Repeability of Frog Morphometric Measurements

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Assessing Repeatability of Morphometric Measurements

We want to measure repeatability of our morphometric measurements, both within individual measurers and between measurers. We plan to combine data with that measured by Julio Rivera in 2015, so we want to know that the data are compatible.

The accuracy we are aiming for is 95%, or 5% measurement error (both within and between individual measurers).

Each measurer measured the same 7 frogs (*Hylophorbus sp.* from Buyetai: JR306,308,311,320,321,324), which was repeated (2 sets of measurements per measurer).

Setup

```
require( googlesheets4 )
require(dplyr)
require(magrittr)
require(ggplot2)
require(cowplot)

if(dir.exists("output")!=TRUE) dir.create("output") # check if output directory out exists
```

Read in our data from a Google Spreadsheet, and convert measurer, session and jr number to factors.

```
file <- "https://docs.google.com/spreadsheets/d/1-w62GXvKwQ868dwiMVzgPdLYbgSkXxSqasE-YoaGO

gs4_deauth() # not a private sheet, so no need for authentication
```

```
alldat <- as.data.frame(read_sheet(file)) %>%  ### INPUT DATA from googlesheet
          filter(!is.na(measurer))           # remove spacer rows
```

```
v Reading from "Frog Repeatability Measurements".
```

```
v Range 'Sheet1'.
```

```
alldat %<>% mutate_at(c("measurer", "session", "jr"), as.factor) %>%
    mutate( shape = case_when( measurer=="JR" ~ 25, measurer!="JR" ~ 19 )) %>%
    mutate( shape = as.factor(shape))
```

Repeatability

This requires two full sets of measurements, so this is still in progress.

```
mod <- with(alldat, summary(aov(lm( svl ~ jr ))))

s2_within <- ms_within <- mod[[1]][2,3]
s2_within
```

```
[1] 0.3019645
```

```
ms_among <- mod[[1]][1,3]
s2_among <- (ms_among-ms_within)/2
ME <- s2_within/(s2_within+s2_among) * 100
ME
```

```
[1] 0.4900875
```

Validating Landmarks

Plot all of our data against the original dataset (JR in green), as well as faceted by individual. The goal here is to validate the landmarks.

This function creates the plots that are repeated for each morphometric variable.

```
dat <- alldat %>% filter(session==0|measurer=="JR")

p <- dat %>% ggplot(aes(svl, femur, color=measurer, label=jr))
v <- dat %>% ggplot(aes(jr, svl, group=jr, color=measurer, shape=measurer))

make_violins <- function(v) {

 v + geom_violin() +
  geom_jitter(aes(x=jr, color=measurer, shape=measurer, size=measurer), width=.2) +
  scale_shape_manual(values=c(19,19,17,19,19,19)) +
  scale_size_manual(values=c(3,3,5,3,3,3))

}

make_plots <- function(p, v) {
  q1 <- p + geom_point(size = 3) +
    geom_smooth( aes(group=measurer), method="lm", alpha=.1) +
    geom_text(nudge_y = .15) +
    theme_bw()

  q2 <- p + geom_point(size = 3) +
    geom_smooth( method="lm", alpha=.1) +
    geom_text(nudge_y = 1) +
    facet_grid( measurer ~ . ) +
    theme_bw()

   plot_grid(q1, q2, labels="AUTO")

 }

# q3 <- v + geom_violin() +
#  geom_jitter(aes(x=jr, color=measurer, shape=measurer), size=3, width=.2) +
#  scale_shape_manual(values=c(19,19,17,19,19,19))

# q3
```

Set up the ggplots:

```
femp <- dat %>% ggplot(aes(svl, femur, color=measurer, label=jr))
tibp <- dat %>% ggplot(aes(svl, tibiofibula, color=measurer, label=jr))
tarp <- dat %>% ggplot(aes(svl, tarsus, color=measurer, label=jr))
```

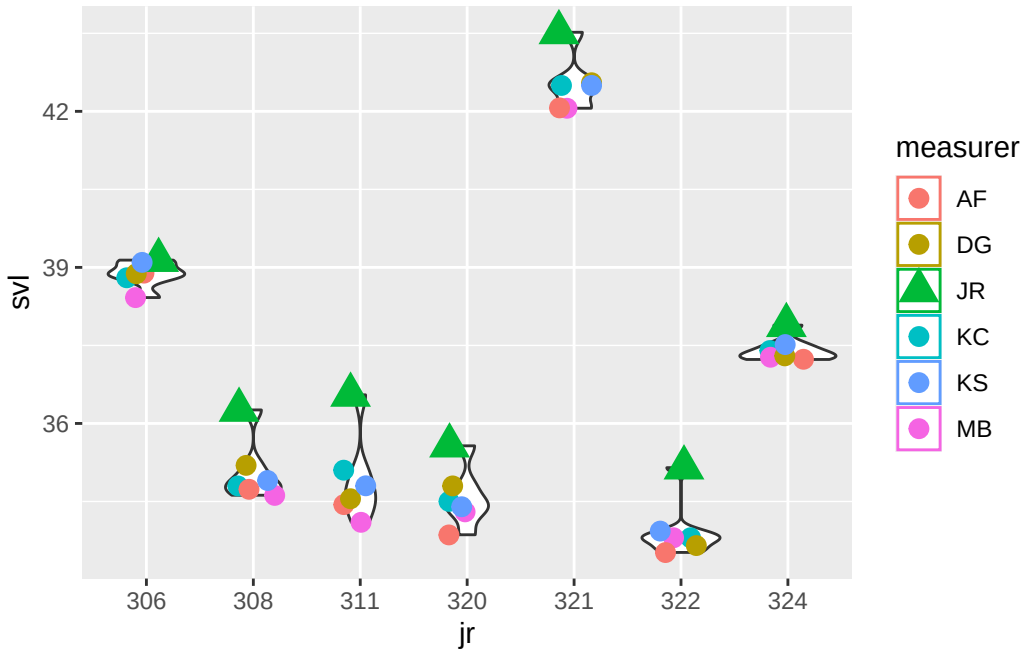
```
footp <- dat %>% ggplot(aes(svl, foot, color=measurer, label=jr))
hwp <- dat %>% ggplot(aes(svl, headW, color=measurer, label=jr))
hlp <- dat %>% ggplot(aes(svl, headL, color=measurer, label=jr))
hump <- dat %>% ggplot(aes(svl, humerus, color=measurer, label=jr))
radp <- dat %>% ggplot(aes(svl, radioulna, color=measurer, label=jr))
handp <- dat %>% ggplot(aes(svl, hand, color=measurer, label=jr))

sv <- dat %>% ggplot(aes(jr, svl, group=jr, color=measurer, shape=measurer))
femv <- dat %>% ggplot(aes(jr, femur, group=jr, color=measurer, shape=measurer))
tibv <- dat %>% ggplot(aes(jr, tibiofibula, group=jr, color=measurer, shape=measurer))
tarv <- dat %>% ggplot(aes(jr, tarsus, group=jr, color=measurer, shape=measurer))
footv <- dat %>% ggplot(aes(jr, foot, group=jr, color=measurer, shape=measurer))
hwv <- dat %>% ggplot(aes(jr, headW, group=jr, color=measurer, shape=measurer))
hlv <- dat %>% ggplot(aes(jr, headL, group=jr, color=measurer, shape=measurer))
humv <- dat %>% ggplot(aes(jr, humerus, group=jr, color=measurer, shape=measurer))
radv <- dat %>% ggplot(aes(jr, radioulna, group=jr, color=measurer, shape=measurer))
handv <- dat %>% ggplot(aes(jr, hand, group=jr, color=measurer, shape=measurer))
```

Make plots:

SVL

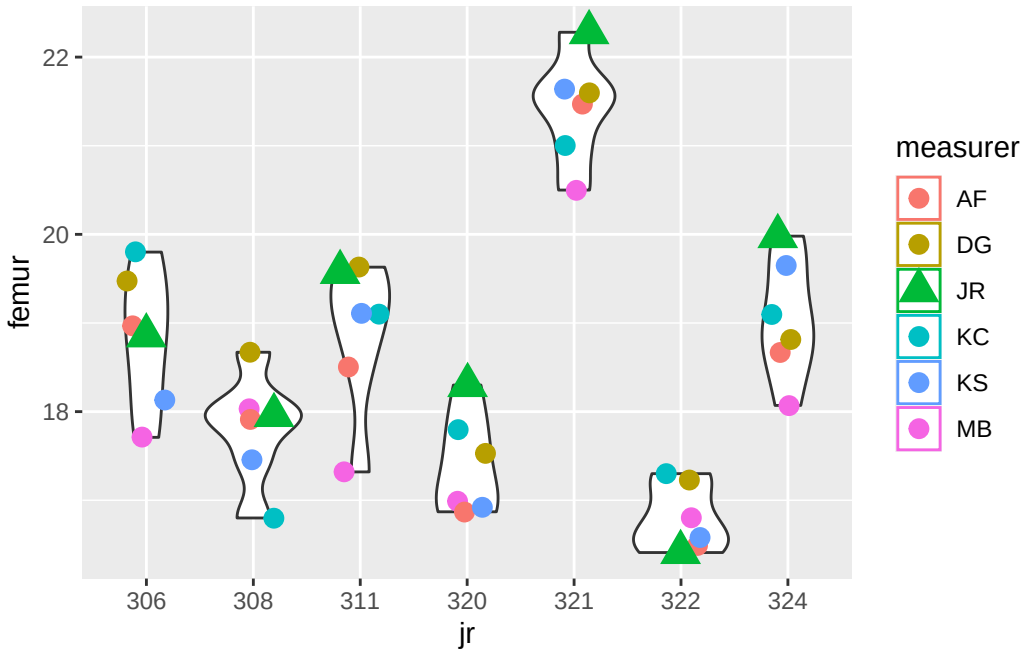
```
make_violins(sv)
```



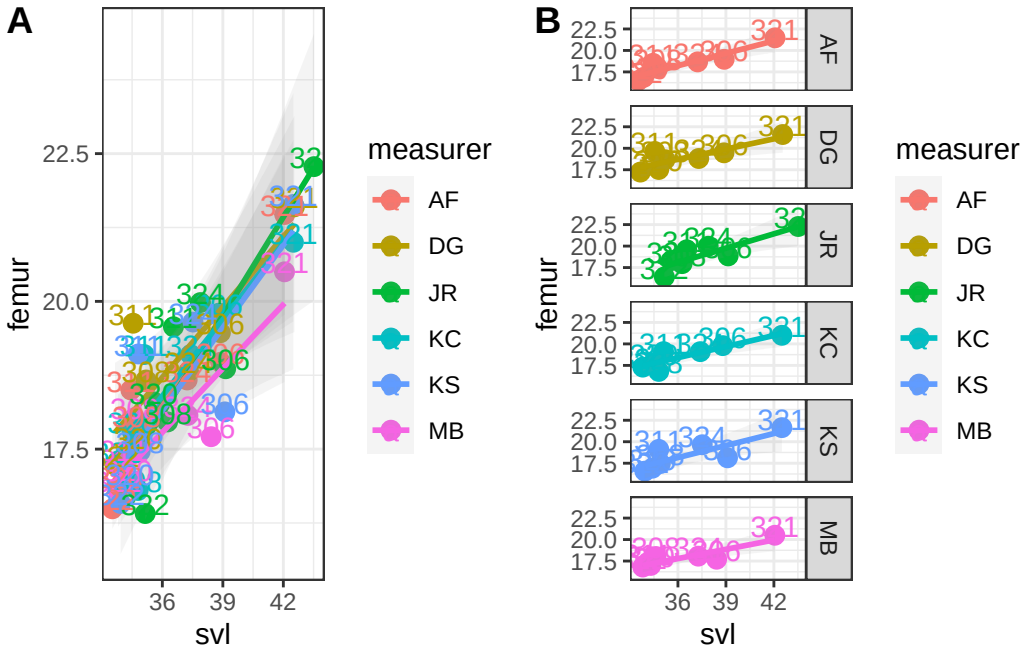
Looks like everyone s SVL are a little short. Basically JR304 and JR306 match well, but the others, JR308, JR311, JR320, JR321, JR322, JR324 are a little short. Did he press them down? Or use a ruler?

Femur

```
make_violins(femv)
```




```
make_plots( femp )
```

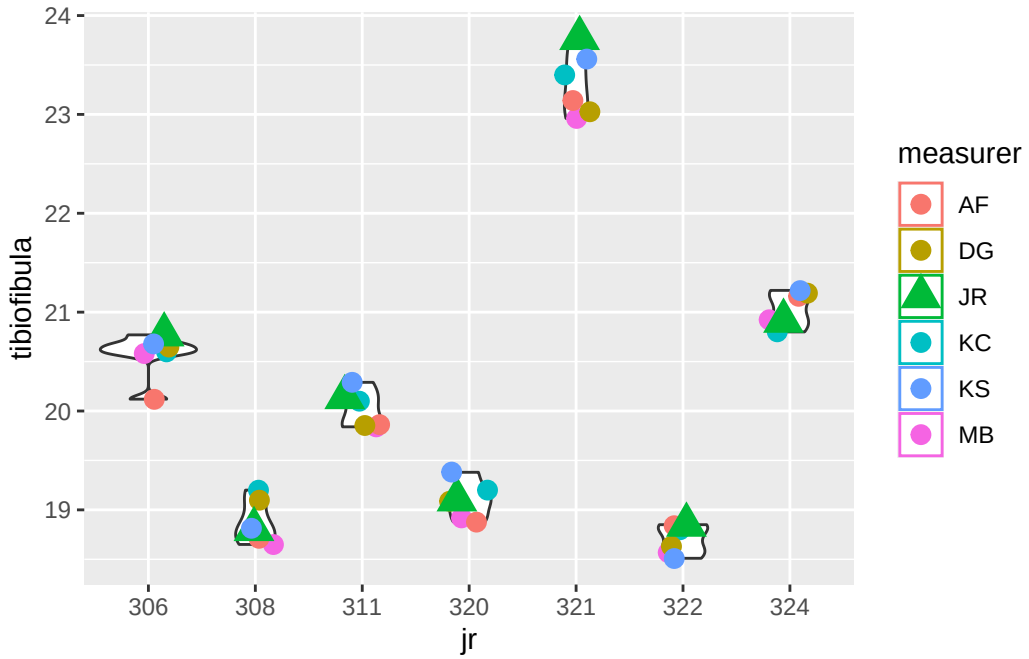


Looks like my femur measurements (MB) are a little short - JR must have measured from the

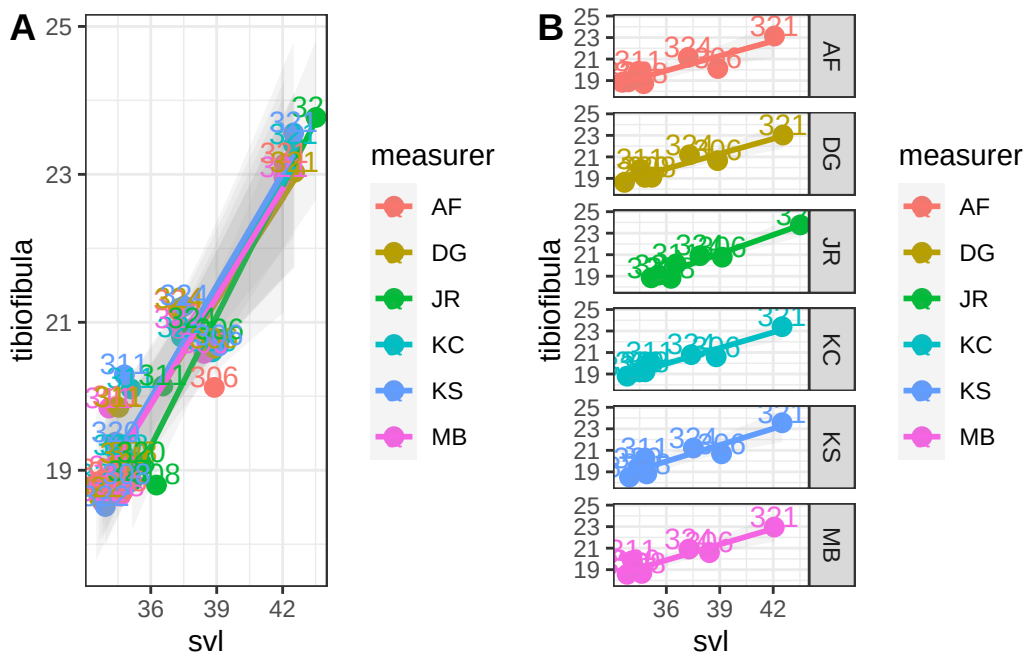
vent rather than from the midline perpendicular to the femur.

Tibiofibula

```
make_violins(tibv)
```



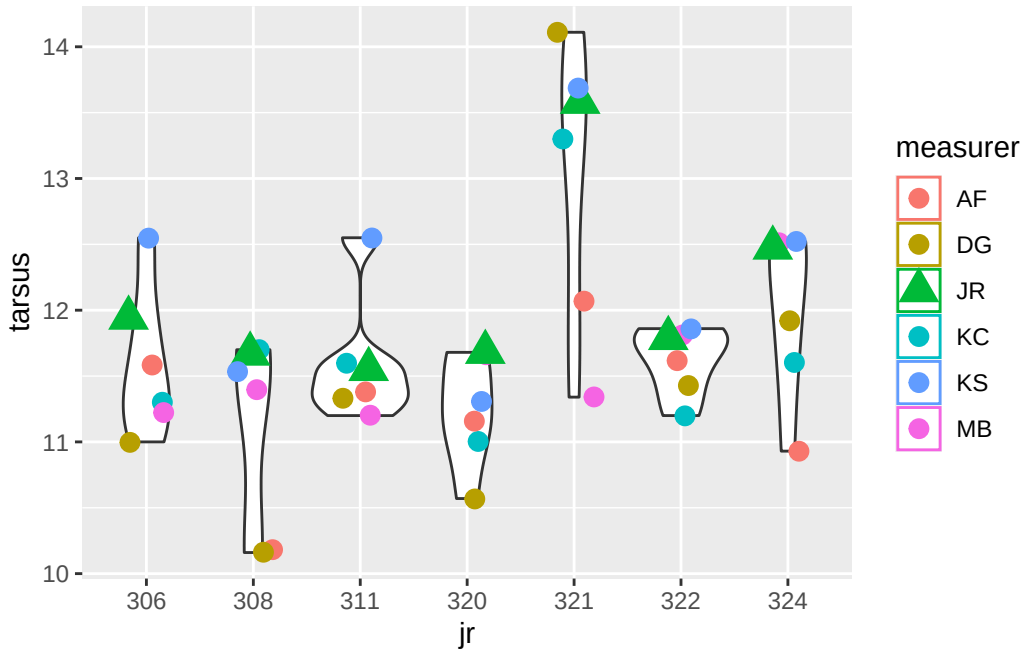

```
make_plots( tibp )
```



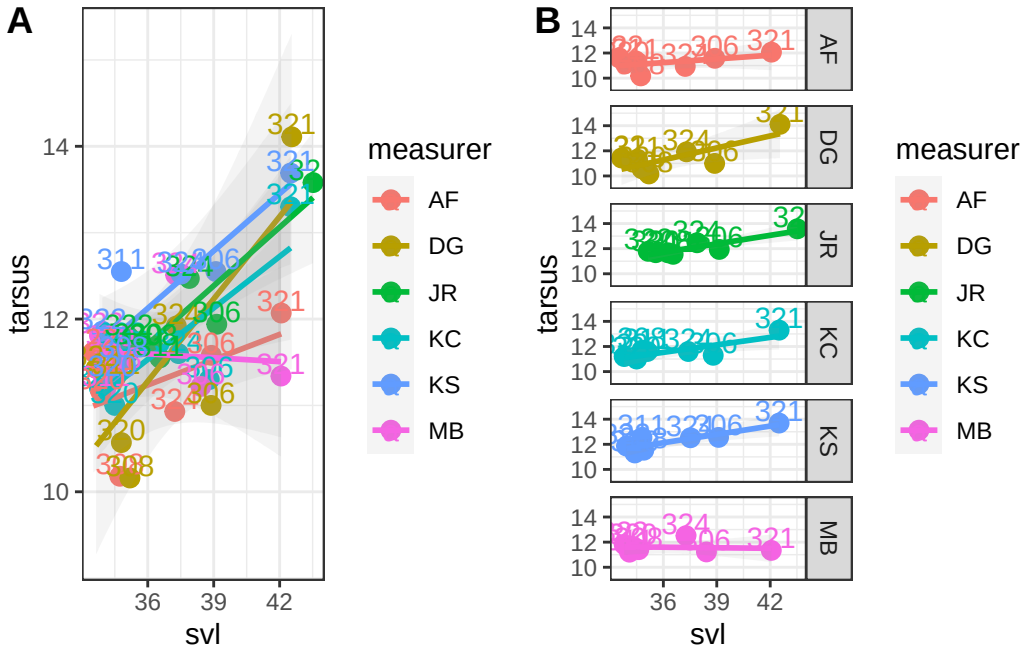
Tibiofibula looks good, except for what looks like a typo in DG s data?

Tarsus

```
make_violins(tarv)
```




```
make_plots( tarp )
```

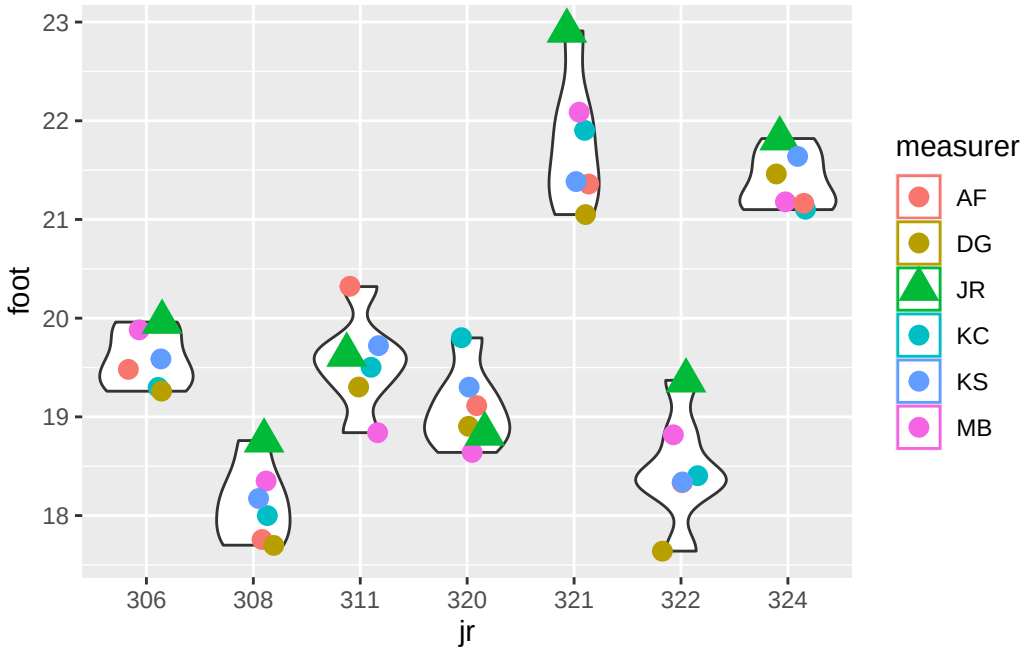


Not sure what I did! Lol. Good example of the unfortunate outlier being the largest throwing

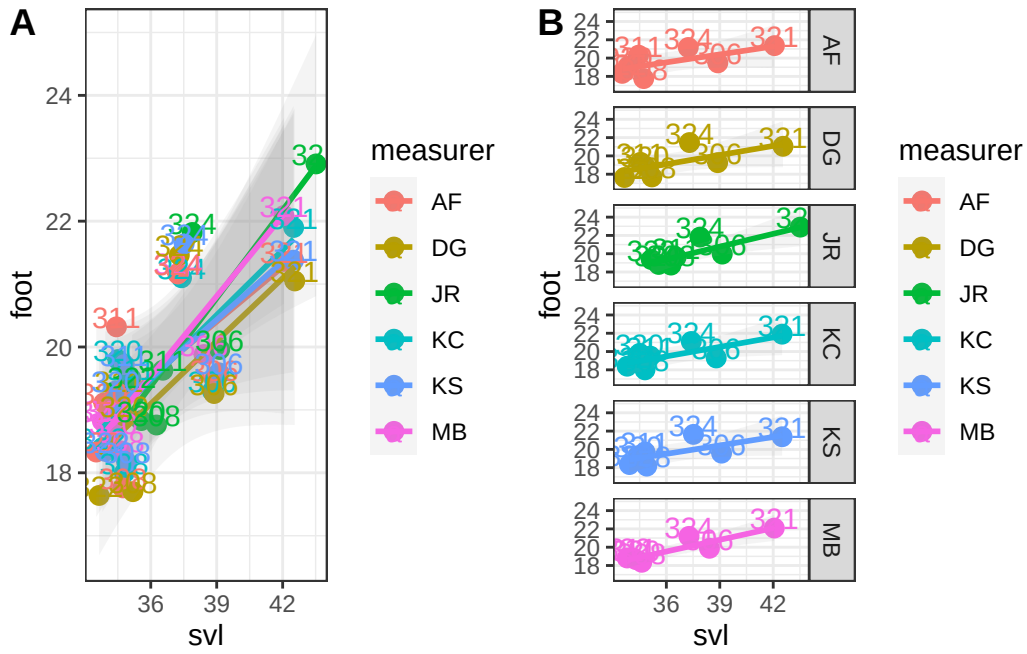
the whole trend off.

Foot

```
make_violins(footv)
```



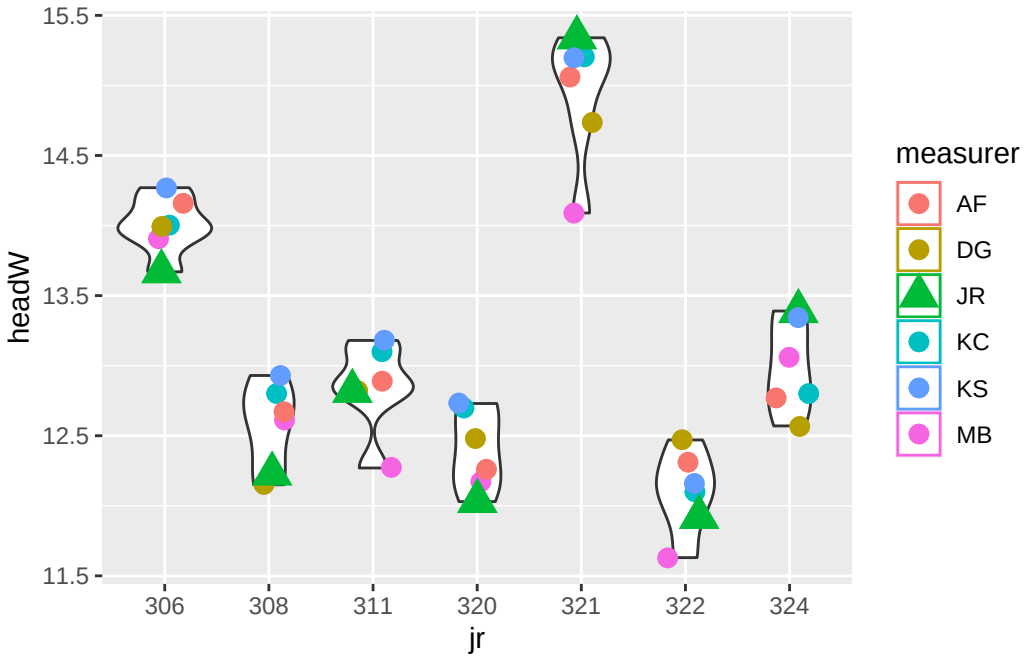

```
make_plots( footp )
```



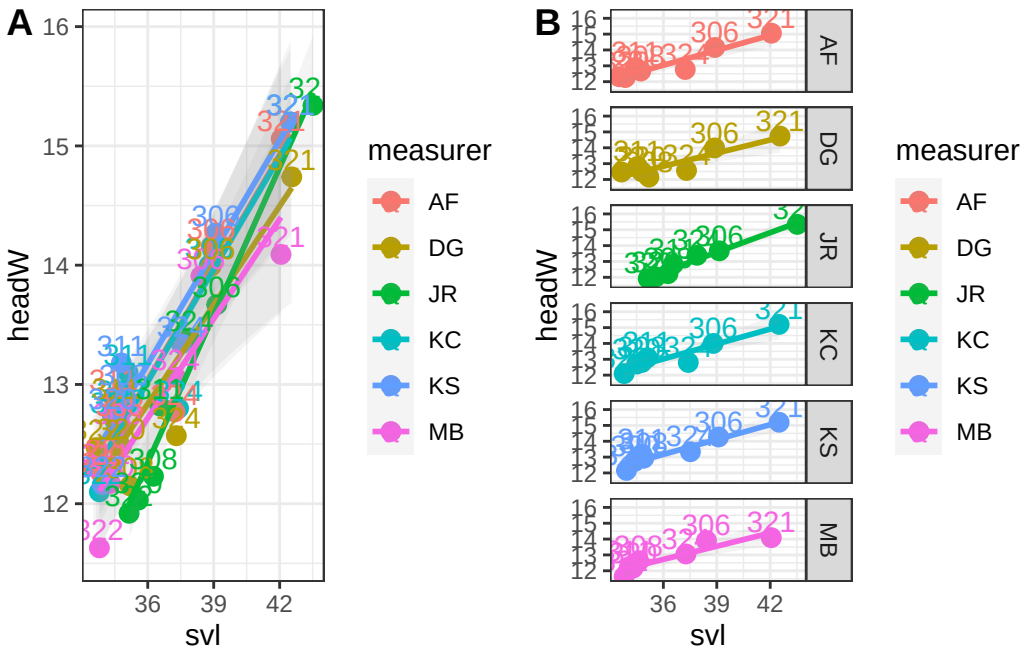
Looks good!

Head Width

```
make_violins(hwv)
```



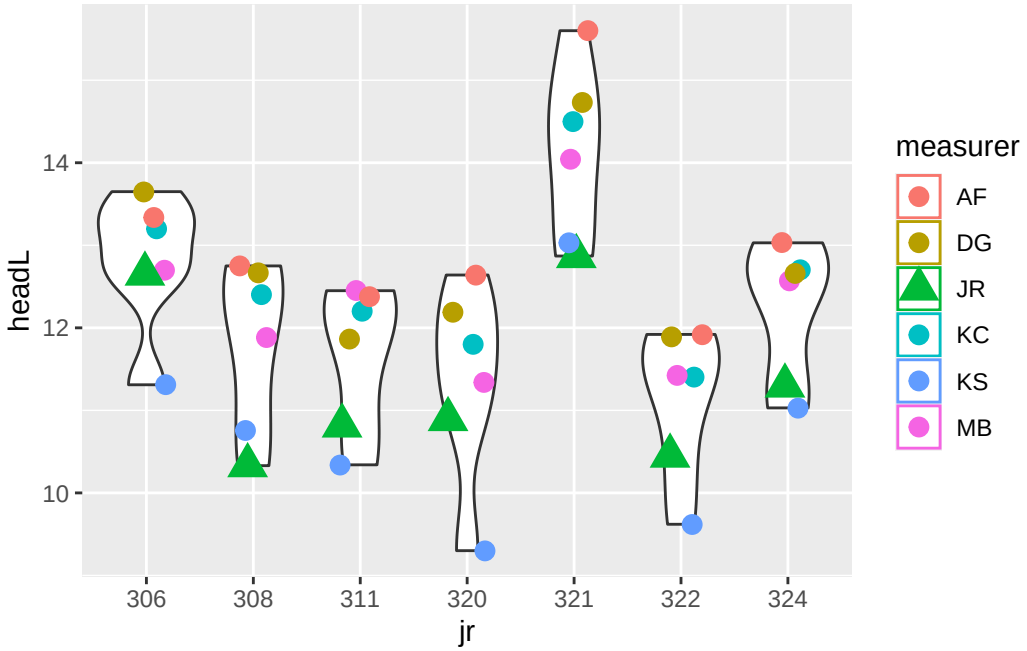

```
make_plots( hwp )
```



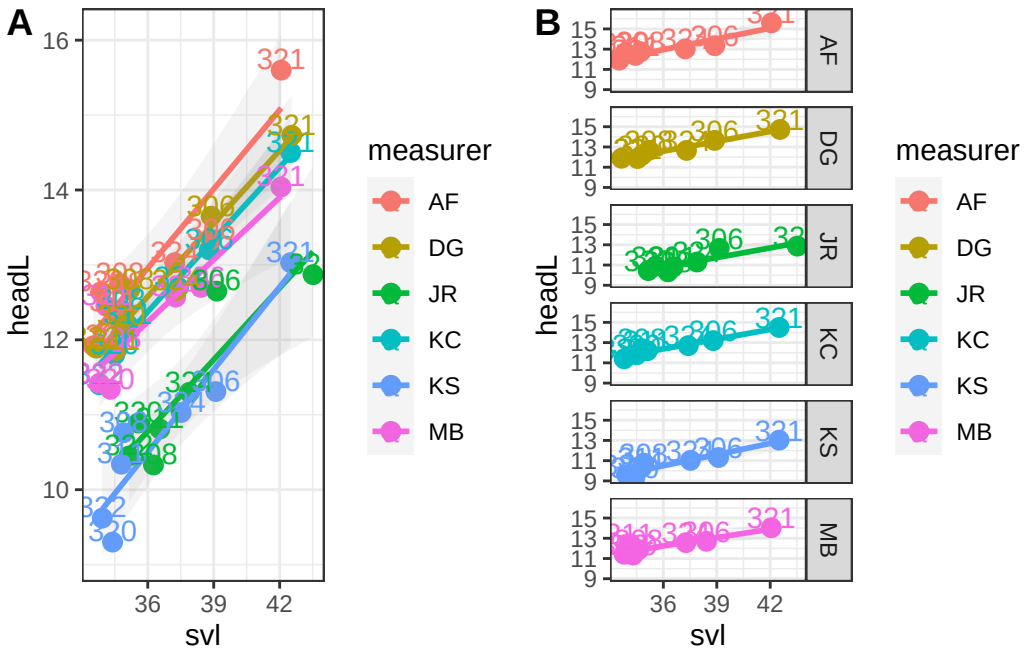
Looks good!

Head Length

```
make_violins(hlv)
```



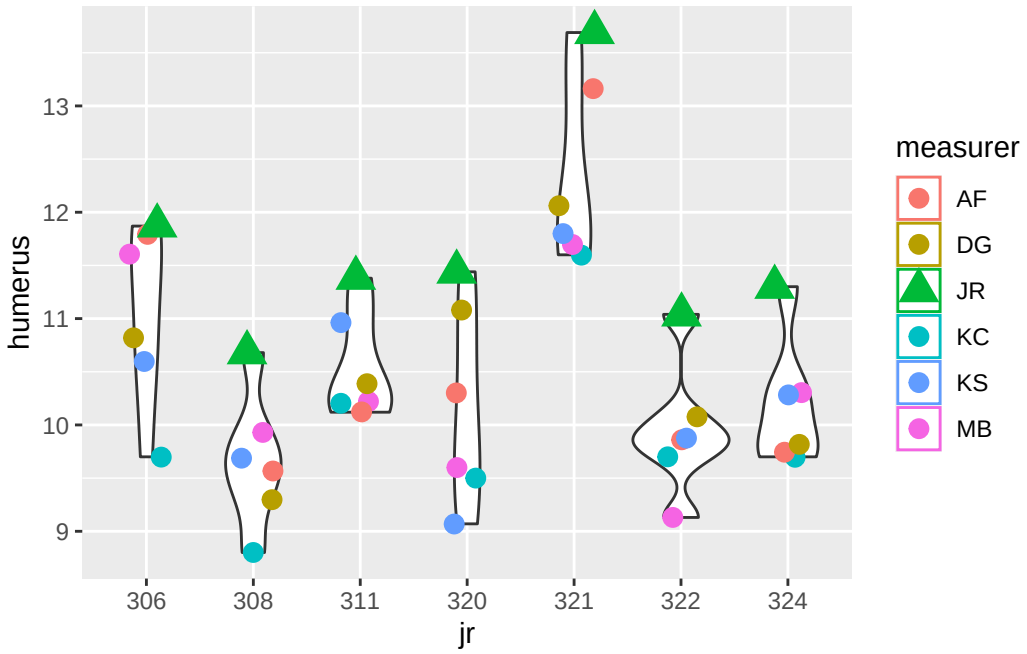

```
make_plots( hlp )
```



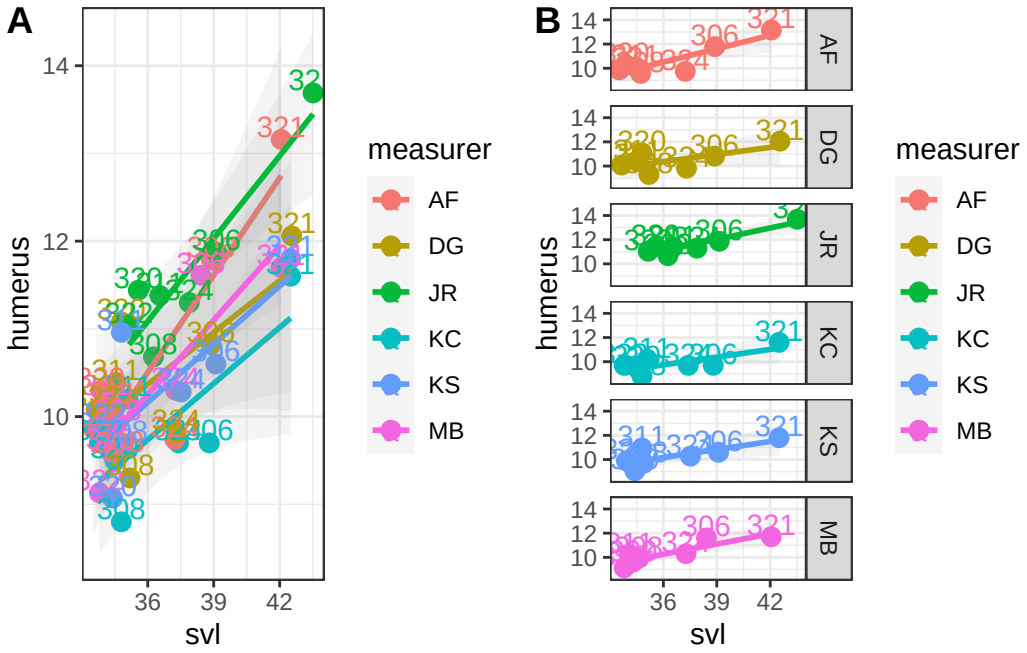
Oh oh. We are not using the right Head Length landmark.

Humerus

```
make_violins(humv)
```



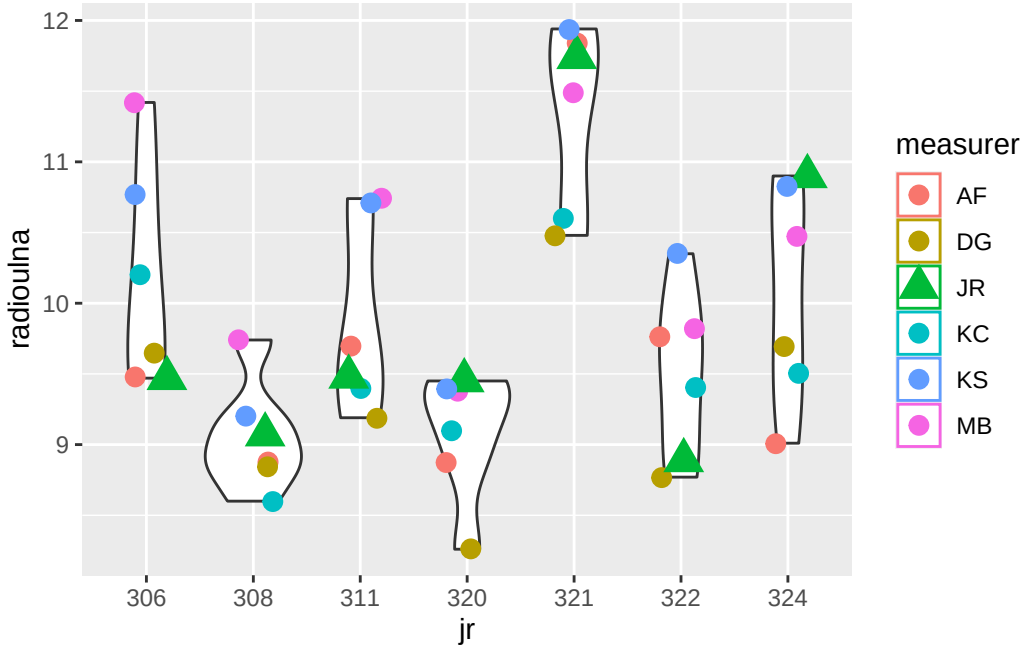

```
make_plots( hump )
```



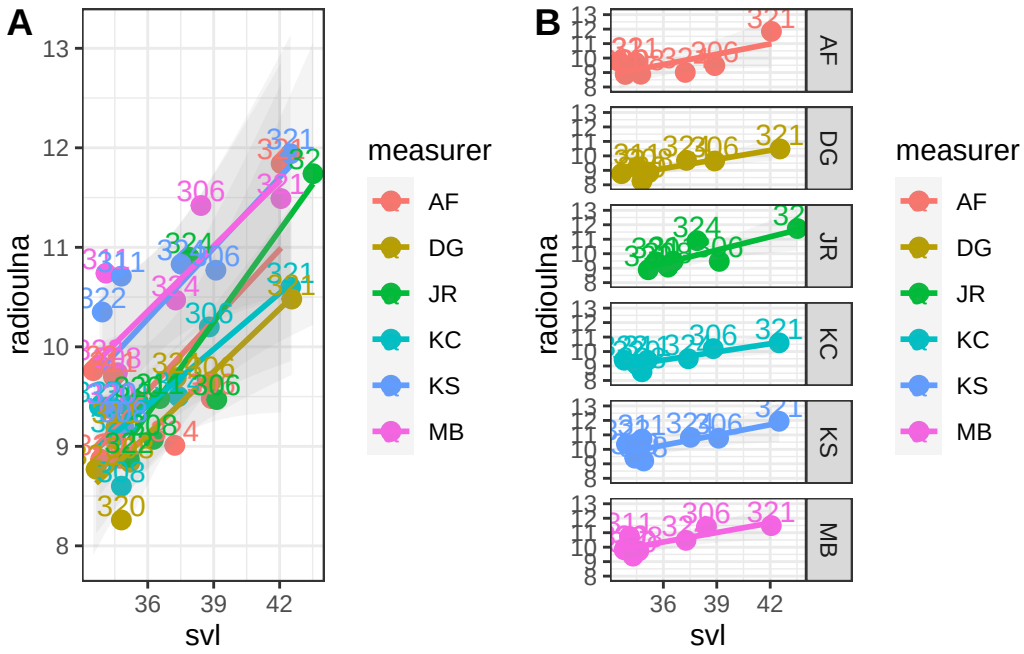
Hmm. We are all a little consistently lower than JR, some more so.

Radioulna

```
make_violins(radv)
```



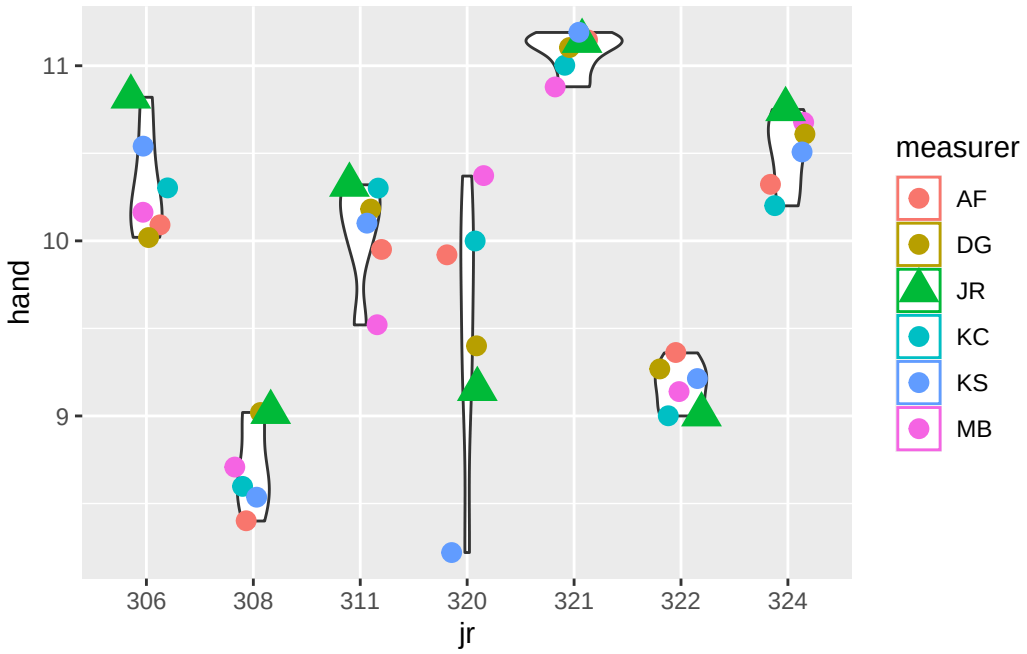

```
make_plots( radp)
```



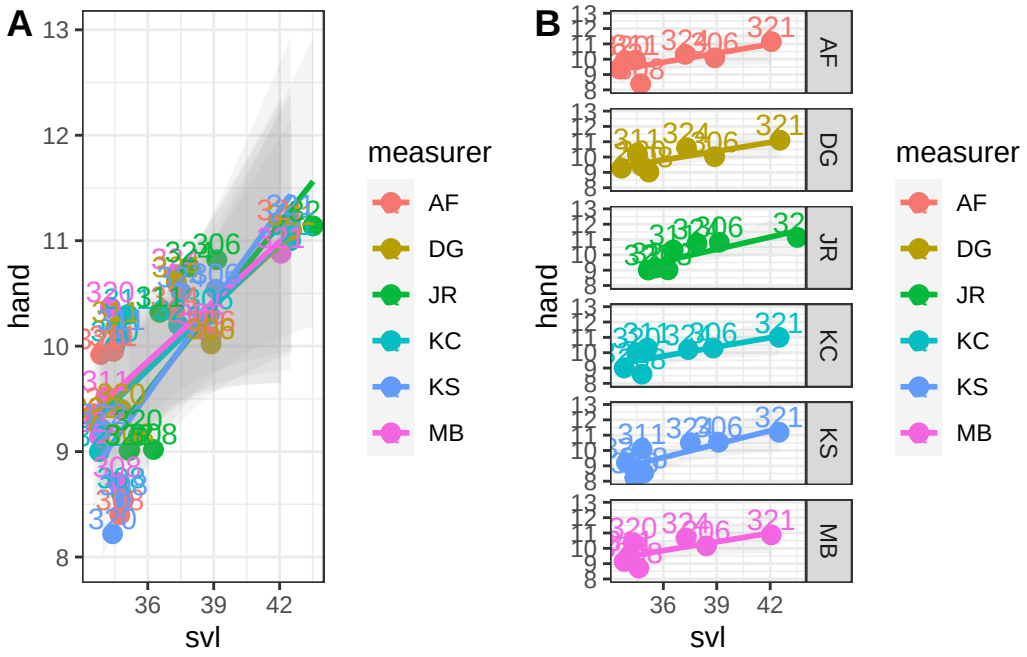
Need to work on this one too.

Hand

```
make_violins(handv)
```




```
make_plots( handp )
```



Looks good!

Conclusions

We need to confirm the landmarks JR used for the limb segment and head length measurements (foot and hand are OK). It looks promising for repeatability but we need to confirm after we get two full sets of measurements.

Session 1

```
dat <- alldat %>% filter(session==1|measurer=="JR")
```

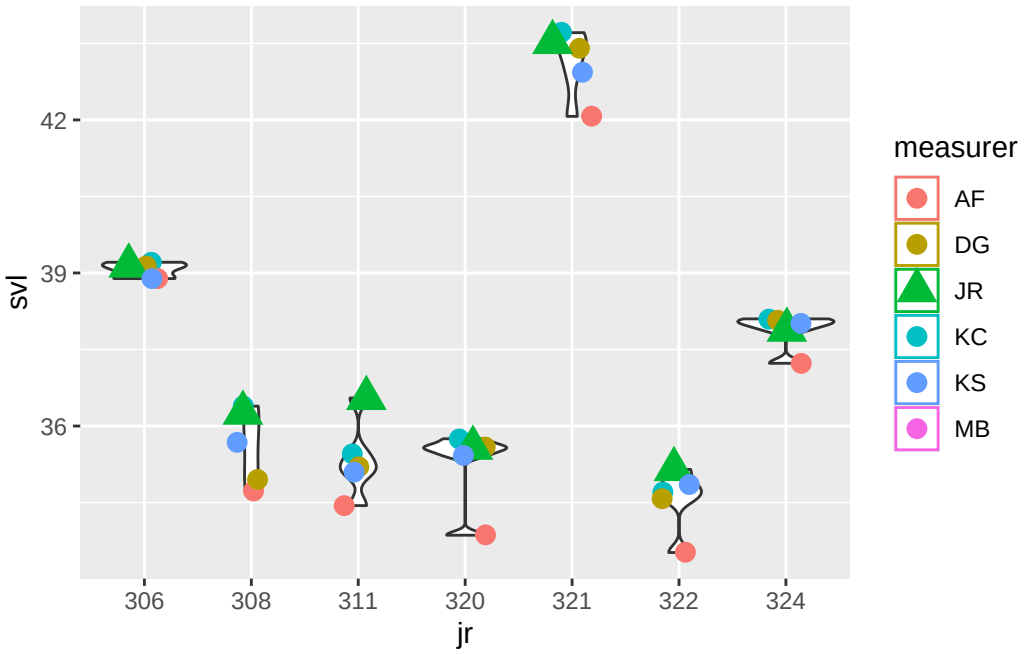
Set up the ggplots:

```
femp <- dat %>% ggplot(aes(svl, femur, color=measurer, label=jr))
tibp <- dat %>% ggplot(aes(svl, tibiofibula, color=measurer, label=jr))
tarp <- dat %>% ggplot(aes(svl, tarsus, color=measurer, label=jr))
footp <- dat %>% ggplot(aes(svl, foot, color=measurer, label=jr))
hwp <- dat %>% ggplot(aes(svl, headW, color=measurer, label=jr))
hlp <- dat %>% ggplot(aes(svl, headL, color=measurer, label=jr))
hump <- dat %>% ggplot(aes(svl, humerus, color=measurer, label=jr))
radp <- dat %>% ggplot(aes(svl, radioulna, color=measurer, label=jr))
handp <- dat %>% ggplot(aes(svl, hand, color=measurer, label=jr))

sv <- dat %>% ggplot(aes(jr, svl, group=jr, color=measurer, shape=measurer))
femv <- dat %>% ggplot(aes(jr, femur, group=jr, color=measurer, shape=measurer))
tibv <- dat %>% ggplot(aes(jr, tibiofibula, group=jr, color=measurer, shape=measurer))
tarv <- dat %>% ggplot(aes(jr, tarsus, group=jr, color=measurer, shape=measurer))
footv <- dat %>% ggplot(aes(jr, foot, group=jr, color=measurer, shape=measurer))
hwv <- dat %>% ggplot(aes(jr, headW, group=jr, color=measurer, shape=measurer))
hlv <- dat %>% ggplot(aes(jr, headL, group=jr, color=measurer, shape=measurer))
humv <- dat %>% ggplot(aes(jr, humerus, group=jr, color=measurer, shape=measurer))
radv <- dat %>% ggplot(aes(jr, radioulna, group=jr, color=measurer, shape=measurer))
handv <- dat %>% ggplot(aes(jr, hand, group=jr, color=measurer, shape=measurer))
```

SVL

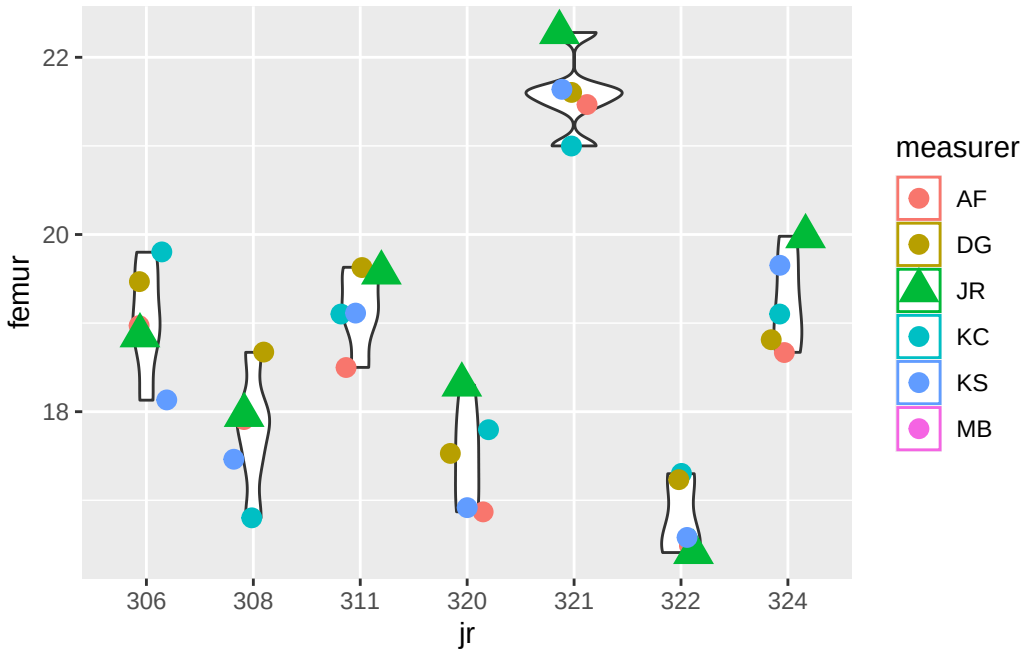
```
make_violins(sv)
```



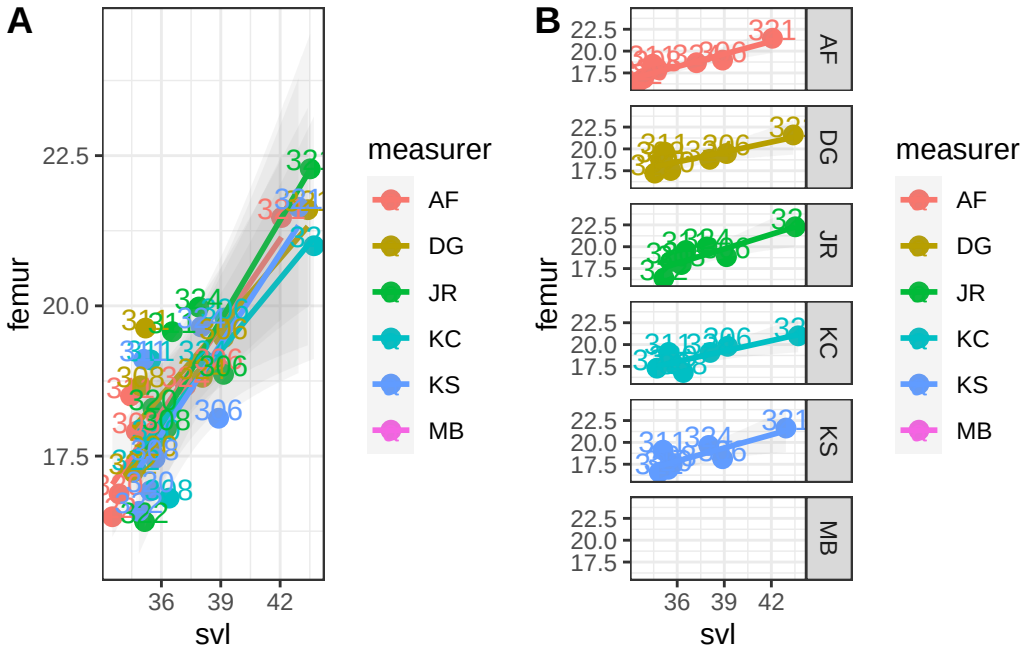
Looks like everyone s SVL are a little short. Basically JR304 and JR306 match well, but the others, JR308, JR311, JR320, JR321, JR322, JR324 are a little short. Did he press them down? Or use a ruler?

Femur

```
make_violins(femv)
```




```
make_plots( femp )
```

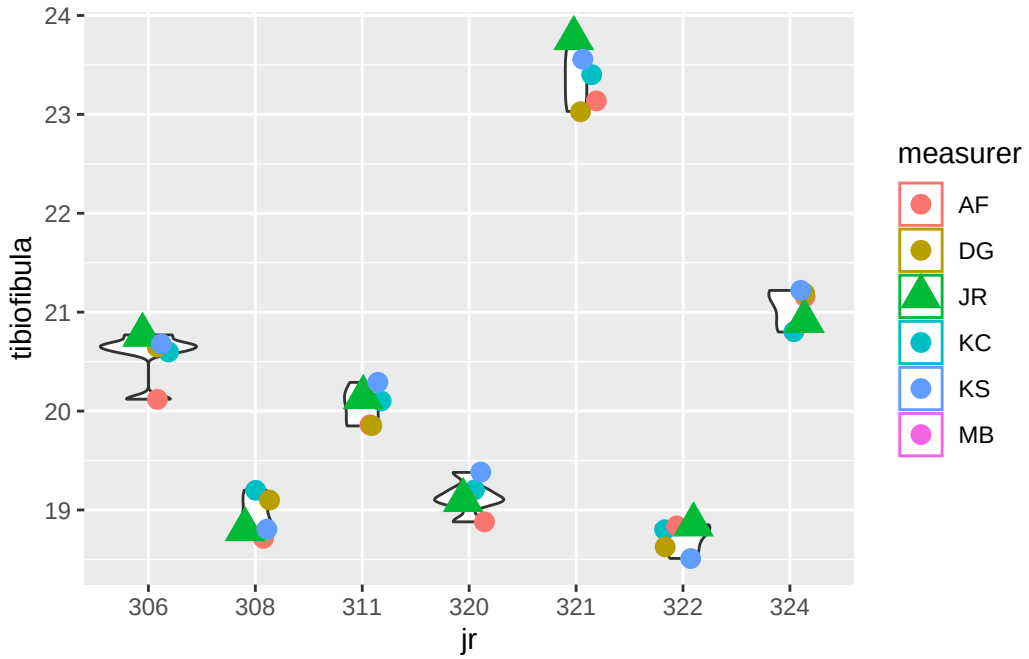


Looks like my femur measurements (MB) are a little short - JR must have measured from the

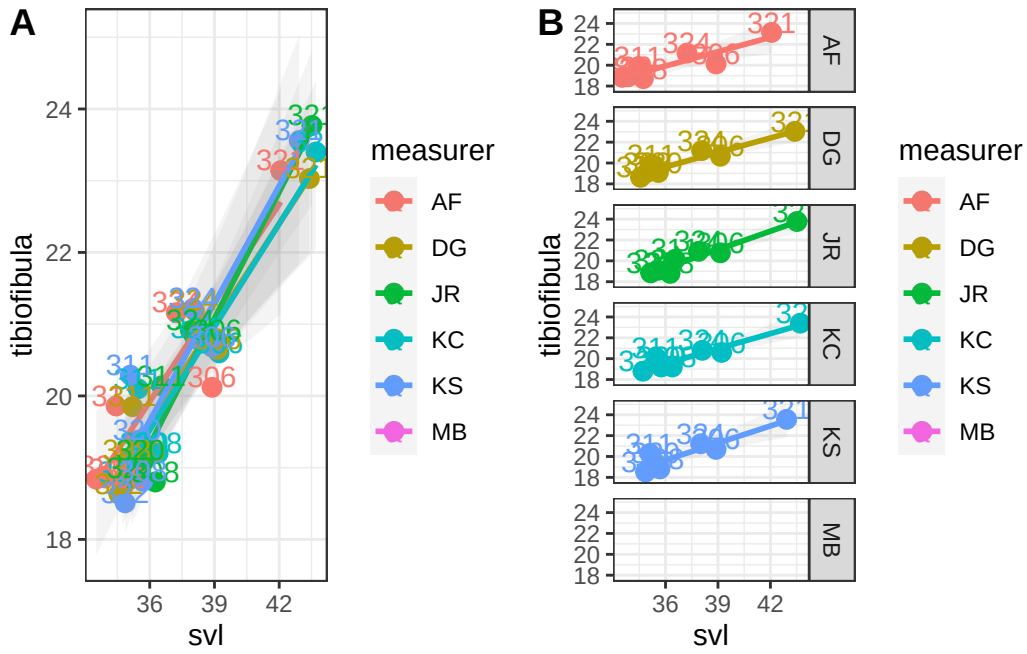
vent rather than from the midline perpendicular to the femur.

Tibiofibula

```
make_violins(tibv)
```



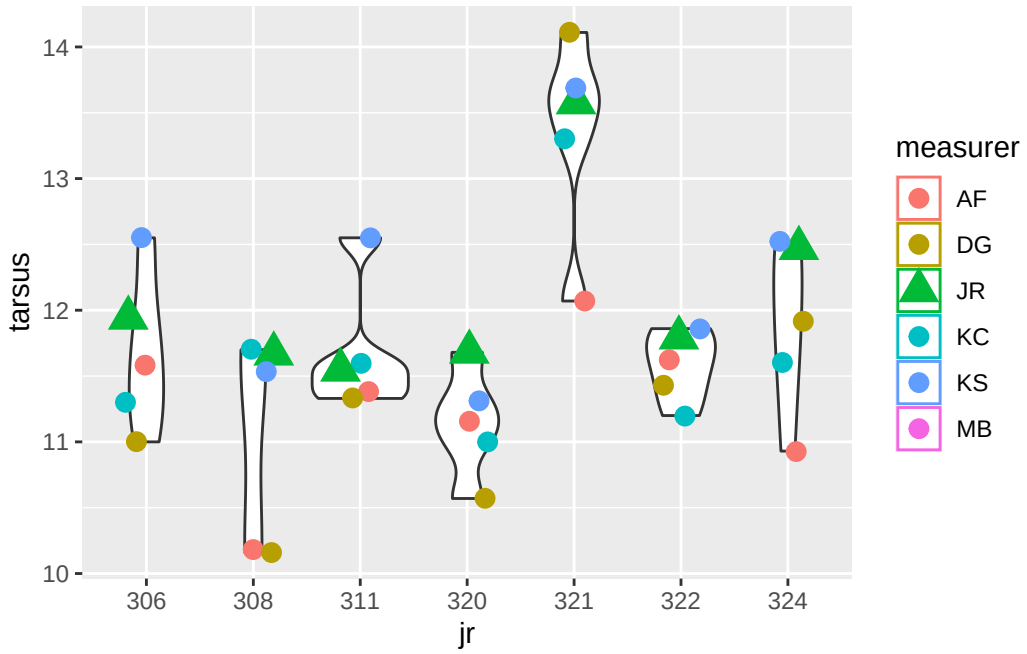

```
make_plots( tibp )
```



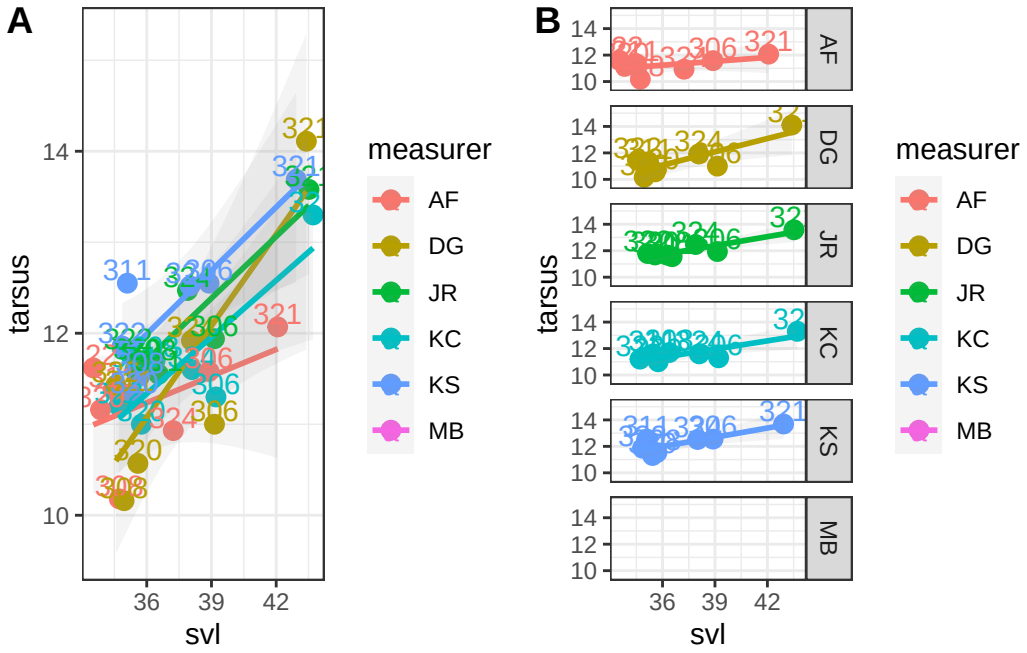
Tibiofibula looks good, except for what looks like a typo in DG s data?

Tarsus

```
make_violins(tarv)
```




```
make_plots( tarp )
```

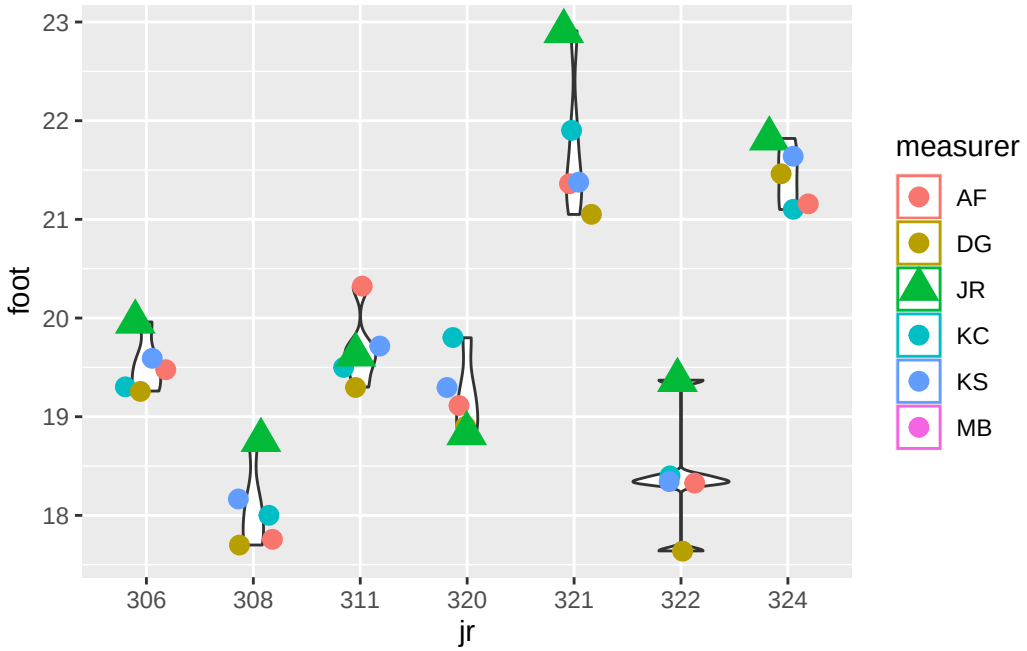


Not sure what I did! Lol. Good example of the unfortunate outlier being the largest throwing

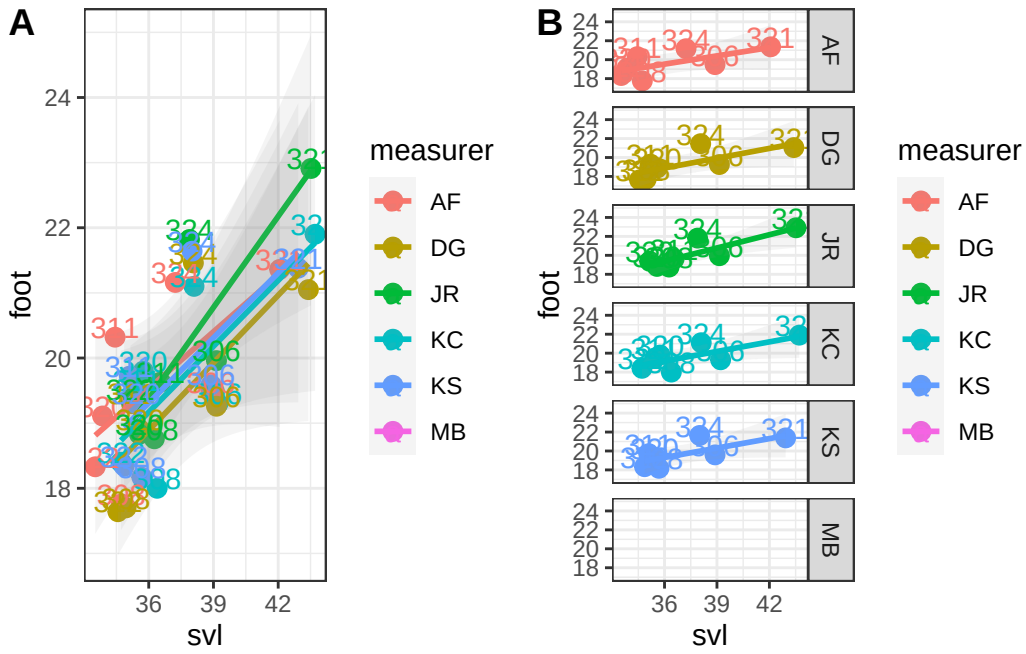
the whole trend off.

Foot

```
make_violins(footv)
```



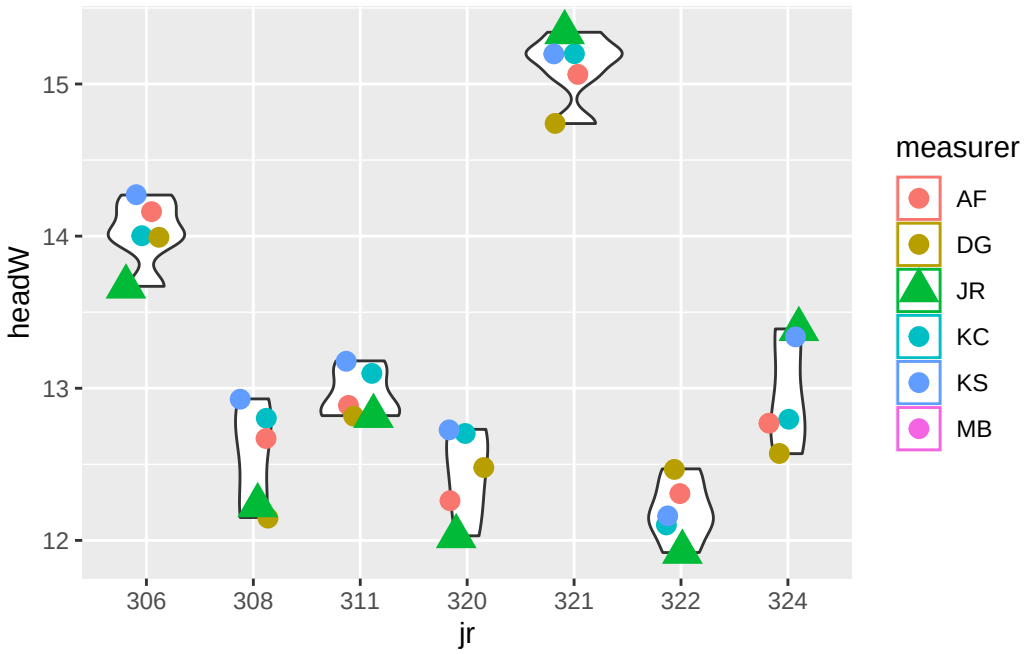

```
make_plots( footp )
```



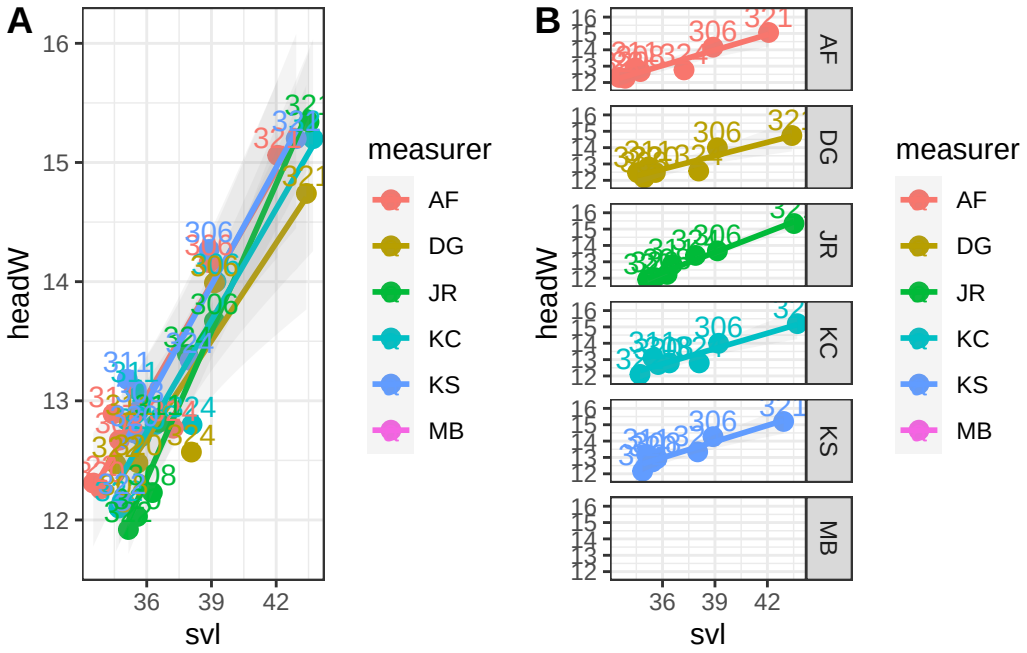
Looks good!

Head Width

```
make_violins(hwv)
```



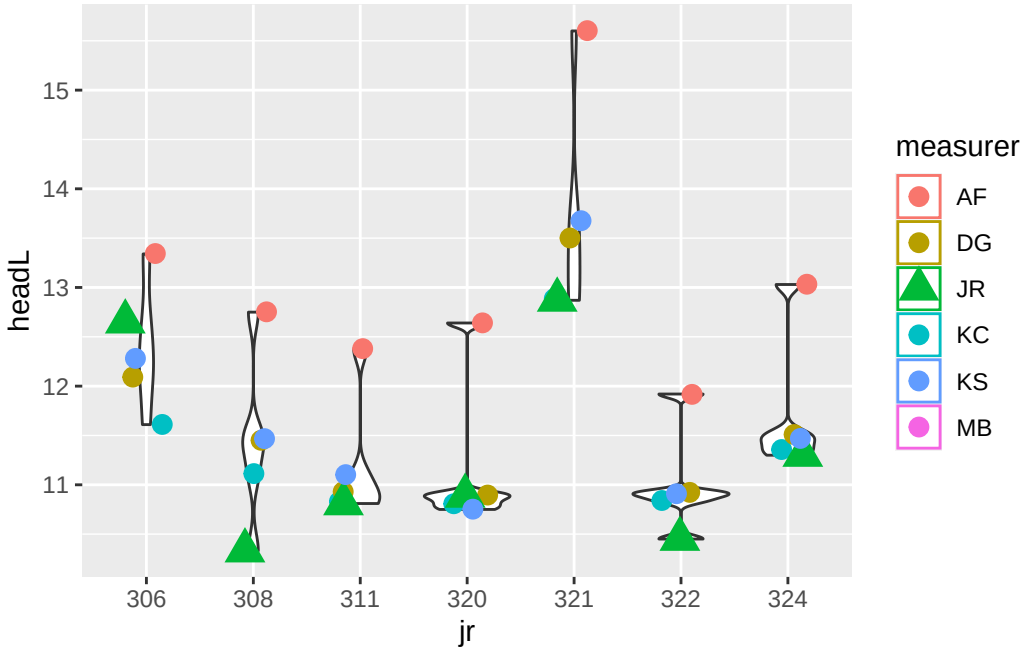

```
make_plots( hwp )
```



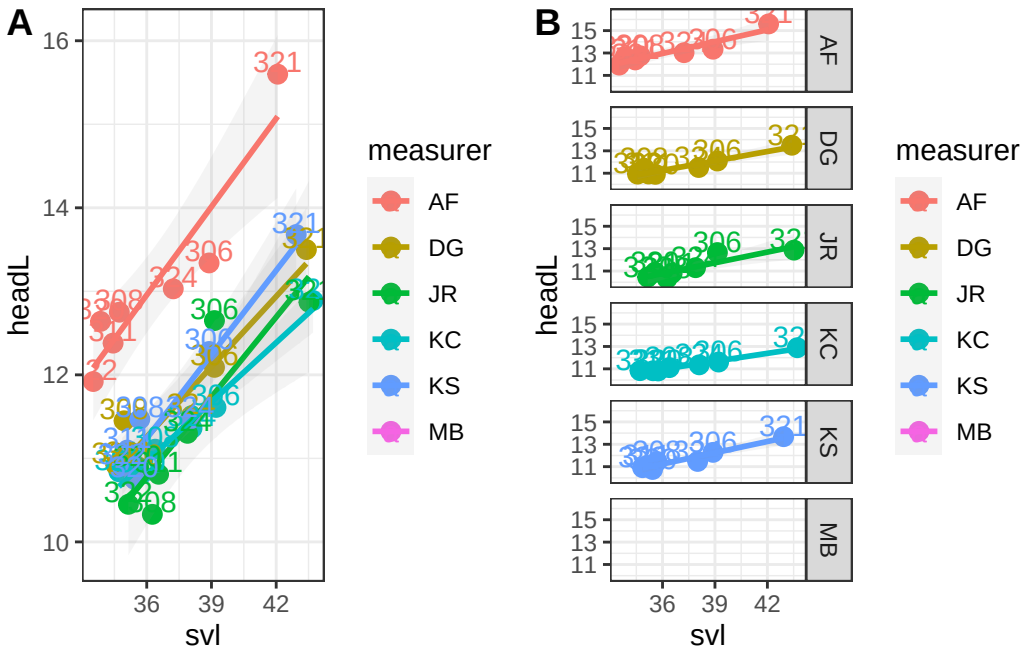
Looks good!

Head Length

```
make_violins(hlv)
```



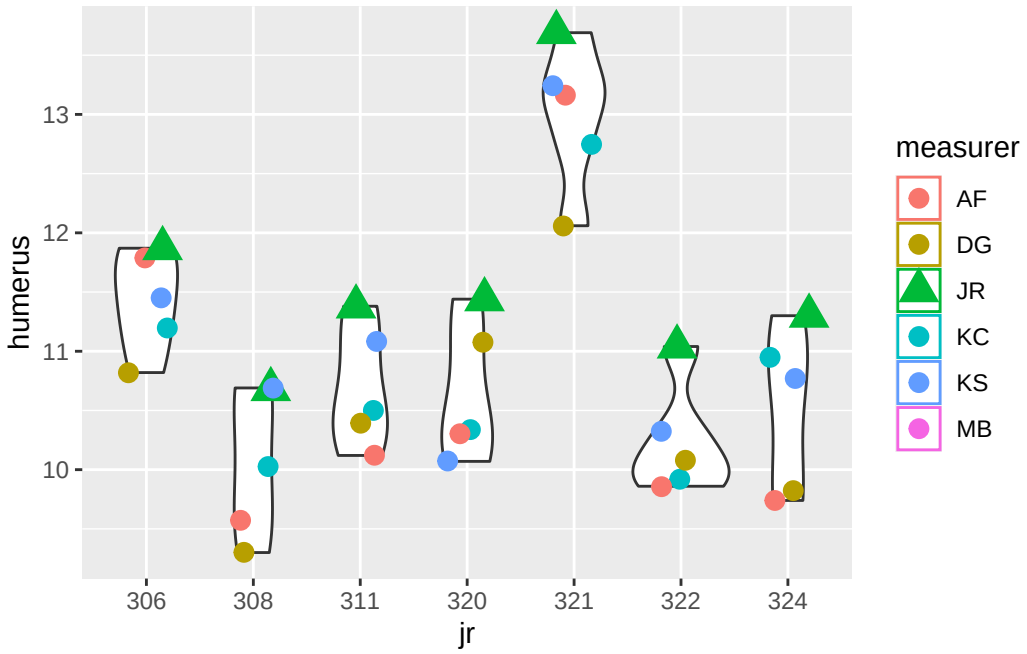

```
make_plots( hlp )
```



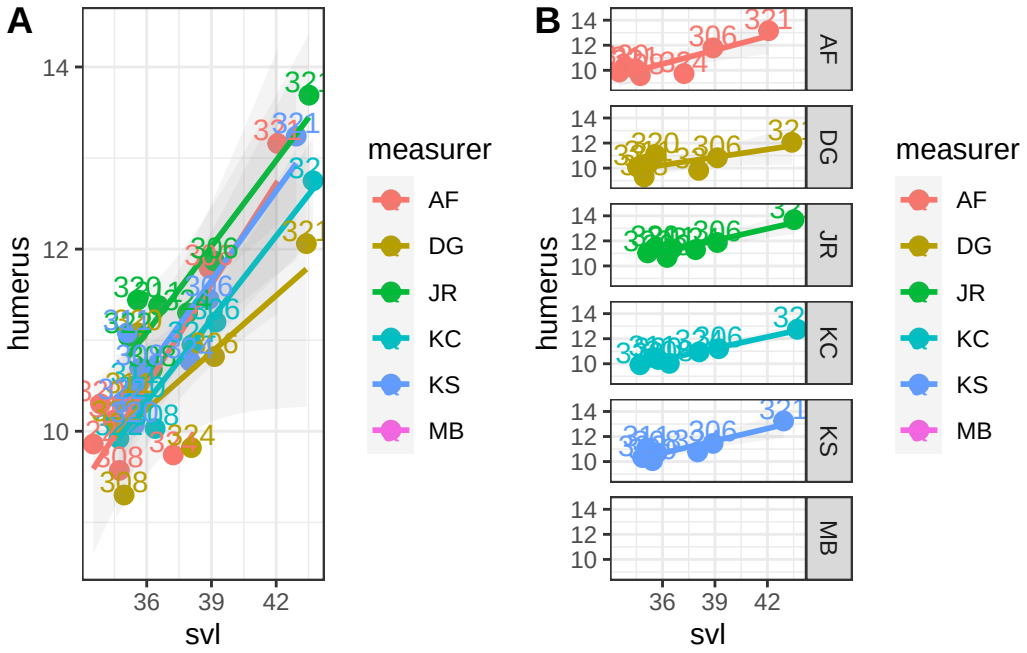
Oh oh. We are not using the right Head Length landmark.

Humerus

```
make_violins(humv)
```



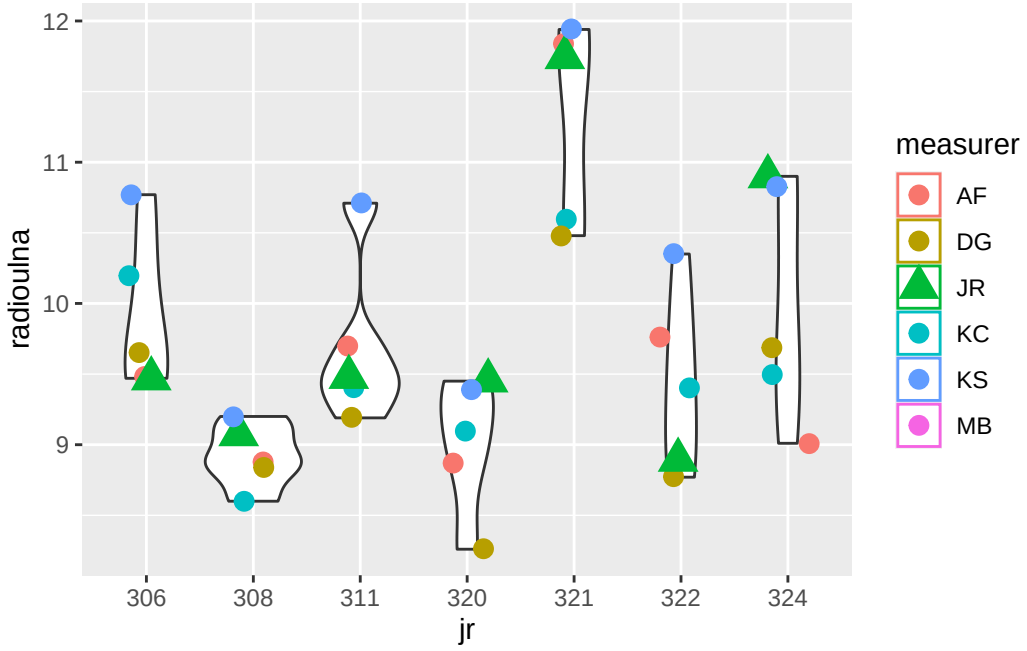

```
make_plots( hump )
```



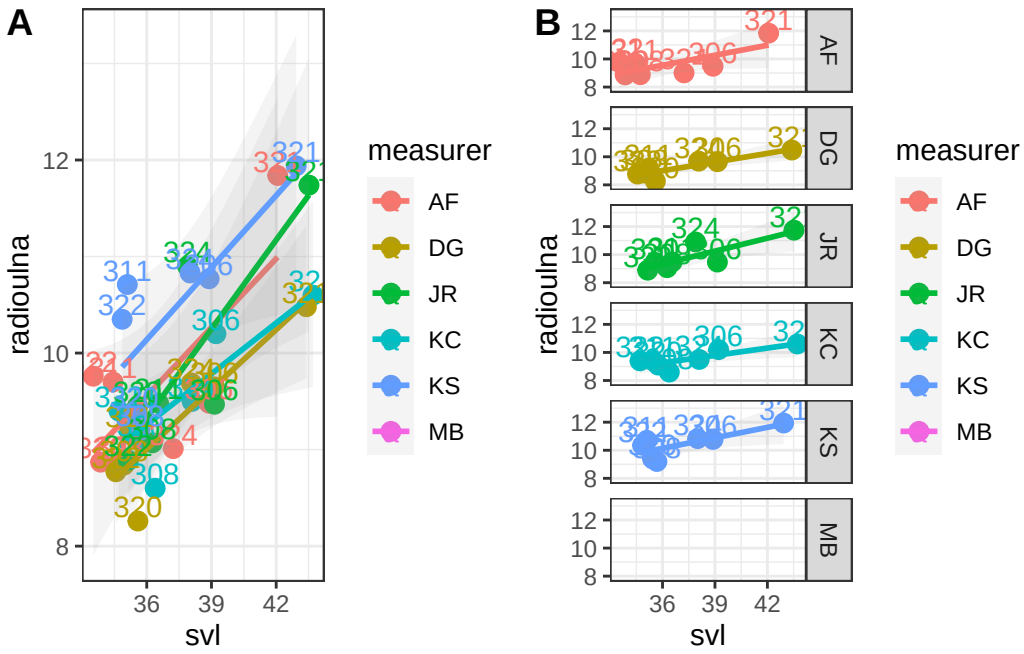
Hmm. We are all a little consistently lower than JR, some more so.

Radioulna

```
make_violins(radv)
```



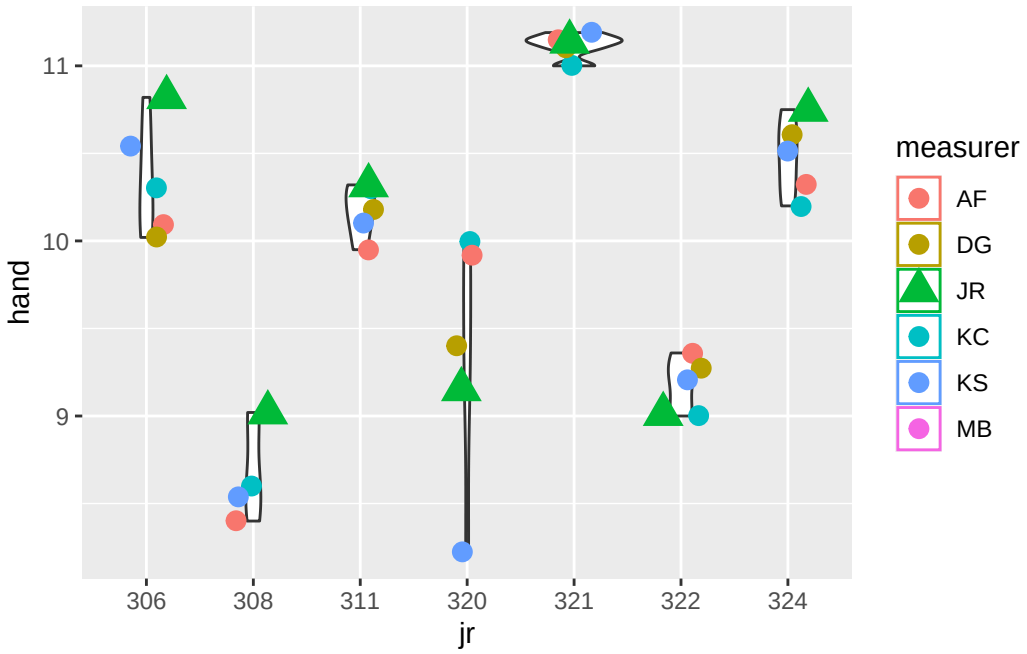

```
make_plots( radp)
```



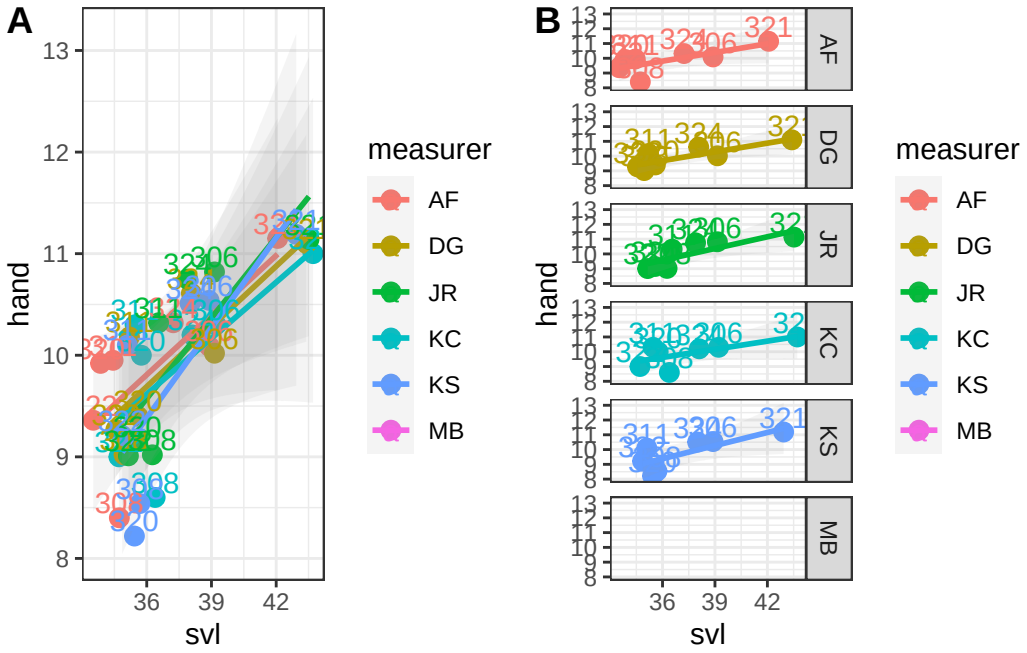
Need to work on this one too.

Hand

```
make_violins(handv)
```




```
make_plots( handp )
```



Looks good!

Conclusions

We need to confirm the landmarks JR used for the limb segment and head length measurements (foot and hand are OK). It looks promising for repeatability but we need to confirm after we get two full sets of measurements.