

SLT_paper

AC

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Contents

History:	1
Read data in	1
Correspondence between lab & zooniverse annotation at the level of segments	2
Precision	5
Recall	6
repeat collapsing	7
Child level descriptors	9

History:

- 2020-08-05 final first version

Read data in

```
#read demo data created by AC from info in paper
demo_data=read.csv("./Data/demo-data.tsv",sep="\t")

# read dataset composed with python
data_all <- read.csv("./Data/new_classifications_PU_zoon.csv")

#remove the word mixed that takes up space and is unnecessary
data_all$Zoon_classif=factor(gsub("Mixed_", "", as.character(data_all$Zoon_classif), fixed=T))

#relevel the factor so that it's easier to read
data_all$Zoon_classif=factor(data_all$Zoon_classif, levels=c("Canonical", "Non-Canonical",
                                                            "Crying", "Laughing", "Junk", levels(data_all$Zoon_classif)))

# create lab column with easier to read correspondance
data_all$lab<-as.character(data_all$Major_Choice)
data_all$lab[data_all$lab=="Non-canonical syllables"]<-"Non-Canonical"
data_all$lab[data_all$lab=="Canonical syllables"]<-"Canonical"
data_all$lab[data_all$lab %in% c("Don't mark", "None")]<-"Junk"
data_all$lab=factor(data_all$lab, levels=levels(data_all$Zoon_classif))
#apply same factor levels as zooniverse so that we can do symmetrical confusion matrices
```

Correspondence between lab & zooniverse annotation at the level of segments

Here we look at to what extent zooniverse and lab annotations match at the level of individual segments. Each data point is one segment (one “vocalization”).

```
table(data_all$lab)
```

```
##
##              Canonical              Non-Canonical
##              271              2669
##              Crying              Laughing
##              54              52
##              Junk              Laughing_Canonical
##              958              0
##              Laughing_Crying      Laughing_Non-Canonical
##              0              0
## Laughing_Non-Canonical_Crying      Non-Canonical_Crying
##              0              0
```

```
table(data_all$Zoon_classif)
```

```
##
##              Canonical              Non-Canonical
##              262              2654
##              Crying              Laughing
##              100              138
##              Junk              Laughing_Canonical
##              614              3
##              Laughing_Crying      Laughing_Non-Canonical
##              5              93
## Laughing_Non-Canonical_Crying      Non-Canonical_Crying
##              7              128
```

```
mycf=confusionMatrix(data_all$lab, data_all$Zoon_classif, dnn = c("Lab","Zooniverse"))
```

```
conf_tab=mycf$table
```

```
# this package uses sensitivity & specificity
#Sensitivity=recall
#Specificity=precision
```

```
mycf
```

```
## Confusion Matrix and Statistics
```

```
##
##              Zooniverse
## Lab          Canonical Non-Canonical Crying Laughing Junk
## Canonical          100          127      3      7    20
## Non-Canonical       60         2155     64     52   183
## Crying              0           17     14      3     3
## Laughing            0            6      2     28     5
## Junk              102         349     17     48   403
## Laughing_Canonical  0            0      0      0     0
## Laughing_Crying     0            0      0      0     0
## Laughing_Non-Canonical 0            0      0      0     0
## Laughing_Non-Canonical_Crying 0            0      0      0     0
```

```

## Non-Canonical_Crying          0          0          0          0          0
##                                Zooniverse
## Lab                            Laughing_Canonical Laughing_Crying
## Canonical                      0              1
## Non-Canonical                  0              3
## Crying                        0              1
## Laughing                      1              0
## Junk                          2              0
## Laughing_Canonical            0              0
## Laughing_Crying               0              0
## Laughing_Non-Canonical        0              0
## Laughing_Non-Canonical_Crying 0              0
## Non-Canonical_Crying          0              0
##                                Zooniverse
## Lab                            Laughing_Non-Canonical
## Canonical                      7
## Non-Canonical                  59
## Crying                        0
## Laughing                      9
## Junk                          18
## Laughing_Canonical            0
## Laughing_Crying               0
## Laughing_Non-Canonical        0
## Laughing_Non-Canonical_Crying 0
## Non-Canonical_Crying          0
##                                Zooniverse
## Lab                            Laughing_Non-Canonical_Crying
## Canonical                      1
## Non-Canonical                  1
## Crying                        2
## Laughing                      1
## Junk                          2
## Laughing_Canonical            0
## Laughing_Crying               0
## Laughing_Non-Canonical        0
## Laughing_Non-Canonical_Crying 0
## Non-Canonical_Crying          0
##                                Zooniverse
## Lab                            Non-Canonical_Crying
## Canonical                      5
## Non-Canonical                  92
## Crying                        14
## Laughing                      0
## Junk                          17
## Laughing_Canonical            0
## Laughing_Crying               0
## Laughing_Non-Canonical        0
## Laughing_Non-Canonical_Crying 0
## Non-Canonical_Crying          0
##
## Overall Statistics
##
## Accuracy : 0.6743
## 95% CI : (0.6596, 0.6888)

```

```

##      No Information Rate : 0.6628
##      P-Value [Acc > NIR] : 0.06382
##
##      Kappa : 0.3692
##
##      McNemar's Test P-Value : NA
##
## Statistics by Class:
##
##      Class: Canonical Class: Non-Canonical Class: Crying
## Sensitivity      0.38168      0.8120      0.140000
## Specificity      0.95430      0.6193      0.989754
## Pos Pred Value   0.36900      0.8074      0.259259
## Neg Pred Value   0.95660      0.6262      0.978228
## Prevalence       0.06543      0.6628      0.024975
## Detection Rate   0.02498      0.5382      0.003497
## Detection Prevalence 0.06768      0.6666      0.013487
## Balanced Accuracy 0.66799      0.7156      0.564877
##
##      Class: Laughing Class: Junk Class: Laughing_Canonical
## Sensitivity      0.202899      0.6564      0.0000000
## Specificity      0.993792      0.8363      1.0000000
## Pos Pred Value   0.538462      0.4207      NaN
## Neg Pred Value   0.972166      0.9307      0.9992507
## Prevalence       0.034466      0.1533      0.0007493
## Detection Rate   0.006993      0.1006      0.0000000
## Detection Prevalence 0.012987      0.2393      0.0000000
## Balanced Accuracy 0.598345      0.7463      0.5000000
##
##      Class: Laughing_Crying Class: Laughing_Non-Canonical
## Sensitivity      0.000000      0.00000
## Specificity      1.000000      1.00000
## Pos Pred Value   NaN      NaN
## Neg Pred Value   0.998751      0.97677
## Prevalence       0.001249      0.02323
## Detection Rate   0.000000      0.00000
## Detection Prevalence 0.000000      0.00000
## Balanced Accuracy 0.500000      0.50000
##
##      Class: Laughing_Non-Canonical_Crying
## Sensitivity      0.000000
## Specificity      1.000000
## Pos Pred Value   NaN
## Neg Pred Value   0.998252
## Prevalence       0.001748
## Detection Rate   0.000000
## Detection Prevalence 0.000000
## Balanced Accuracy 0.500000
##
##      Class: Non-Canonical_Crying
## Sensitivity      0.00000
## Specificity      1.00000
## Pos Pred Value   NaN
## Neg Pred Value   0.96803
## Prevalence       0.03197
## Detection Rate   0.00000
## Detection Prevalence 0.00000
## Balanced Accuracy 0.50000

```

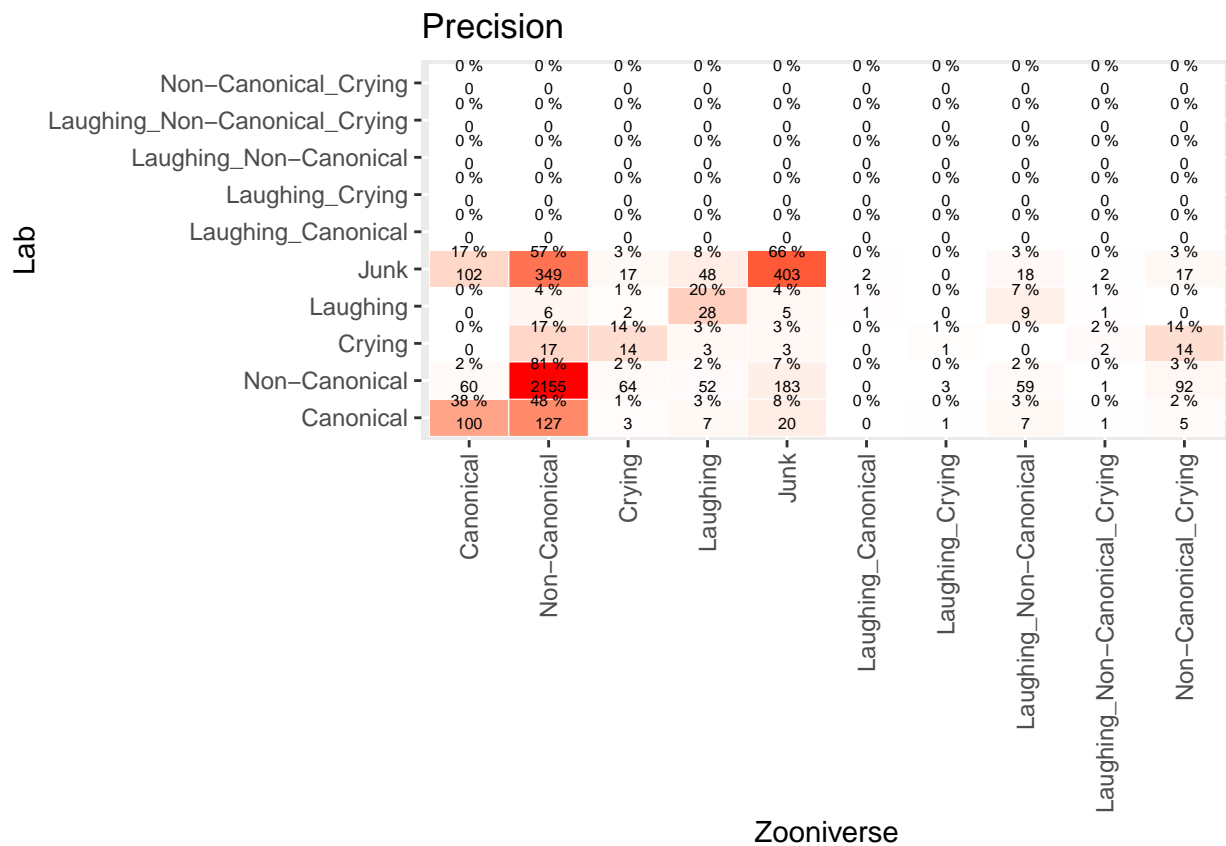
Precision

Precision means: If a segment was called X by zooniverse coders, what proportion of the time was it called X by lab coders?

```
prop_cat=data.frame(conf_tab/colSums(conf_tab)*100) #generates precision because columns
prop_cat$id=paste(prop_cat$Lab,prop_cat$Zooniverse)
colnames(prop_cat)[3]<-"pr"
```

```
data.frame(conf_tab)->stall
stall$id=paste(stall$Lab,stall$Zooniverse)
stall=merge(stall,prop_cat[c("id","pr")])
```

```
ggplot(data = stall, mapping = aes(y = Lab, x=Zooniverse)) +
  geom_tile(aes(fill= rescale(pr)), colour = "white") +
  geom_text(aes(label = paste(round(pr,"%")), vjust = -1,size=2) +
  geom_text(aes(label = Freq, vjust = 1,size=2) +
  scale_fill_gradient(low = "white", high = "red", name = "Percentage") +
  theme(legend.position = "none") +
  xlab("Zooniverse") + ylab("Lab") +
  ggtitle("Precision")+ theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```



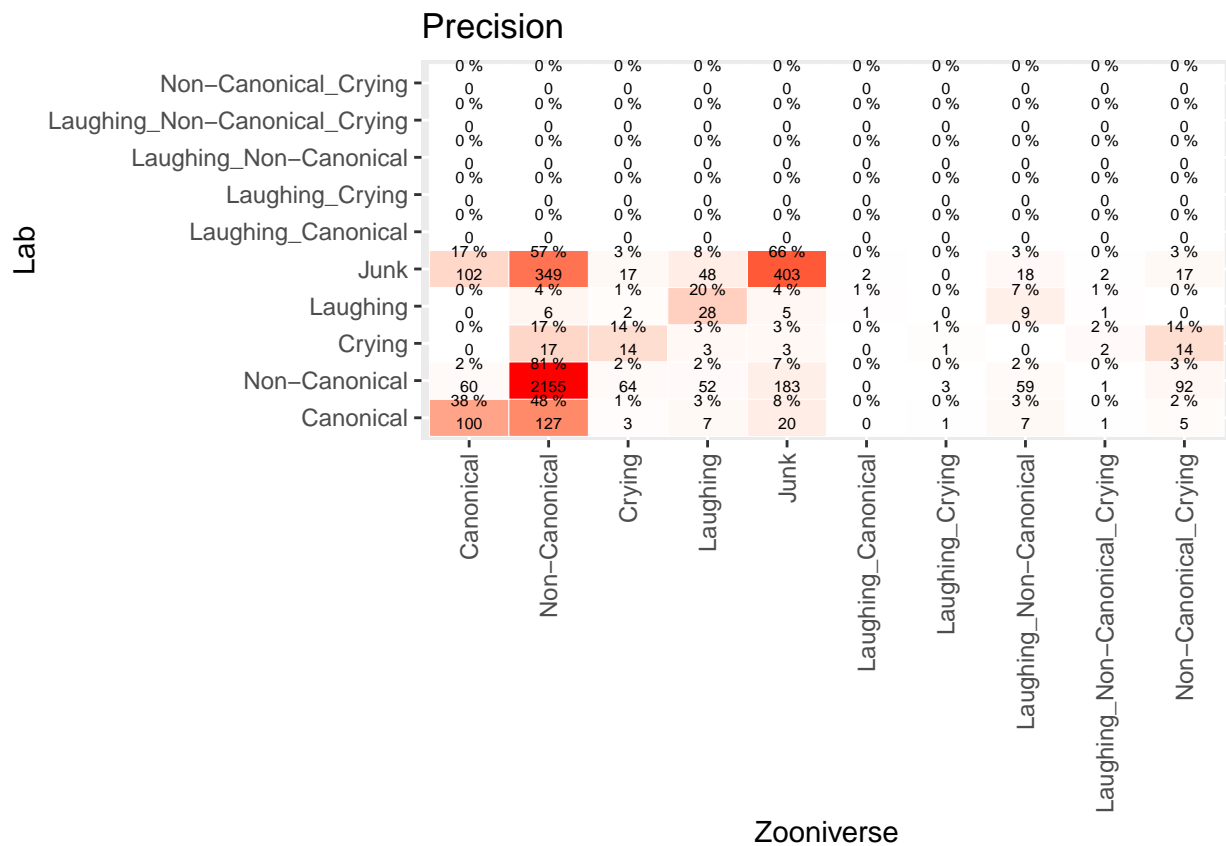
Recall

Recall means: If a segment was called X by lab coders, what proportion of the time was it called X by zooniverse coders?

```
prop_cat=data.frame(conf_tab/colSums(conf_tab)*100) #generates precision because columns
prop_cat$id=paste(prop_cat$Lab,prop_cat$Zooniverse)
colnames(prop_cat)[3]<-"pr"
```

```
data.frame(conf_tab)->stall
stall$id=paste(stall$Lab,stall$Zooniverse)
stall=merge(stall,prop_cat[c("id","pr")])
```

```
ggplot(data = stall, mapping = aes(y = Lab, x=Zooniverse)) +
  geom_tile(aes(fill= rescale(pr)), colour = "white") +
  geom_text(aes(label = paste(round(pr,"%")), vjust = -1,size=2) +
  geom_text(aes(label = Freq, vjust = 1,size=2) +
  scale_fill_gradient(low = "white", high = "red", name = "Percentage") +
  theme(legend.position = "none") +
  xlab("Zooniverse") + ylab("Lab") +
  ggtitle("Precision")+ theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```



repeat collapsing

```
#given results above, we map the mixed
data_all$Zoon_classif[data_all$Zoon_classif=="Laughing_Canonical"]<-"Canonical"
data_all$Zoon_classif[data_all$Zoon_classif=="Laughing_Non-Canonical"]<-"Non-Canonical"
data_all$Zoon_classif[data_all$Zoon_classif=="Laughing_Non-Canonical_Crying"]<-"Non-Canonical"
data_all$Zoon_classif[data_all$Zoon_classif=="Laughing_Crying"]<-"Crying"
data_all$Zoon_classif[data_all$Zoon_classif=="Non-Canonical_Crying"]<-"Non-Canonical"
data_all$Zoon_classif[data_all$Zoon_classif=="Non-Canonical_Laughing_Crying"]<-"Non-Canonical"

#and reset the factors for cleanliness
data_all$Zoon_classif=factor(data_all$Zoon_classif)
data_all$lab=factor(data_all$lab)

mycf=confusionMatrix(data_all$lab, data_all$Zoon_classif, dnn = c("Lab","Zooniverse"))
conf_tab=mycf$table

# this package uses sensitivity & specificity
#Sensitivity=recall
#Specificity=precision

mycf

## Confusion Matrix and Statistics
##
##              Zooniverse
## Lab      Canonical Non-Canonical Crying Laughing Junk
## Canonical      100         140      4         7    20
## Non-Canonical   60        2307     67        52   183
## Crying           0          33     15          3     3
## Laughing         1          16      2         28     5
## Junk           104         386     17         48   403
##
## Overall Statistics
##
##              Accuracy : 0.7125
##              95% CI : (0.6982, 0.7265)
##      No Information Rate : 0.7198
##      P-Value [Acc > NIR] : 0.8503
##
##              Kappa : 0.3989
##
## Mcnemar's Test P-Value : <2e-16
##
## Statistics by Class:
##
##              Class: Canonical Class: Non-Canonical Class: Crying
## Sensitivity           0.37736           0.8005      0.142857
## Specificity           0.95427           0.6774      0.989997
## Pos Pred Value        0.36900           0.8644      0.277778
## Neg Pred Value        0.95580           0.5693      0.977215
## Prevalence            0.06618           0.7198      0.026224
## Detection Rate        0.02498           0.5762      0.003746
## Detection Prevalence  0.06768           0.6666      0.013487
```

```
## Balanced Accuracy          0.66581          0.7389          0.566427
##                               Class: Laughing Class: Junk
## Sensitivity                0.202899          0.6564
## Specificity                0.993792          0.8363
## Pos Pred Value             0.538462          0.4207
## Neg Pred Value             0.972166          0.9307
## Prevalence                 0.034466          0.1533
## Detection Rate             0.006993          0.1006
## Detection Prevalence       0.012987          0.2393
## Balanced Accuracy          0.598345          0.7463
```

```
pdf("./Results/precision.pdf",height=10,width=10)
colsums=colSums(conf_tab)
my_conf_tab=conf_tab
for(i in 1:5) my_conf_tab[,i]=my_conf_tab[,i]/colsums[i]
colSums(my_conf_tab)
```

```
##      Canonical Non-Canonical      Crying      Laughing      Junk
##           1           1           1           1           1
```

```
prop_cat=data.frame(my_conf_tab*100) #generates precision because columns
prop_cat$id=paste(prop_cat$Lab,prop_cat$Zooniverse)
colnames(prop_cat)[3]<-"pr"
```

```
data.frame(conf_tab)->stall
stall$id=paste(stall$Lab,stall$Zooniverse)
stall=merge(stall,prop_cat[c("id","pr")])
```

```
ggplot(data = stall, mapping = aes(y = Lab, x=Zooniverse)) +
  geom_tile(aes(fill= rescale(pr)), colour = "white") +
  geom_text(aes(label = paste(round(pr,"%")), vjust = -1,size=8) +
  geom_text(aes(label = Freq), vjust = 1,size=8) +
  scale_fill_gradient(low = "white", high = "red", name = "Proportion") +
  theme(legend.position = "none") +
  xlab("Zooniverse") + ylab("Lab") +
  ggtitle("Precision")+theme(text = element_text(size=20),
    axis.text.x = element_text(angle=90, hjust=1))
dev.off()
```

```
## pdf
## 2
```

```
pdf("./Results/recall.pdf",height=10,width=10)
prop_cat=data.frame(conf_tab/rowSums(conf_tab)*100) #generates recall because rows
prop_cat$id=paste(prop_cat$Lab,prop_cat$Zooniverse)
colnames(prop_cat)[3]<-"rec"
```

```
data.frame(conf_tab)->stall
stall$id=paste(stall$Lab,stall$Zooniverse)
stall=merge(stall,prop_cat[c("id","rec")])
```

```
ggplot(data = stall, mapping = aes(y = Lab, x=Zooniverse)) +
  geom_tile(aes(fill= rescale(rec)), colour = "white") +
  geom_text(aes(label = paste(round(rec,"%")), vjust = -1,size=8) +
```



```

geom_text(aes(label = Freq), vjust = 1,size=8) +
scale_fill_gradient(low = "white", high = "red", name = "Proportion") +
  theme(legend.position = "none") +
xlab("Zooniverse") + ylab("Lab") +
ggtitle("Recall")+theme(text = element_text(size=20),
  axis.text.x = element_text(angle=90, hjust=1))

dev.off()

## pdf
## 2

```

Child level descriptors

Although there may be errors at the level of the segment, what we really care about is whether Zooniverse annotations give a reliable image of the child's individual development. This is what we look at in this section. In all of these graphs, red points correspond to children diagnosed with Angelman Syndrome, black for low-risk control.

```

#get the ns by child, then calculate the linguistic ratio & canonical ratio, separately for zooniverse
ztab=table(data_all$ChildID,data_all$Zoon_classif)
z_lr=rowSums(ztab[,c("Canonical","Non-Canonical")])/rowSums(ztab[,~which(colnames(ztab) %in% c("Junk"))])
z_cr=ztab[,c("Canonical")]/rowSums(ztab[,c("Canonical","Non-Canonical")])

ltab=table(data_all$ChildID,data_all$lab)
l_lr=rowSums(ltab[,c("Canonical","Non-Canonical")])/rowSums(ltab[,~which(colnames(ztab) %in% c("Junk"))])
l_cr=ltab[,c("Canonical")]/rowSums(ltab[,c("Canonical","Non-Canonical")])

#put all the ratios together
if(sum(rownames(ztab)==rownames(ltab))==dim(ztab)[1]) ratios=cbind(rownames(ztab),z_lr,z_cr,l_lr,l_cr)
colnames(ratios)[1]<-"ChildID"

#add age
#ages=aggregate(data_all$Age,by=list(data_all$ChildID),mean) #this is a weird way of adding ages, since
#improvement: now we merge with a demo data tab, but note this is merged with child id, so the problem

merge(ratios,demo_data,by="ChildID")->ratios
colnames(ratios)[dim(ratios)[2]]<-"Age"

#cbinding results in text, so we numerize the ratios
for(thisvar in c("z_lr","z_cr","l_lr","l_cr")) ratios[,thisvar]=as.numeric(as.character(ratios[,thisvar]))
summary(ratios)

```

```

##      ChildID      z_lr      z_cr      l_lr
## 1111_1 :1  Min.   :0.7667  Min.   :0.02872  Min.   :0.8289
## 1151_1 :1  1st Qu.:0.8967  1st Qu.:0.03864  1st Qu.:0.9383
## 1801_1 :1  Median :0.9321  Median :0.06747  Median :0.9650
## 2881_1 :1  Mean    :0.9120  Mean    :0.10022  Mean    :0.9524
## 3021_1 :1  3rd Qu.:0.9547  3rd Qu.:0.14691  3rd Qu.:0.9840
## 3041_1 :1  Max.    :0.9710  Max.    :0.23474  Max.    :1.0000
## (Other):4
##      l_cr      Diagnosis Sex      Age

```

```
## Min.      :0.01701   AngelmanSyndrome:9   F:3   Min.      :11.83
## 1st Qu.:0.06450   Low-RiskControl :1   M:7   1st Qu.:23.11
## Median :0.07924                                     Median :43.78
## Mean    :0.10246                                     Mean    :35.49
## 3rd Qu.:0.11905                                     3rd Qu.:46.27
## Max.    :0.23529                                     Max.    :53.26
##
```

We first look generally at two measures that have been found to relate to age:

- linguistic ratio = (“Canonical”+“Non-Canonical”)/“All vocalizations” (i.e. we remove junk)
- canonical ratio = “Canonical”/(“Canonical”+“Non-Canonical”) (i.e. we remove junk + non-linguistic vocalizations)

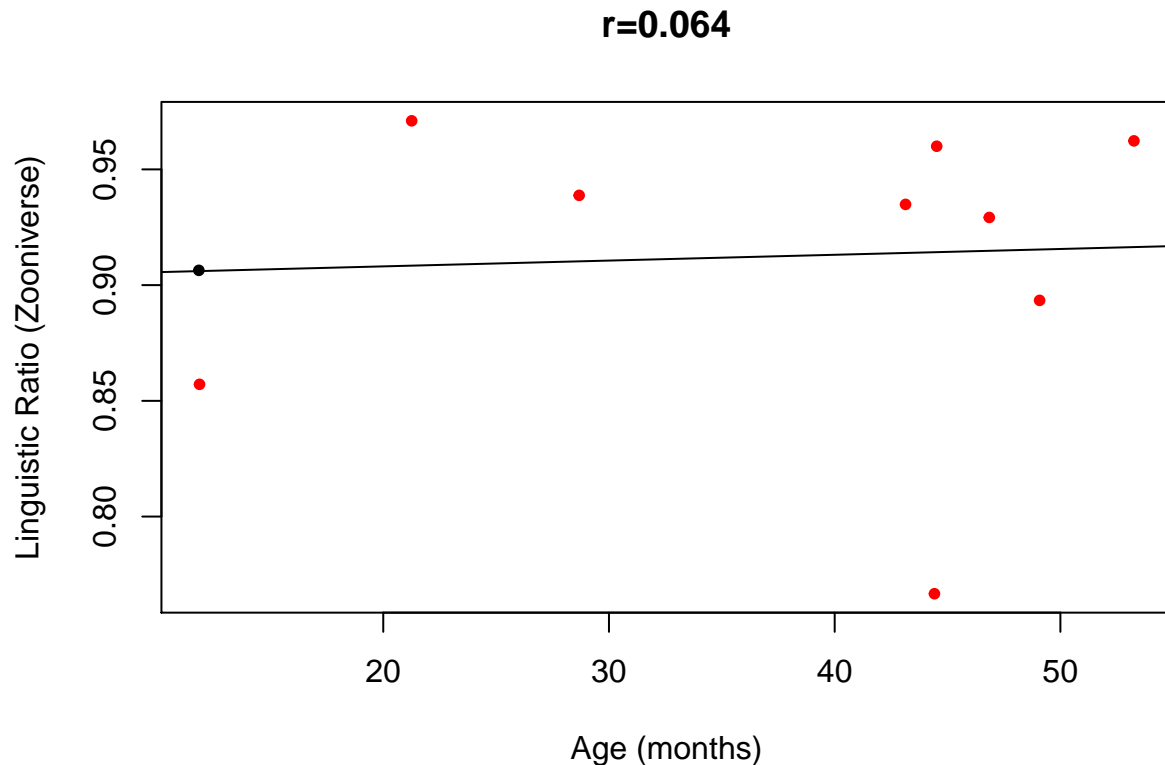
As expected, linguistic ratio goes up with age.

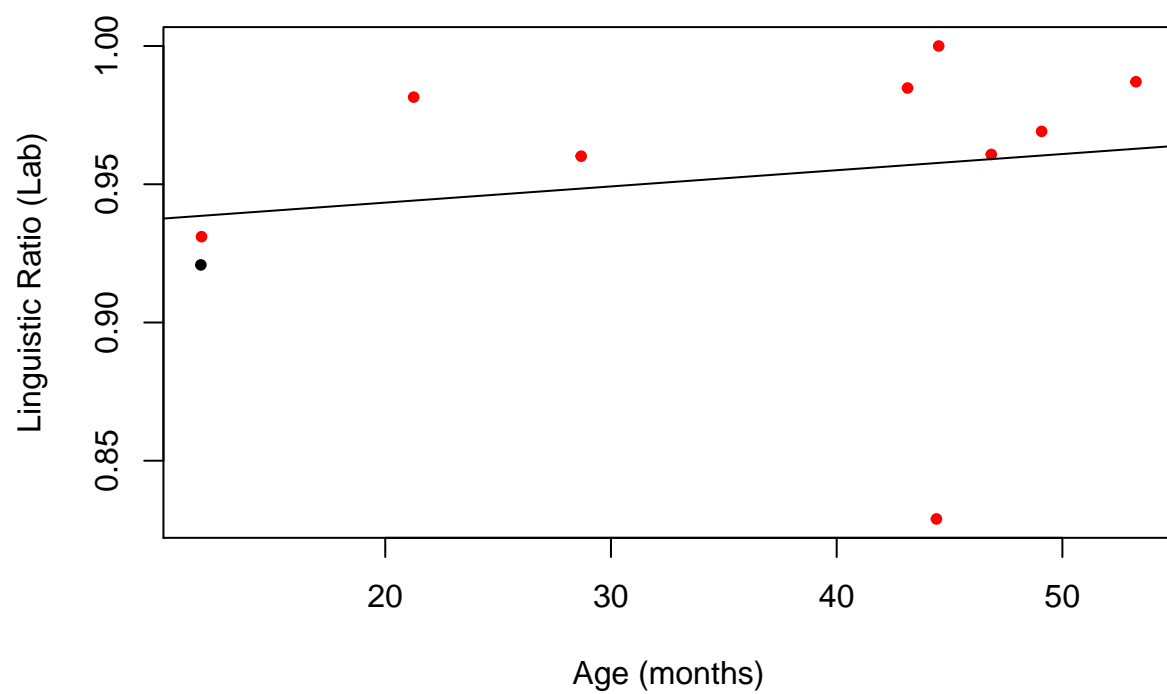
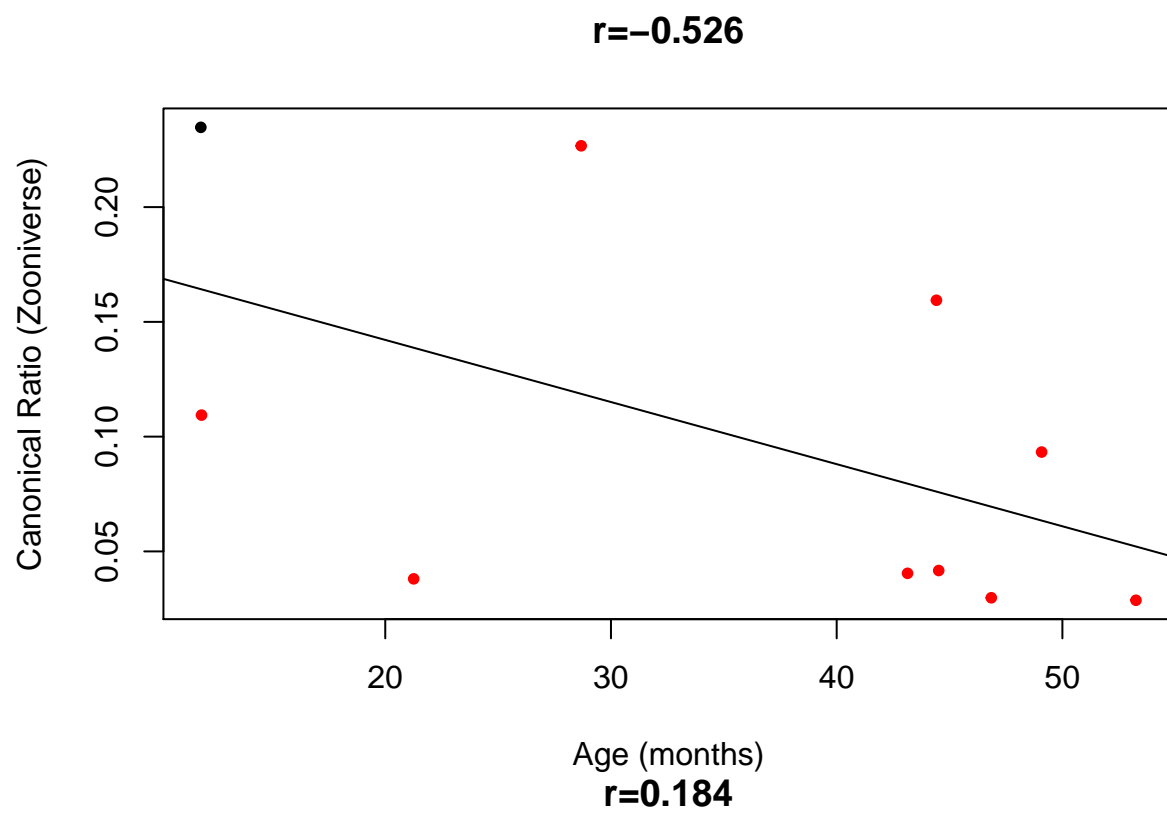
Surprisingly, canonical ratio goes DOWN with age.

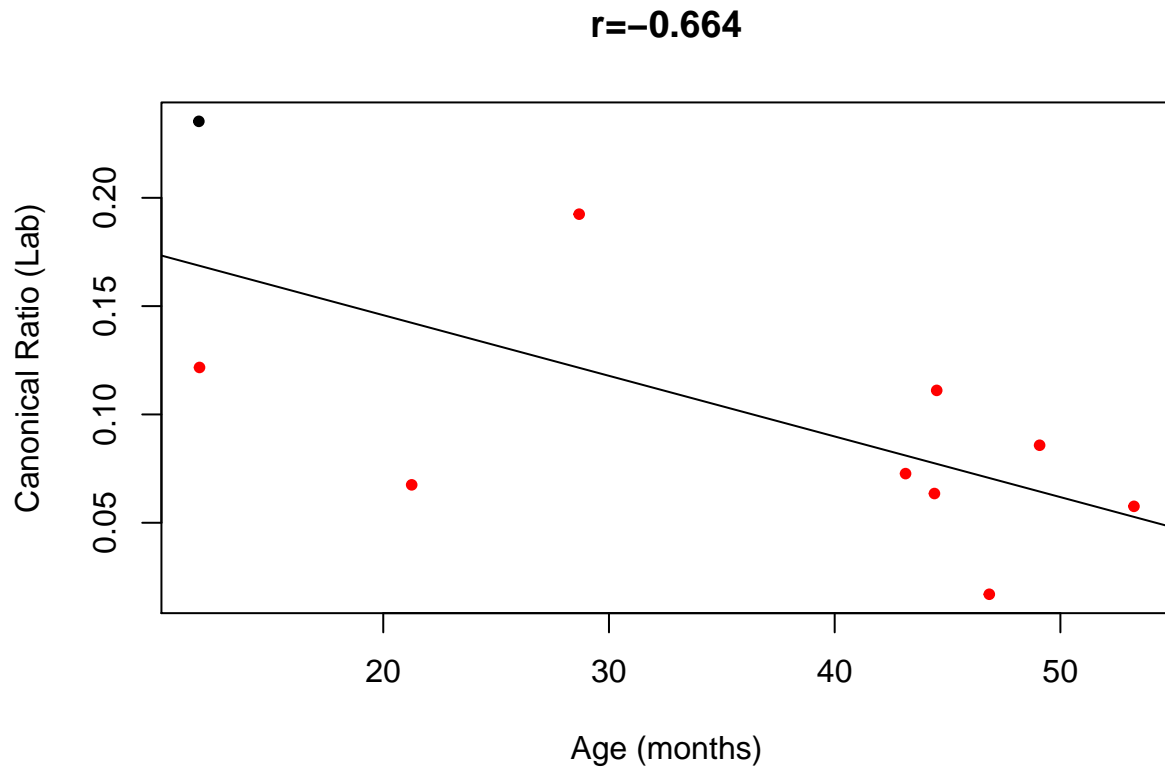
```
prettynames=c("Linguistic Ratio (Zooniverse)","Canonical Ratio (Zooniverse)",
              "Linguistic Ratio (Lab)","Canonical Ratio (Lab)" )
names(prettynames)<-c("z_lr","z_cr","l_lr","l_cr")

#### this is working the opposite than it should! but note that to get angsynd kids to come out in red,
mycols=c("red","black")
names(mycols)<-c("Low-RiskControl","AngelmanSyndrome")

for(thisvar in c("z_lr","z_cr","l_lr","l_cr")) {
  myr=round(cor.test(ratios[,thisvar],ratios$Age)$estimate,3)
  plot(ratios[,thisvar]~ratios$Age, pch=20,xlab="Age (months)",ylab=prettynames[thisvar],main=paste0("r=",myr))
  col=mycols[ratios$Diagnosis]
  abline(lm(ratios[,thisvar]~ratios$Age))
}
```







But the key thing for us: Are Zooniverse annotations describing children similar to lab annotations? The answer is clearly yes.

```
#Ling ratio
pdf("./Results/ling_rat_z_vs_l.pdf",height=5,width=5)
lims=range(c(ratios["z_lr"],ratios["l_lr"]))
myr=round(cor.test(ratios["z_lr"],ratios["l_lr"])$estimate,3)
plot(ratios["z_lr"]~ratios["l_lr"], pch=20,xlab=prettynames["l_lr"],ylab=prettynames["z_lr"],main=p
      xlim=lims,ylim=lims,
      col=mycols[ratios$Diagnosis])
abline(lm(ratios["z_lr"]~ratios["l_lr"]))
lines(c(0,1),c(0,1),lty=2,col="darkgray")
dev.off()
```

```
## pdf
## 2
```

```
#CR
pdf("./Results/can_rat_z_vs_l.pdf",height=5,width=5)
lims=range(c(ratios["z_cr"],ratios["l_cr"]))
myr=round(cor.test(ratios["z_cr"],ratios["l_cr"])$estimate,3)
plot(ratios["z_cr"]~ratios["l_cr"], pch=20,xlab=prettynames["l_cr"],ylab=prettynames["z_cr"],main=p
      xlim=lims,ylim=lims,
      col=mycols[ratios$Diagnosis])
abline(lm(ratios["z_cr"]~ratios["l_cr"]),col="darkgray")
lines(c(0,1),c(0,1),lty=2,col="darkgray")
dev.off()
```

```
## pdf
## 2
```

```

#COMBINED to save space
pdf("./Results/combined.pdf",height=5,width=5)
lims=range(c(ratios[, "z_lr"],ratios[, "l_lr"]),c(ratios[, "z_cr"],ratios[, "l_cr"]))
#myr=round(cor.test(ratios[, "z_lr"],ratios[, "l_lr"])$estimate,3)

plot(ratios[, "z_lr"]~ratios[, "l_lr"],xlab="Laboratory annotations",ylab="Zooniverse annotations",
     xlim=lims,ylim=lims,
     pch=20,col=mycols[ratios$Diagnosis])
points(ratios[, "z_cr"]~ratios[, "l_cr"], pch=2, col=mycols[ratios$Diagnosis])
abline(lm(ratios[, "z_cr"]~ratios[, "l_cr"]))
abline(lm(ratios[, "z_lr"]~ratios[, "l_lr"]),lty=3)
# lines(c(0,1),c(0,1),lty=2,col="darkgray")
dev.off()

## pdf
## 2

```