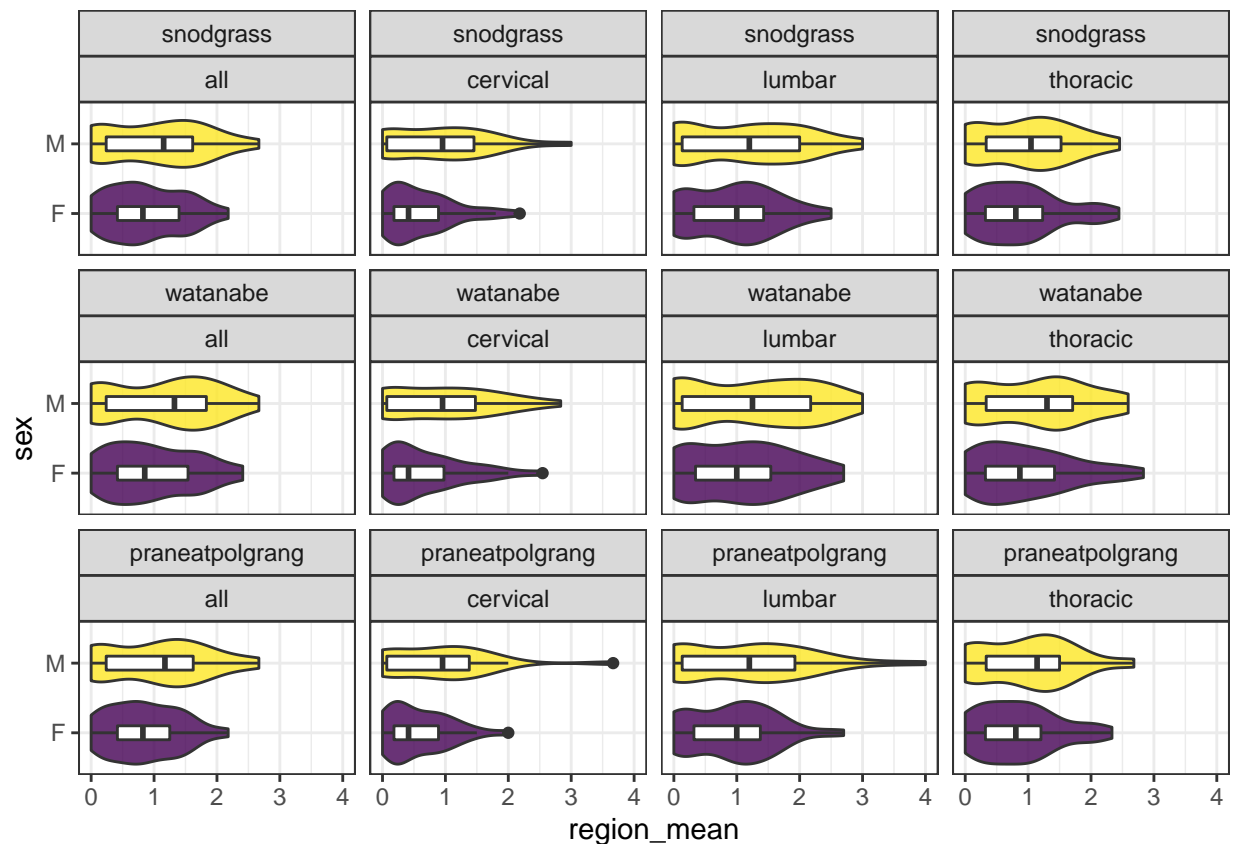

Figure 2: Comparing osteophyte scores between sex, separated by region and method.

2 Correlation tests

```
cor_test <- region_means_all %>%
  filter(region == "all", sex == "F", method == "snodgrass") %>%
  dplyr::select(region_mean, known_age)
cor_f <- cor.test(cor_test$region_mean, cor_test$known_age) %>%
  tidy()

cor_test <- region_means_all %>%
  filter(region == "all", sex == "M", method == "snodgrass") %>%
  dplyr::select(region_mean, known_age)
cor_m <- cor.test(cor_test$region_mean, cor_test$known_age) %>%
  tidy()

cor_f %>%
  bind_rows(cor_m) %>%
  mutate(sex = c("F", "M"), .before = 1) %>%
  knitr::kable(caption = "Pearson correlation coefficients for Snodgrass osteophyte score for combined r
```

Table 4: Pearson correlation coefficients for Snodgrass osteophyte score for combined regions, and age-at-death. Separated by Sex.

sex	estimate	statistic	p.value	parameter	conf.low	conf.high	method	alt
F	0.7176649	6.989546	0	46	0.5445767	0.8321192	Pearson's product-moment correlation	tw
M	0.8664245	10.696801	0	38	0.7600529	0.9275805	Pearson's product-moment correlation	tw

Males (0.8664245) have a higher correlation between osteophyte score and age than females (0.7176649). Both have strong correlations.

3   Weighted least squares regression

Models were built using weights estimated with a standard deviation function regressing the absolute values of the residuals on the predictor, i.e. known age. The weights were then calculated as the inverse of the squared standard deviation function.

$$w_i = \frac{1}{\sigma_i^2}$$

```
# Code to generate wls regression lines for facet plot
reg_plots <- region_means_all %>%
  #group_by(feat, known_age, sex, region, method) %>%
  #summarise(region_mean = mean(score, na.rm = T)) %>%
  ggplot(aes(x = region_mean, known_age)) +
    geom_point(aes(col = sex)) +
    scale_color_viridis_d(name = "Sex") +
    facet_wrap(~ method + region) +
    theme_bw() +
    labs(x = "Mean Osteophyte Score", y = "Age-at-Death")

# Insert coefficients into table
snodgrass_coefs <- lapply(snodgrass_wls, coef) %>%
  unlist() %>%
  matrix(byrow = T, nrow = 4, ncol = 2)
watanabe_coefs <- lapply(watanabe_wls, coef) %>%
  unlist() %>%
  matrix(byrow = T, nrow = 4, ncol = 2)
praneatpolgrang_coefs <- lapply(praneatpolgrang_wls, coef) %>%
  unlist() %>%
  matrix(byrow = T, nrow = 4, ncol = 2)
all_coefs <- rbind(praneatpolgrang_coefs, snodgrass_coefs, watanabe_coefs)
# Create data frame to pass to geom_abline
reg_coefs <- data.frame("method" = c(rep("praneatpolgrang", 4),
                                     rep("snodgrass", 4),
                                     rep("watanabe", 4)),
                        "region" = rep(c("all", "cervical", "lumbar", "thoracic")),
                        "slope" = all_coefs[,1],
                        "intercept" = all_coefs[,2])
reg_plots +
    geom_abline(aes(slope = slope, intercept = intercept), reg_coefs)
```
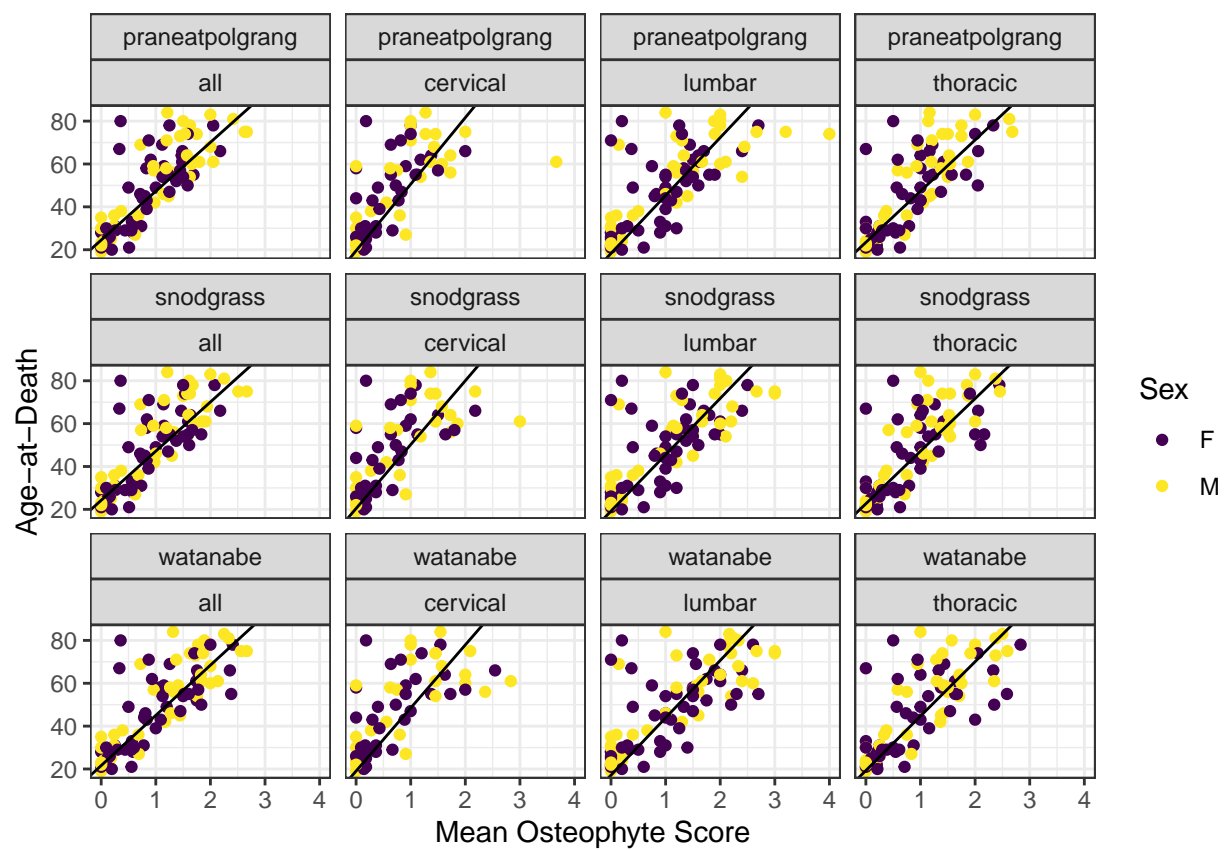
Figure 3: Regression plots for all regions and methods. F = Female, M = Male.

```
ggsave(here("fig_output", "wls_plots.jpg"),
       dpi = 600, height = 6, width = 7.5, units = "in")
```

3.1 Snodgrass

```
lapply(snodgrass_wls, extract_eq, use_coefs = T)
```

$all

$$\widehat{known\_age} = 22.93 + 24.22(\text{region\_mean}) \tag{1}$$

$cervical

$$\widehat{known\_age} = 29.81 + 20.4(\text{region\_mean}) \tag{2}$$

$lumbar

$$\widehat{known\_age} = 26.3 + 19.17(\text{region\_mean}) \tag{3}$$

$thoracic

$$\widehat{known\_age} = 24.53 + 22.62(\text{region\_mean}) \tag{4}$$

3.2 Watanabe et al.

```
lapply(watanabe_wls, extract_eq, use_coefs = T)
```

$all

$$\widehat{known\_age} = 23.41 + 21.6(\text{region\_mean}) \tag{5}$$

$cervical

$$\widehat{known\_age} = 29.43 + 19.04(\text{region\_mean}) \tag{6}$$

$lumbar

$$\widehat{known\_age} = 26.77 + 17.1(\text{region\_mean}) \tag{7}$$

$thoracic

$$\widehat{known\_age} = 25.39 + 19.29(\text{region\_mean}) \tag{8}$$

3.3 Praneatpolgrang et al.

```
lapply(praneatpolgrang_wls, extract_eq, use_coefs = T)
```

$all

$$\widehat{known\_age} = 22.8 + 24.5(\text{region\_mean}) \tag{9}$$

$cervical

Table 5: Evaluation of combined regions models.

method	R2	SEE	RMSE	AIC	accuracy	accuracy_5	accuracy_10	accuracy_15
snodgrass	0.7408885	11.98932	11.85230	655.3249	73.86364	43.18182	70.45455	86.36364
watanabe	0.7383007	11.88823	11.75236	656.2994	76.13636	45.45455	71.59091	86.36364
praneatpolgrang	0.7432913	12.03182	11.89431	654.4726	72.72727	45.45455	69.31818	87.50000

Table 6: Evaluation of cervical region models.

R2	SEE	RMSE	AIC	accuracy	accuracy_5	accuracy_10	accuracy_15	method
0.4946757	15.24596	14.99805	503.7397	67.74194	27.41935	54.83871	75.80645	snodgrass
0.5087869	15.26382	15.01561	501.8177	66.12903	27.41935	53.22581	72.58065	watanabe
0.4540794	15.59793	15.34429	508.7065	69.35484	32.25806	54.83871	75.80645	praneatpolgrang

$$\widehat{known\_age} = 31.05 + 19.54(region\_mean) \tag{10}$$

$lumbar

$$\widehat{known\_age} = 27.02 + 18.27(region\_mean) \tag{11}$$

$thoracic

$$\widehat{known\_age} = 23.87 + 23.47(region\_mean) \tag{12}$$

3.4 Model evaluation

Models from each of the three methods (Snodgrass, Watanabe et al., and Praneatpolgrang et al.) and four regions (combined, cervical, thoracic, and lumbar) were evaluated using R^2, standard error of the estimate (SEE), AIC, and accuracy. Accuracy is calculated as the total number of prediction intervals that contain the known age, and total number of estimates that are within 5, 10, and 15 years of the known age.

```
all_eval_tbl %>%
  relocate(method, .before = 1) %>%
  knitr::kable(caption = "Evaluation of combined regions models.")

knitr::kable(cerv_eval_tbl, caption = "Evaluation of cervical region models.")

knitr::kable(thor_eval_tbl, caption = "Evaluation of thoracic region models.")

knitr::kable(lumb_eval_tbl, caption = "Evaluation of lumbar region models.")
```

3.4.1 Diagnostic plots for the combined regions

Snodgrass

Table 7: Evaluation of thoracic region models.

R2	SEE	RMSE	AIC	accuracy	accuracy_5	accuracy_10	accuracy_15	method
0.6373824	13.54765	13.37507	615.8977	72.15190	37.97468	67.08861	79.74684	snodgrass
0.6161718	13.76330	13.58797	620.5676	72.15190	39.24051	69.62025	78.48101	watanabe
0.6636872	13.12377	12.95659	609.7794	70.88608	39.24051	67.08861	82.27848	praneatpolgrang

Table 8: Evaluation of lumbar region models.

| R2	SEE	RMSE	AIC	accuracy	accuracy_5	accuracy_10	accuracy_15	method
0.6305082	13.79961	13.63820	673.3420	79.06977	38.37209	69.76744	80.23256	snodgrass
0.6207949	13.80715	13.64565	675.5420	77.90698	39.53488	67.44186	80.23256	watanabe
0.6057519	14.30967	14.14230	678.9124	73.25581	39.53488	67.44186	77.90698	praneatpolgrang

```
autoplot(snodgrass_wls$all)
```
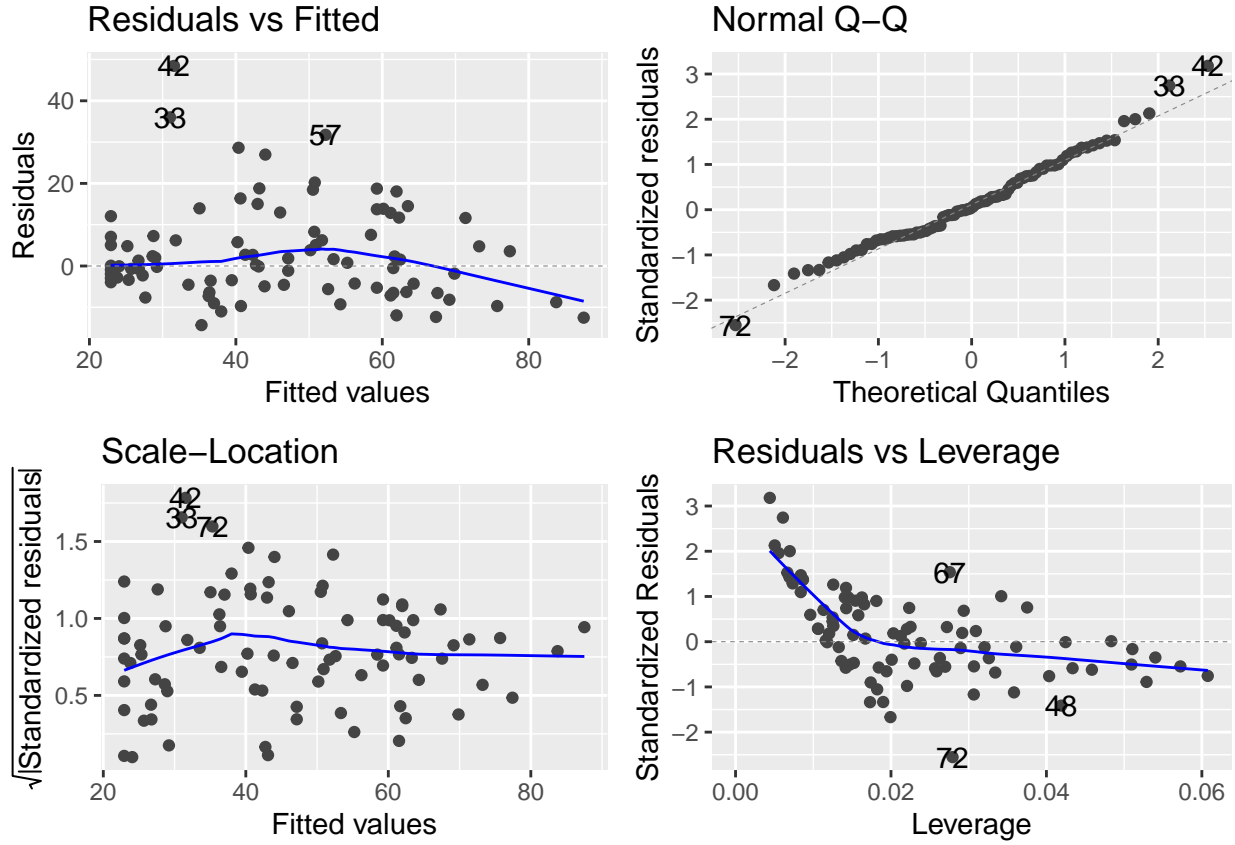

Watanabe

```
autoplot(watanabe_wls$all)
```
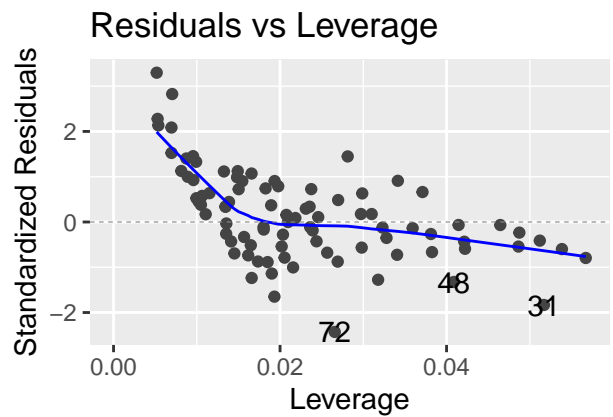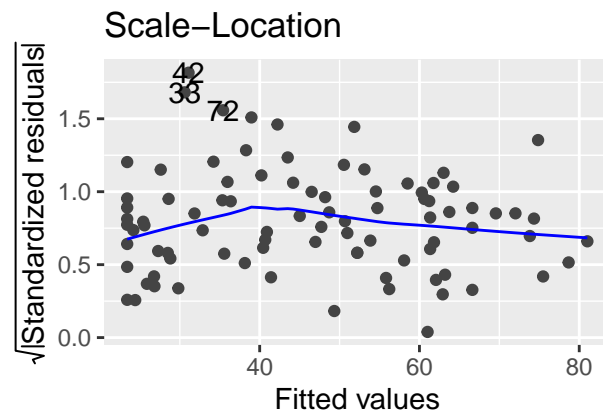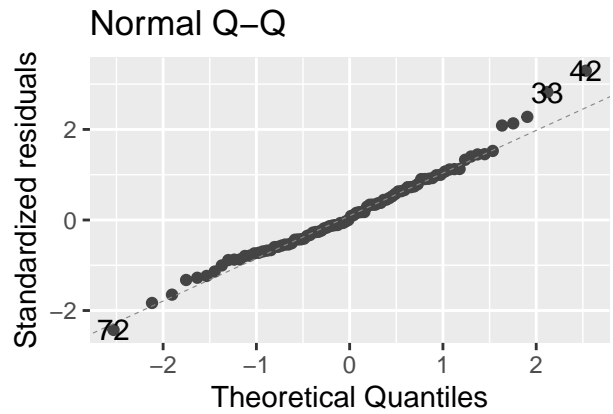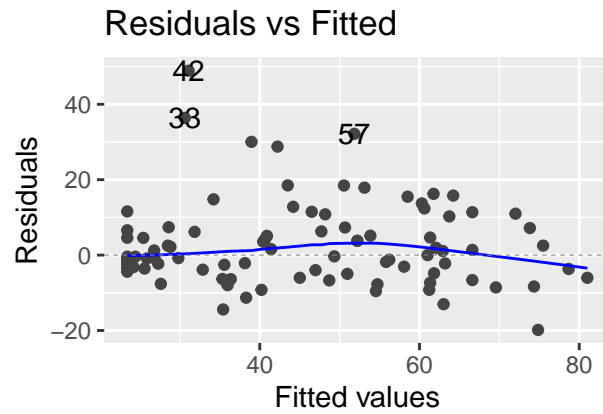
Praneatpolgrang

```
autoplot(praneatpolgrang_wls$all)
```
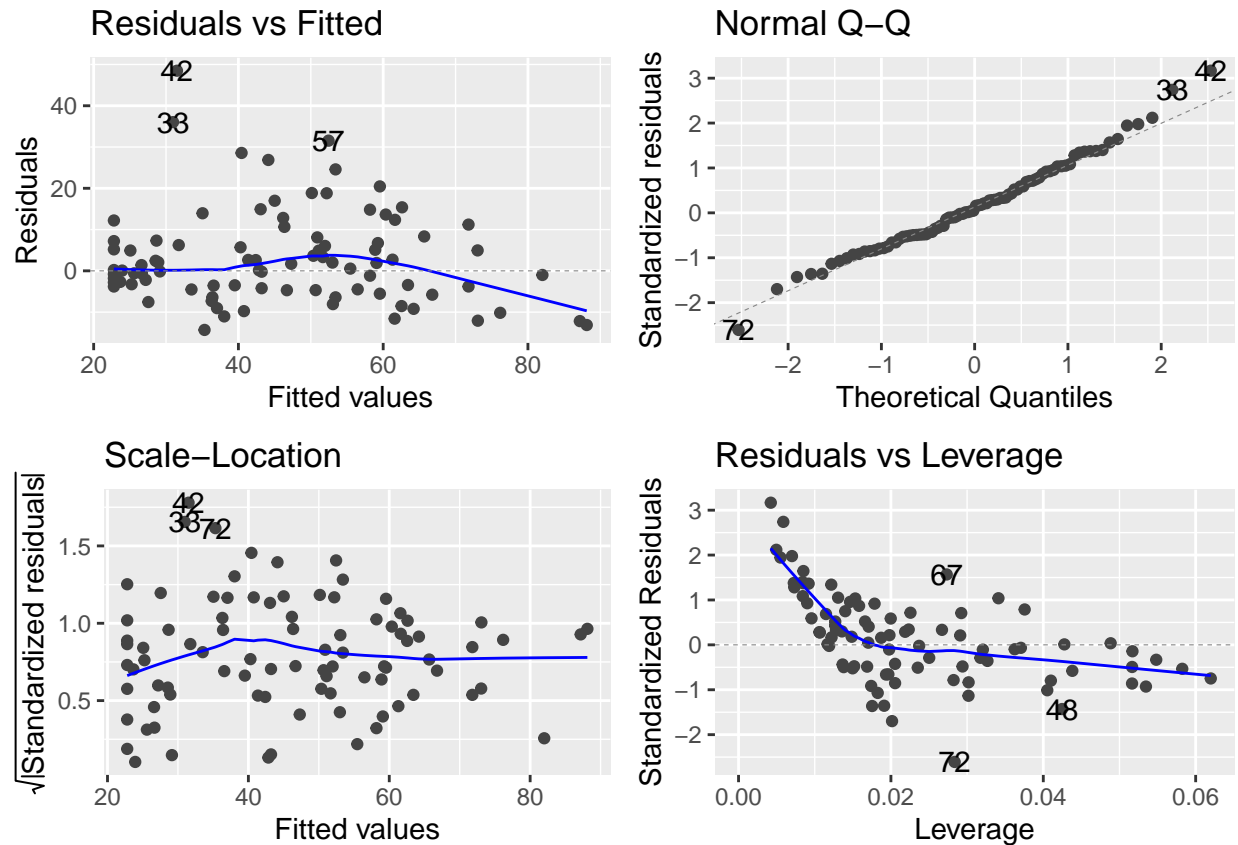
4 Biases

Does the number of elements present influence accuracy?

Graphs show the number of elements and the absolute value of the residuals for the Snodgrass method, to see if there is any relationship between the number of elements scored and the accuracy of the age estimate.

```
n_elements <- element_data_long %>%
  group_by(id,method,region) %>%
  summarise(n = sum(!is.na(score))) %>%
  ungroup()

n_elements_all <- n_elements %>%
  group_by(id, method) %>%
  summarise(n = sum(n)) %>%
  mutate(region = "all") %>%
  ungroup()

n_all_snodgrass <- n_elements_all %>%
  filter(method == "snodgrass") %>%
  mutate(residual = snodgrass_all_res$residual,
         age = snodgrass_all_res$known_age,
         sex = snodgrass_all_res$sex)

n_all_snodgrass %>%
  ggplot(aes(x = n, y = abs(residual))) +
```

```
    geom_point(aes(col = sex)) +
    geom_smooth(method = "lm", se = F, col = "black", size = 0.5) +
    scale_color_viridis_d() +
    theme_minimal()
```
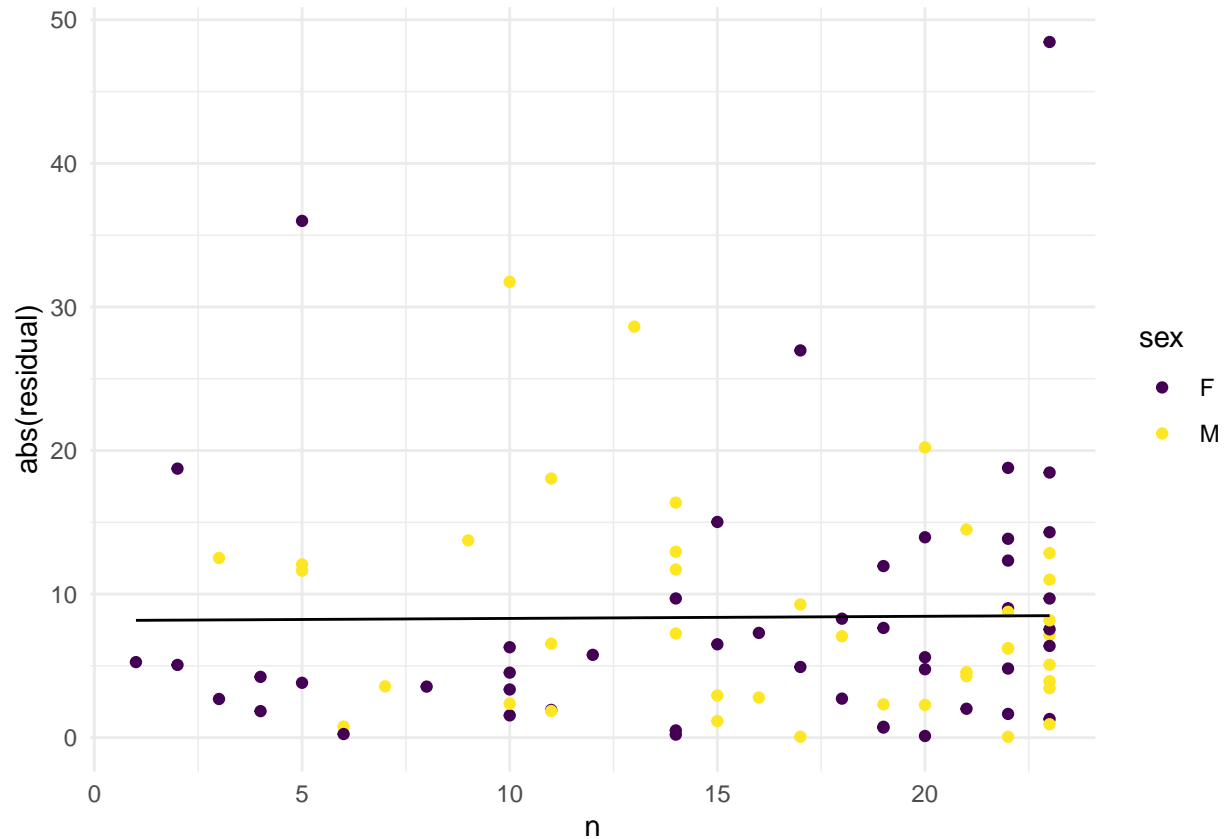

Figure 4: Number of elements (n) plotted against the absolute value of the residuals for Snodgrass method, combined regions.

The graph shows that there is no apparent relationship between the number of elements scored and the accuracy of the age, meaning there is no theoretical minimum number of elements that needs to be scored; however, I would recommend that at least 3 elements are scored (preferably more) to obtain reliable results.

```
n_elements <- element_data_long %>%
  group_by(id,method,region) %>%
  summarise(n = sum(!is.na(score))) %>%
  ungroup()

n_elements_cerv <- n_elements %>%
  filter(region == "cervical") %>%
  group_by(id, method) %>%
  summarise(n = sum(n)) %>%
  #mutate(region = "cervical") %>%
  ungroup()

n_cerv_snodgrass <- n_elements_cerv %>%
  filter(method == "snodgrass", n != 0) %>%
```

```
  mutate(residual = snodgrass_cerv_res$residual,
         age = snodgrass_cerv_res$known_age,
         sex = snodgrass_cerv_res$sex)

n_cerv_snodgrass %>%
  ggplot(aes(x = n, y = abs(residual))) +
    geom_point(aes(col = sex)) +
    geom_smooth(method = "lm", se = F, col = "black", size = 0.5) +
    scale_color_viridis_d() +
    theme_minimal()
```
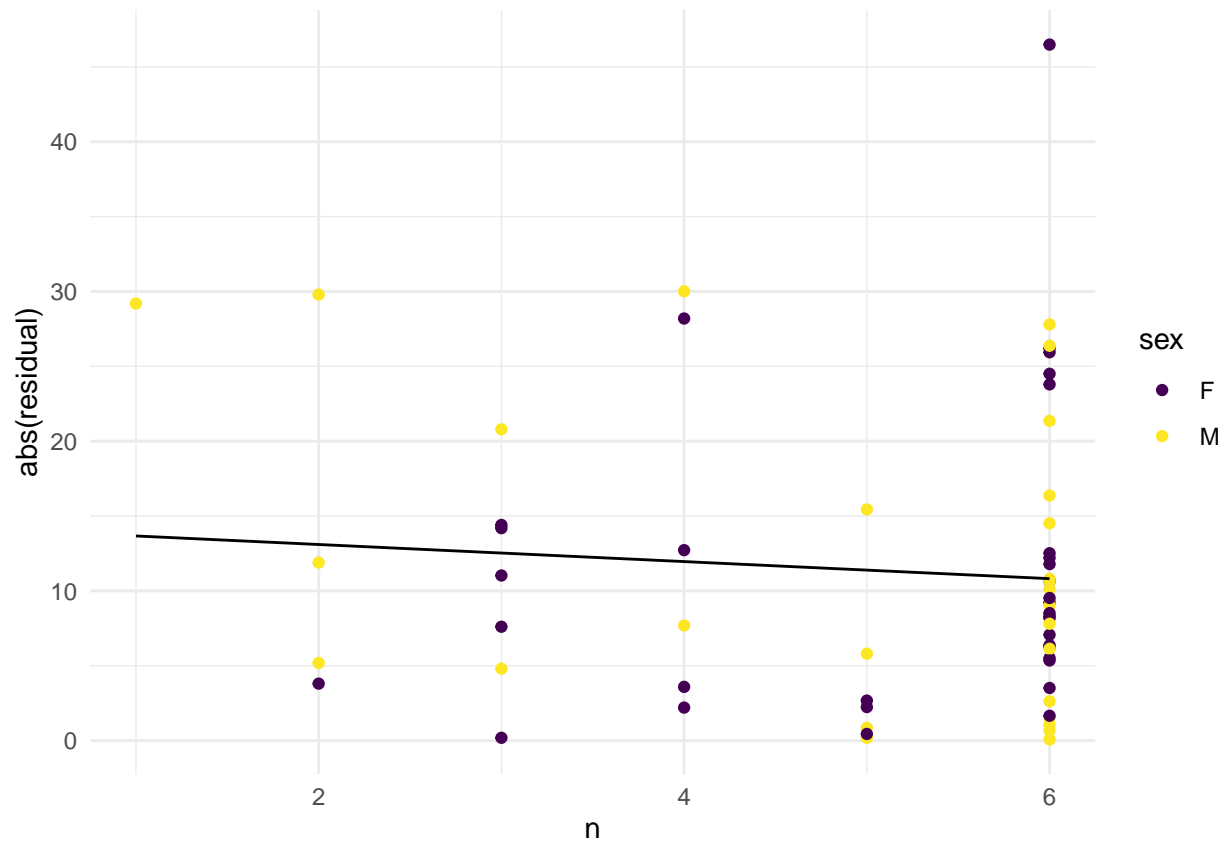

Figure 5: Number of elements (n) plotted against the absolute value of the residuals for Snodgrass method, cervical region.

```
n_elements <- element_data_long %>%
  group_by(id,method,region) %>%
  summarise(n = sum(!is.na(score))) %>%
  ungroup()

n_elements_thor <- n_elements %>%
  filter(region == "thoracic") %>%
  group_by(id, method) %>%
  summarise(n = sum(n)) %>%
  #mutate(region = "thoracic") %>%
  ungroup()
```

```
n_thor_snodgrass <- n_elements_thor %>%
  filter(method == "snodgrass", n != 0) %>%
  mutate(residual = snodgrass_thor_res$residual,
         age = snodgrass_thor_res$known_age,
         sex = snodgrass_thor_res$sex)

n_thor_snodgrass %>%
  ggplot(aes(x = n, y = abs(residual))) +
    geom_point(aes(col = sex)) +
    geom_smooth(method = "lm", se = F, col = "black", size = 0.5) +
    scale_color_viridis_d() +
    theme_minimal()
```
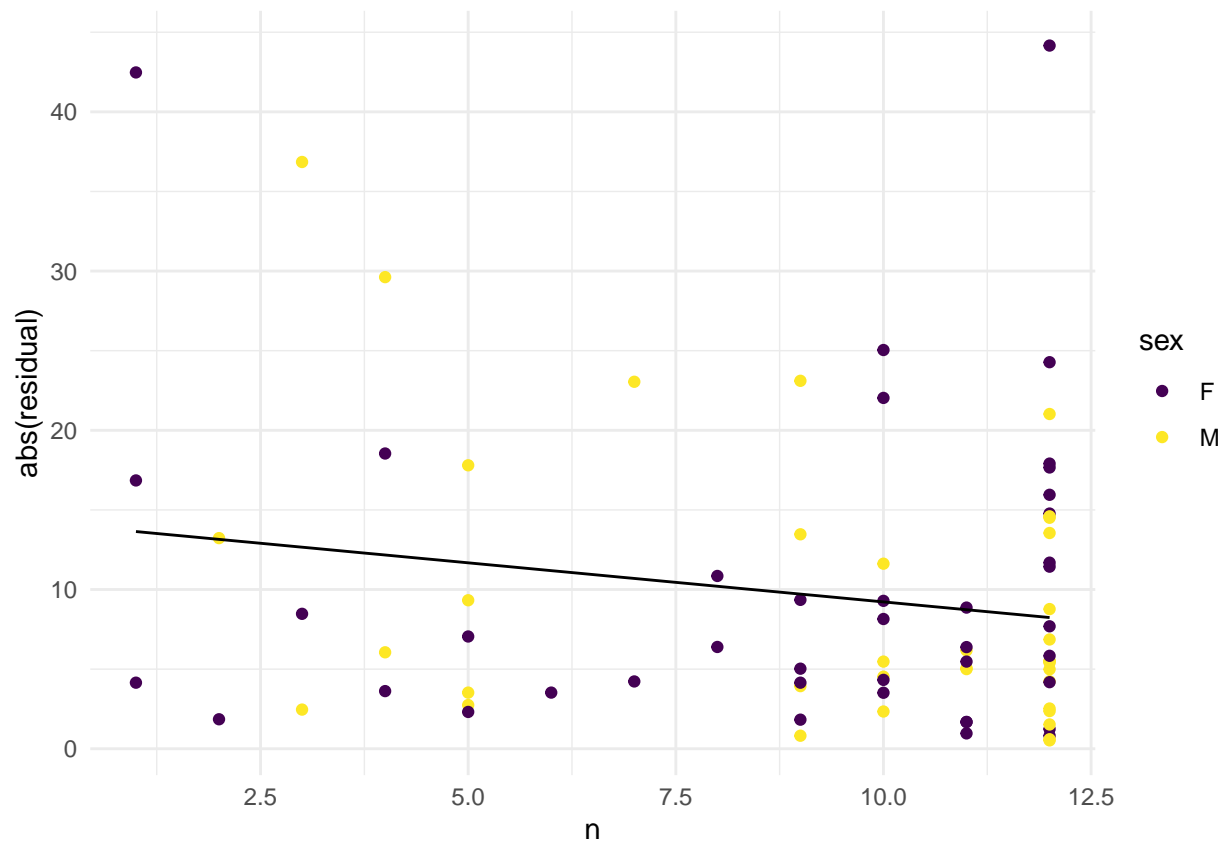

Figure 6: Number of elements (n) plotted against the absolute value of the residuals for Snodgrass method, thoracic region.

```
n_elements <- element_data_long %>%
  group_by(id,method,region) %>%
  summarise(n = sum(!is.na(score))) %>%
  ungroup()

n_elements_lumb <- n_elements %>%
  filter(region == "lumbar") %>%
  group_by(id, method) %>%
  summarise(n = sum(n)) %>%
```

```
  #mutate(region = "lumbar") %>%
  ungroup()

n_lumb_snodgrass <- n_elements_lumb %>%
  filter(method == "snodgrass", n != 0) %>%
  mutate(residual = snodgrass_lumb_res$residual,
         age = snodgrass_lumb_res$known_age,
         sex = snodgrass_lumb_res$sex)

n_lumb_snodgrass %>%
  ggplot(aes(x = n, y = abs(residual))) +
    geom_point(aes(col = sex)) +
    geom_smooth(method = "lm", se = F, col = "black", size = 0.5) +
    scale_color_viridis_d() +
    theme_minimal()
```
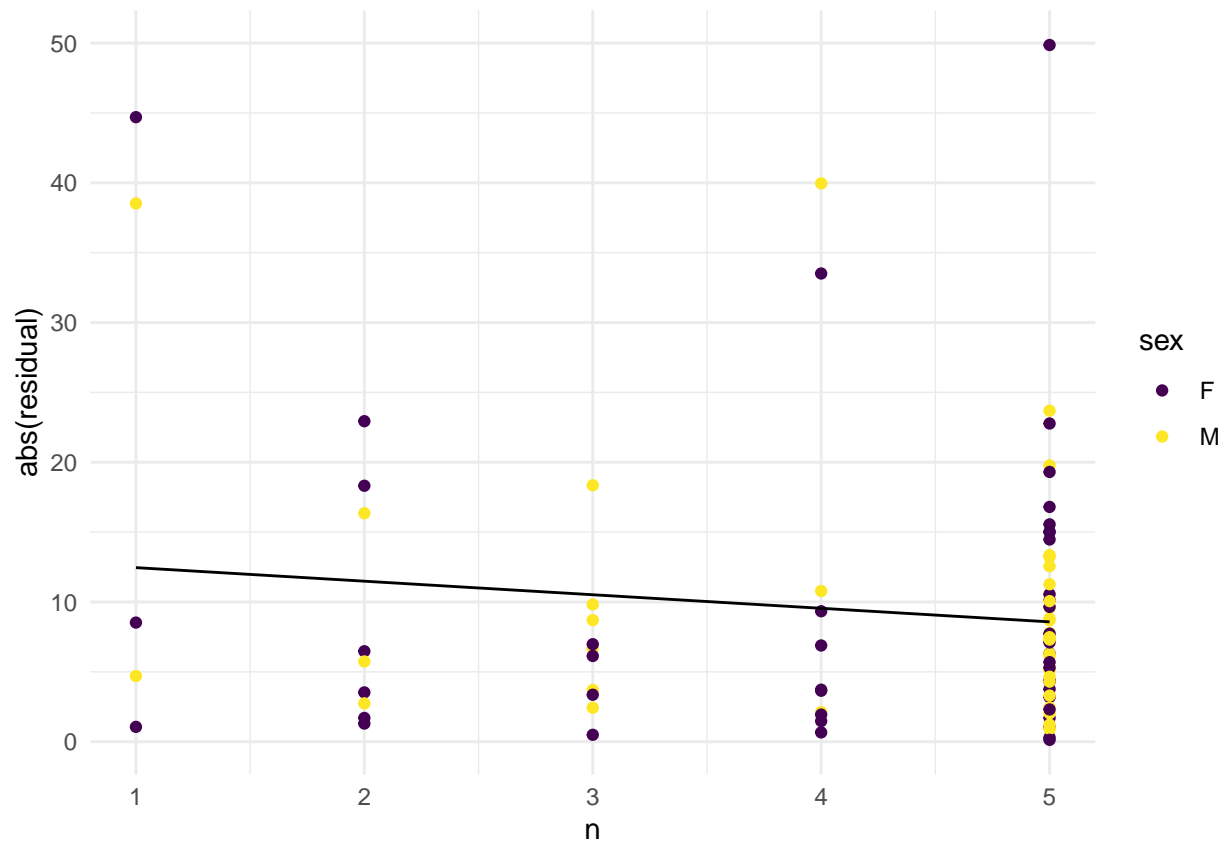

Figure 7: Number of elements (n) plotted against the absolute value of the residuals for Snodgrass method, lumbar region.

4.1 Age bias

```
data.frame(
  "known_age" = sep_regions$snodgrass$all$known_age,
  "residuals" = snodgrass_wls$all$residuals,
```

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```
  "sex" = sep_regions$snodgrass$all$sex) %>%
ggplot(aes(x = known_age, y = residuals, col = sex)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  theme_bw() +
  labs(y = "Residuals", x = "Age-at-Death") +
  scale_colour_viridis_d(name = "Sex")
```
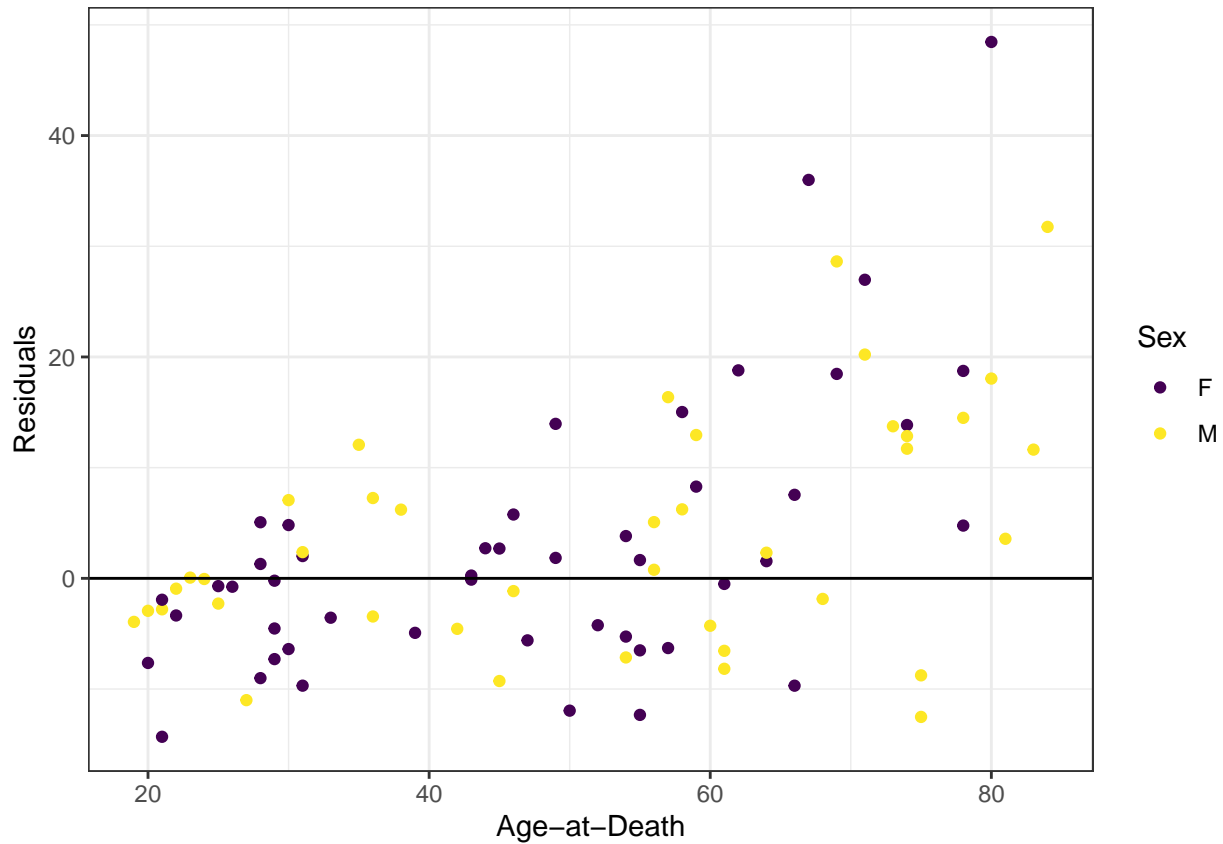

Figure 8: Residuals for Snodgrass method, combined regions, plotted against known age-at-death.

```
data.frame(
  "known_age" = na.omit(sep_regions$snodgrass$cervical)$known_age,
  "residuals" = snodgrass_wls$cervical$residuals) %>%
ggplot(aes(x = known_age, y = residuals)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  theme_minimal()
```

```
data.frame(
  "known_age" = na.omit(sep_regions$snodgrass$thoracic)$known_age,
  "residuals" = snodgrass_wls$thoracic$residuals) %>%
ggplot(aes(x = known_age, y = residuals)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  theme_minimal()
```
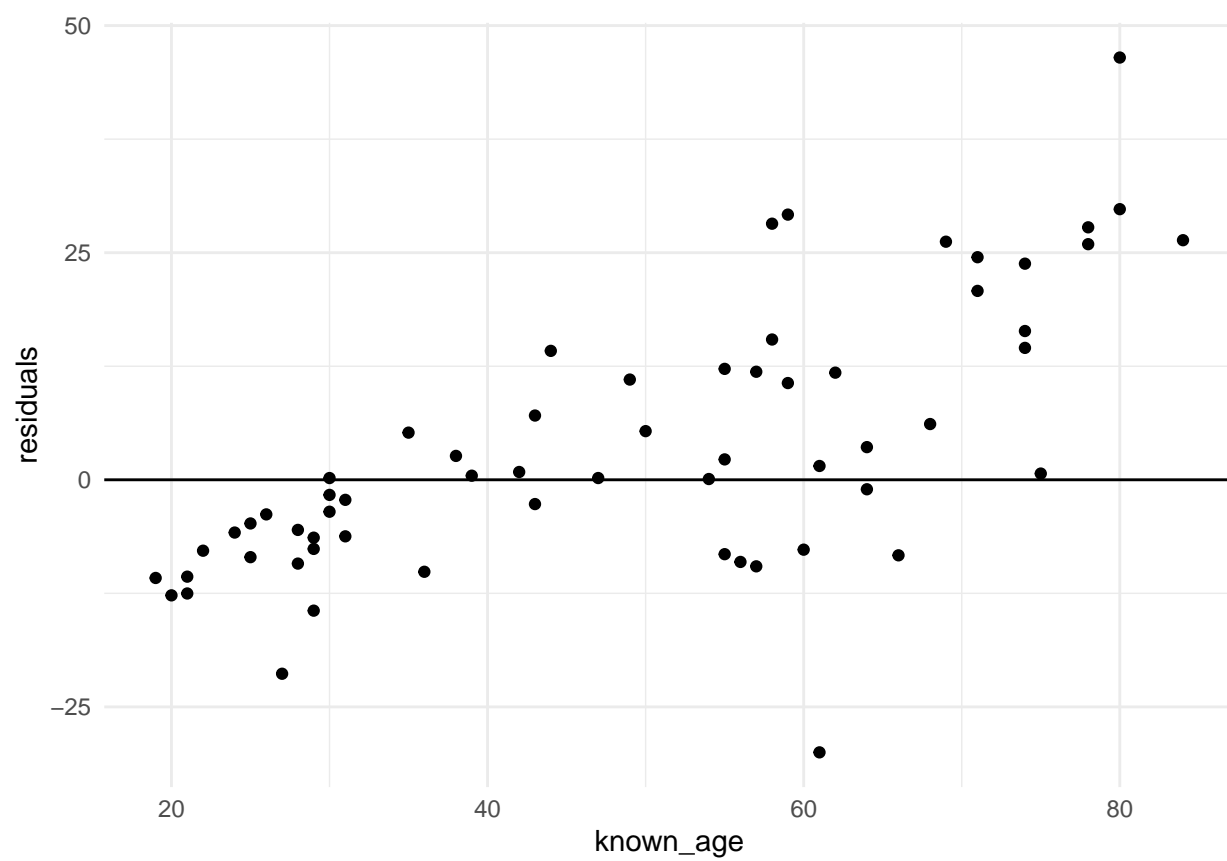
Figure 9: Residuals for Snodgrass method, cervical region, plotted against known age-at-death.
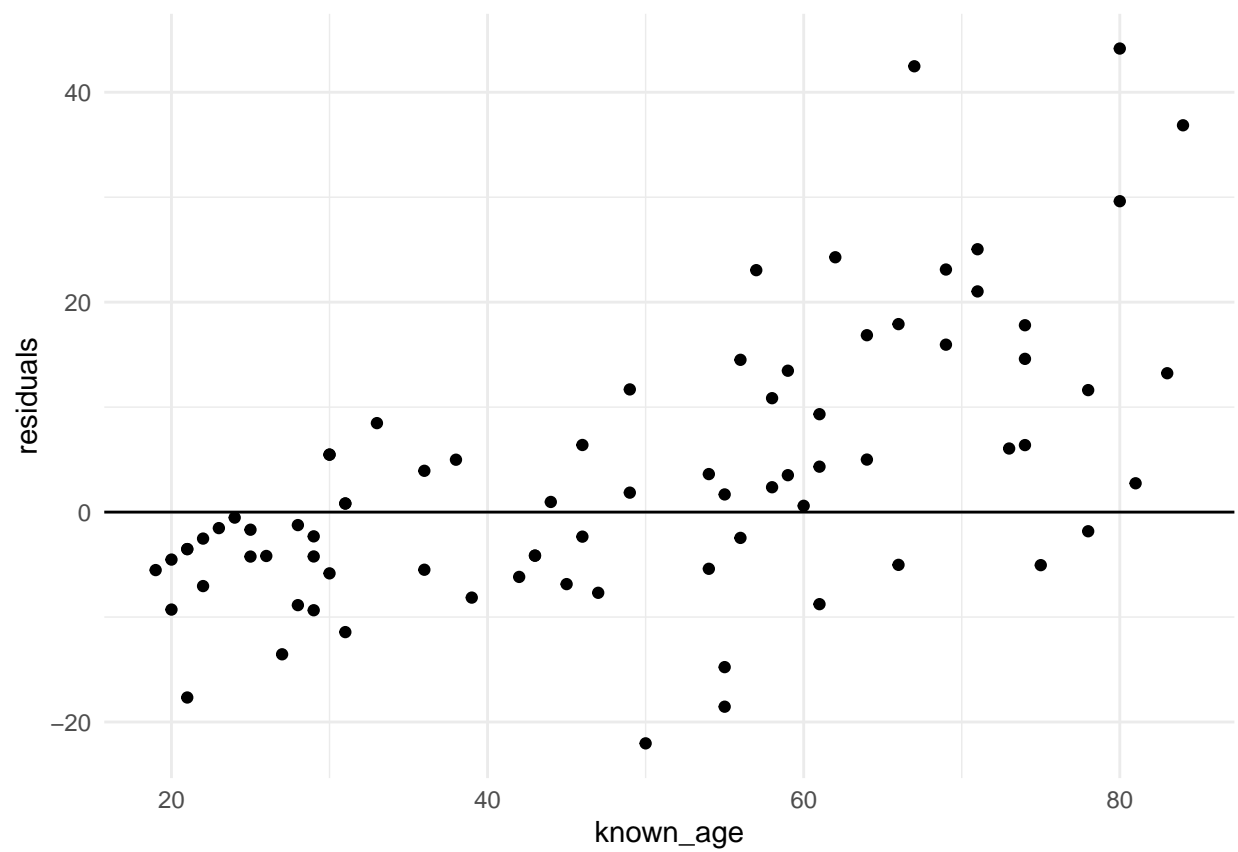
Figure 10: Residuals for Snodgrass method, thoracic region, plotted against known age-at-death.

```
data.frame(
  "known_age" = na.omit(sep_regions$snodgrass$lumbar)$known_age,
  "residuals" = snodgrass_wls$lumbar$residuals) %>%
ggplot(aes(x = known_age, y = residuals)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  theme_minimal()
```
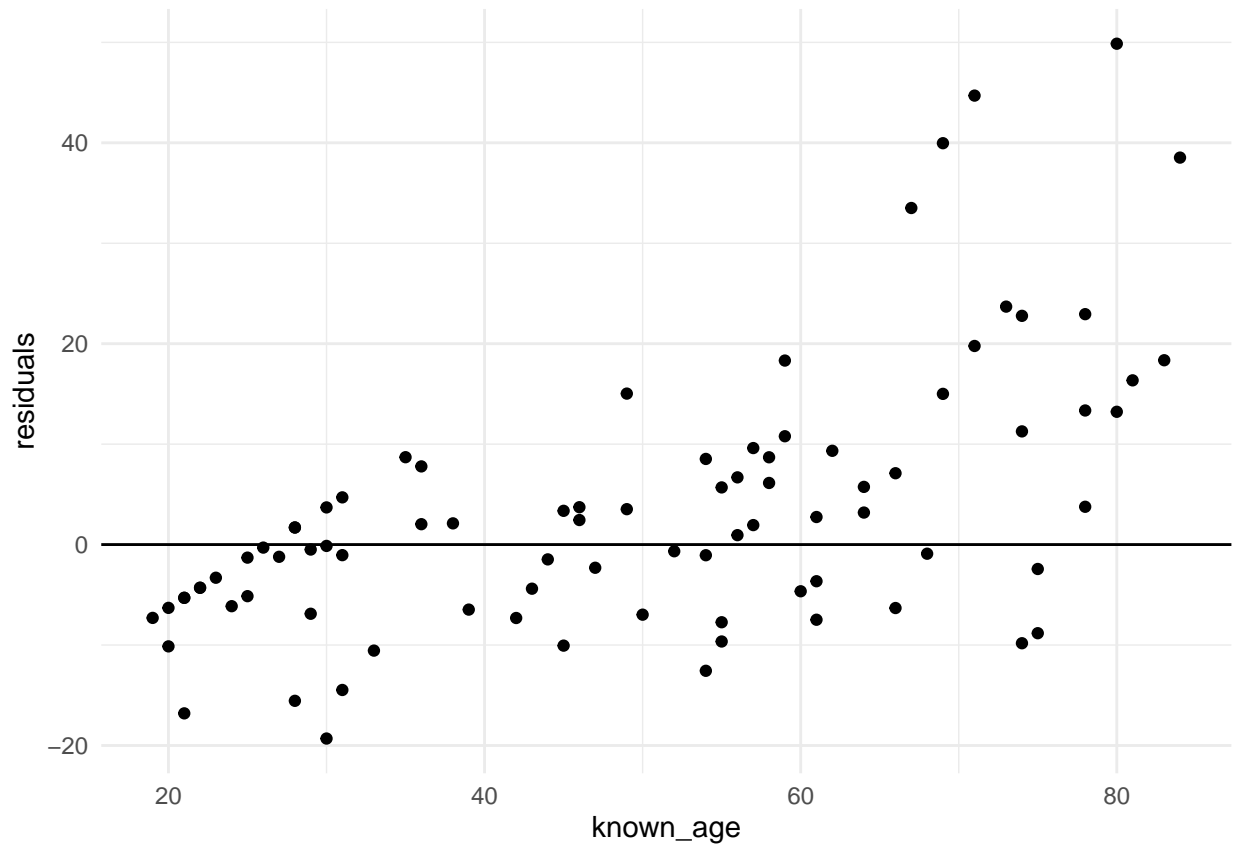

Figure 11: Residuals for Snodgrass method, lumbar region, plotted against known age-at-death.

```
data.frame(
  "known_age" = sep_regions$watanabe$all$known_age,
  "residuals" = watanabe_wls$all$residuals,
  "sex" = sep_regions$watanabe$all$sex) %>%
ggplot(aes(x = known_age, y = residuals, col = sex)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  theme_bw() +
  labs(y = "Residuals", x = "Age-at-Death") +
  scale_colour_viridis_d(name = "Sex")
```

```
data.frame(
  "known_age" = sep_regions$praneatpolgrang$all$known_age,
  "residuals" = praneatpolgrang_wls$all$residuals,
  "sex" = sep_regions$praneatpolgrang$all$sex) %>%
ggplot(aes(x = known_age, y = residuals, col = sex)) +
```
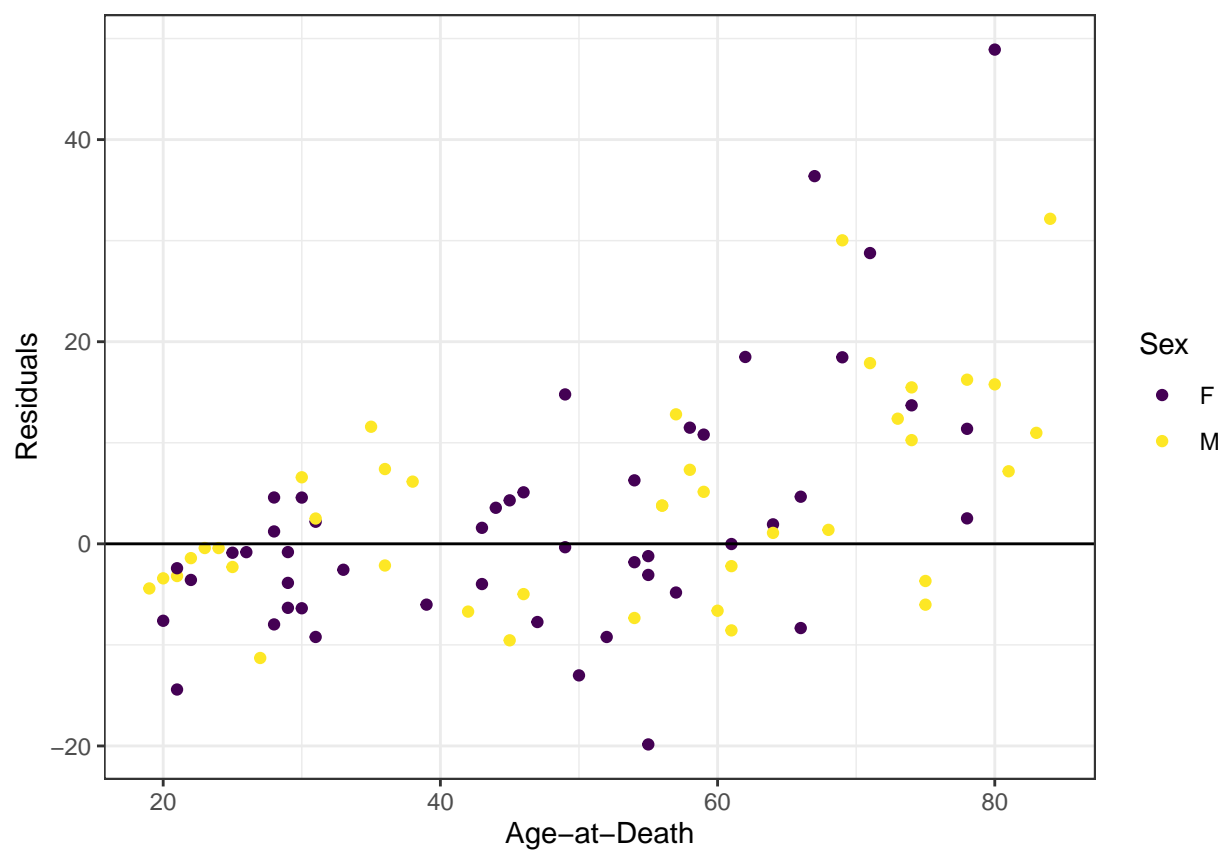
Figure 12: (#fig:watanabe-all-res,)Residuals for Watanabe method, combined regions, plotted against known age-at-death.

```
  geom_point() +
  geom_hline(yintercept = 0) +
  theme_bw() +
  labs(y = "Residuals", x = "Age-at-Death") +
  scale_colour_viridis_d(name = "Sex")
```
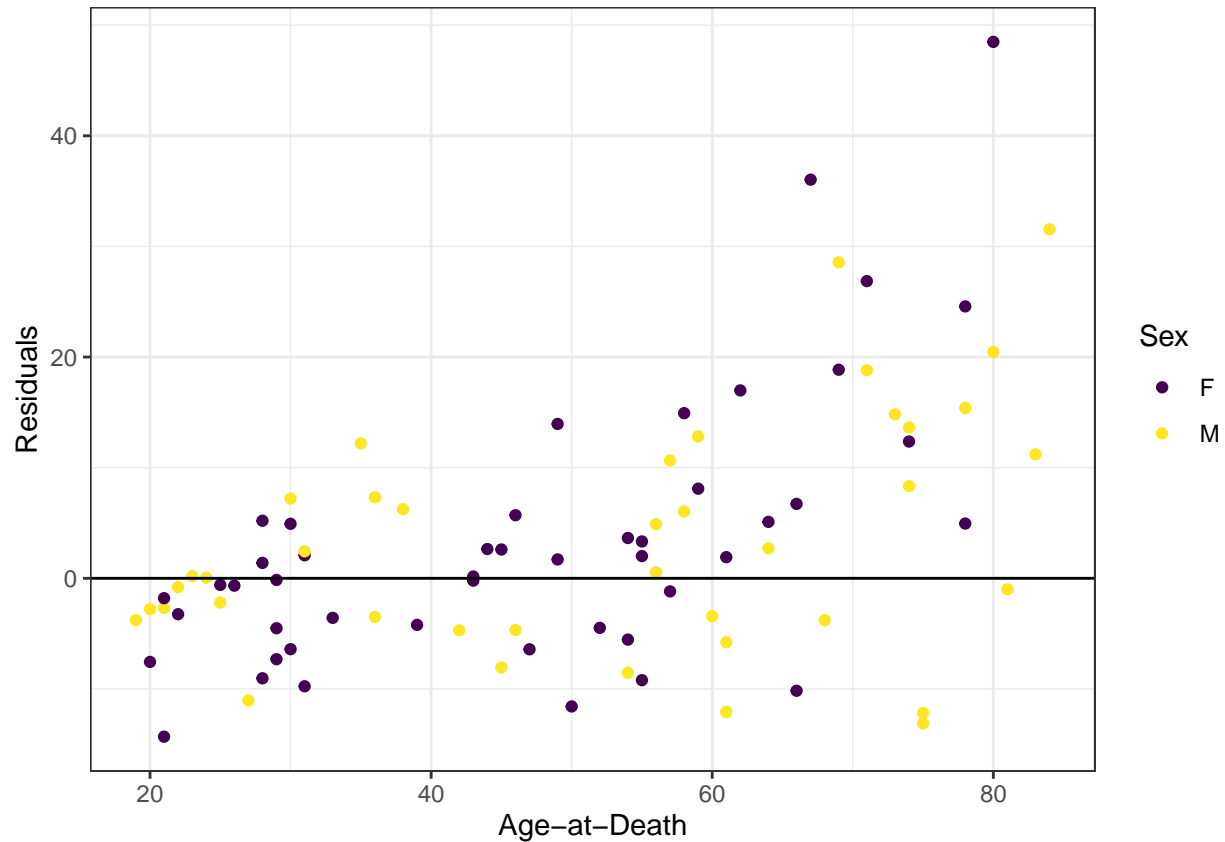

Figure 13: Residuals for Praneatpolgrang method, combined regions, plotted against known age-at-death.

What is the accuracy and average residuals (not squared or absolute) per age category?

```
snodgrass_all_bias <- snodgrass_all_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            bias_snodgrass = mean(residual))

watanabe_all_bias <- watanabe_all_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            bias_watanabe = mean(residual))

praneatpolgrang_all_bias <- praneatpolgrang_all_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            bias_praneat = mean(residual))

all_bias <- list(snodgrass_all_bias, watanabe_all_bias, praneatpolgrang_all_bias)
```

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Table 9: Prediction bias by age for combined regions

age_group	n	bias_snodgrass	bias_watanabe	bias_praneat
1	1	-3.9329403	-4.4137666	-3.7969539
2	19	-3.3326893	-3.4383567	-3.2546827
3	12	1.1486175	1.2234272	1.2460393
4	11	0.5936718	-0.3583449	0.2461556
5	16	1.0287878	0.0678360	1.6502734
6	13	6.3261776	6.6678678	6.2793092
7	11	10.5518121	10.8119426	10.4041769
8	5	22.6911167	23.0021529	22.1403238

Table 10: Prediction bias by age for cervical region

age_group	n	snodgrass_bias	watanabe_bias	praneat_bias
1	1	-10.8086074	-10.4307692	-12.0532597
2	14	-9.3672309	-8.6663419	-10.4068141
3	9	-1.6982159	-0.9720792	-2.7217721
4	6	5.1117731	5.2581261	4.2796978
5	12	7.3745547	6.2795447	8.3063558
6	9	0.2435072	1.1252385	0.3830655
7	8	19.2991972	19.8042854	20.0121335
8	3	34.2163107	34.5945123	34.2963433

```
all_mean_bias <- all_bias %>%
  reduce(inner_join, by = c("age_group", "n"))

knitr::kable(all_mean_bias, caption = "Prediction bias by age for combined regions")
```

```
snodgrass_cerv_bias <- snodgrass_cerv_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            snodgrass_bias = mean(residual))

watanabe_cerv_bias <- watanabe_cerv_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            watanabe_bias = mean(residual))

praneatpolgrang_cerv_bias <- praneatpolgrang_cerv_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            praneat_bias = mean(residual))

cerv_bias <- list(snodgrass_cerv_bias, watanabe_cerv_bias, praneatpolgrang_cerv_bias)

cerv_mean_bias <- cerv_bias %>%
  reduce(inner_join, by = c("age_group", "n"))

knitr::kable(cerv_mean_bias, caption = "Prediction bias by age for cervical region")
```

Table 11: Prediction bias by age for thoracic region

age__group	n	snodgrass__bias	watanabe__bias	praneat__bias
1	1	-5.5256740	-6.3887656	-4.8695061
2	18	-5.5445962	-5.8268562	-5.0920400
3	11	-0.0845294	-0.0842103	0.3581641
4	10	-1.0468731	-2.8772647	-1.5781927
5	13	0.7576514	1.3798364	1.5967547
6	12	12.1684760	12.4541515	11.8964329
7	9	10.6273014	11.5278913	9.7542369
8	5	25.3214421	25.5489227	22.8387228

```
snodgrass_thor_bias <- snodgrass_thor_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            snodgrass_bias = mean(residual))

watanabe_thor_bias <- watanabe_thor_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            watanabe_bias = mean(residual))

praneatpolgrang_thor_bias <- praneatpolgrang_thor_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            praneat_bias = mean(residual))

thor_bias <- list(snodgrass_thor_bias, watanabe_thor_bias, praneatpolgrang_thor_bias)

thor_mean_bias <- thor_bias %>%
  reduce(inner_join, by = c("age_group", "n"))

knitr::kable(thor_mean_bias, caption = "Prediction bias by age for thoracic region")
```

```
snodgrass_lumb_bias <- snodgrass_lumb_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            snodgrass_bias = mean(residual))

watanabe_lumb_bias <- watanabe_lumb_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            watanabe_bias = mean(residual))

praneatpolgrang_lumb_bias <- praneatpolgrang_lumb_res %>%
  group_by(age_group) %>%
  summarise(n = n(),
            praneat_bias = mean(residual))

lumb_bias <- list(snodgrass_lumb_bias, watanabe_lumb_bias, praneatpolgrang_lumb_bias)

lumb_mean_bias <- lumb_bias %>%
```

Table 12: Prediction bias by age for lumbar region

age_group	n	snodgrass_bias	watanabe_bias	praneat_bias
1	1	-7.2991963	-7.7693094	-8.0168617
2	18	-4.9639622	-5.2623760	-5.5375607
3	12	-1.9137817	-2.2956140	-2.2092975
4	10	0.2545196	-0.0382005	0.4354296
5	16	2.4181210	1.3541013	2.7671487
6	13	7.1993127	7.2729990	8.8715273
7	11	12.8360094	13.5599795	11.8832422
8	5	27.2639918	27.6389654	28.6810396

```
  reduce(inner_join, by = c("age_group", "n"))

knitr::kable(lumb_mean_bias, caption = "Prediction bias by age for lumbar region")
```