

Analyses for JSLHR version

2020-10-17

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History:

- 2020-08-05 final first version
- 2020-10-10 (rehaul),
- latest minor edits 2020-10-17

TODO:

- pipeline is still not transparent
- there are duplicate files across raw and derived data
- there are a bunch of files with similar names
- README is old
- a note said read demo data created by AC from info in paper - should be replaced with real demo data
- add code to print out the results paragraphs

Read data in

```
# read datasets

demo_data=read.csv("../Derived_Data/demo-data.tsv",sep="\t")
data_ang <- read.csv("../Derived_Data/classifications_PU_zoon_final17.csv",header=T,sep=",")
data_td <- read.csv("../Derived_Data/classifications_PU_zoon_final.csv")
data_all<-rbind(data_ang, data_td)

#add filenames to demo data
demo_data_fn <- demo_data %>%
  left_join(select(data_all, filename, ChildID), by = c("ChildID"))

## Warning: Column `ChildID` joining factors with different levels, coercing to
## character vector
```

```

demo_data_fn<-unique(demo_data_fn)

#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",
# 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

```

Data post-processing

We collected a total of 169,628 judgments provided for 33,880 500-ms chunks, corresponding to 11,984 LENA segments. Nearly a fifth of chunks did not have at least 3 labels in agreement out of the 5 Zooniverse labels ($N = 6,585$, 19% of all chunks). Of the chunks without a majority agreement, 4341 (66%) contained one or two Junk judgements (out of 5), 6523 (99.9%) had at least two matching judgements (the threshold used for lab-annotated segments), and only 61 (0.01%) had 5 different judgements. Future work may explore different ways of setting the minimal requirement for convergence, but for further analyses here, we focused on the 81% of chunks that did have at least 3 labels in agreement; this represented 136,703 labels for 27,295 chunks, corresponding to 11,593 LENA segments. As the segments average 1.12 seconds in length, this means about 3.8 hours of audio data were annotated by 8 different annotators (3 in the laboratory, 5 on Zooniverse).

```

# remove non-majority labels
#TODO

# 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"
data_all$Zoon_classif[data_all$Zoon_classif=="Crying_Canonical"]<-"Canonical"
# +
data_all$Zoon_classif[data_all$Zoon_classif=="Canonical_Crying"]<-"Canonical"
data_all$Zoon_classif[data_all$Zoon_classif=="Canonical_Laughing"]<-"Canonical"
data_all$Zoon_classif[data_all$Zoon_classif=="Laughing_Canonical_Crying"]<-"Non-Canonical"

data_all$Zoon_classif[data_all$Zoon_classif=="Crying_Laughing"]<-"Crying"
data_all$Zoon_classif[data_all$Zoon_classif=="Crying_Canonical_Laughing"]<-"Canonical"
data_all$Zoon_classif[data_all$Zoon_classif=="Crying_Laughing_Non-Canonical"]<-"Non-Canonical"
data_all$Zoon_classif[data_all$Zoon_classif=="Crying_Non-Canonical"]<-"Non-Canonical"
data_all$Zoon_classif[data_all$Zoon_classif=="Crying_Non-Canonical_Laughing"]<-"Non-Canonical"
data_all$Zoon_classif[data_all$Zoon_classif=="Non-Canonical_Laughing"]<-"Non-Canonical"

#and reset the factors for cleanliness
data_all$Zoon_classif=factor(data_all$Zoon_classif)
data_all$lab=factor(data_all$lab)
sample_data<-cbind(data_all$lab, data_all$Zoon_classif)

```

```

#get the ns by child, then calculate the linguistic ratio & canonical ratio, separately for zooniverse
ztab=table(data_all$filename,data_all$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$filename,data_all$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]<-"filename"

#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

# Created demo_data with filenames. Use filenames instead of childIDs to merge ratios and demo data.

merge(ratios,demo_data_fn,by="filename")->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)

```

```

##          filename      z_lr      z_cr
## 20180206_110905_009463: 1   Min.   :0.5927   Min.   :0.02882
## 20180419_111712_022875: 1   1st Qu.:0.8058   1st Qu.:0.05891
## 20180530_180405_024879: 1   Median :0.8785   Median :0.14065
## 20180530_181101_022875: 1   Mean    :0.8511   Mean    :0.19128
## 20180808_111325_024882: 1   3rd Qu.:0.9313   3rd Qu.:0.28454
## 20180906_133011_022875: 1   Max.    :0.9740   Max.    :0.51084
## (Other)                  :14
##      l_lr      l_cr      ChildID      Diagnosis
## Min.   :0.3880   Min.   :0.01488   Length:20   AngelmanSyndrome:10
## 1st Qu.:0.9130   1st Qu.:0.06609   Class :character   Low-RiskControl :10
## Median :0.9578   Median :0.11115   Mode  :character
## Mean    :0.9131   Mean    :0.19129
## 3rd Qu.:0.9787   3rd Qu.:0.26529
## Max.    :0.9968   Max.    :0.60000
##
## Sex      Age
## F: 7     Min.   : 4.67
## M:13     1st Qu.:12.13
##          Median :17.50
##          Mean    :25.04
##          3rd Qu.:43.46
##          Max.    :53.26
##

```

Results

Descriptive analyses

In this section, we provide descriptive analyses of our dataset. According to lab annotators, 16% of segments were canonical, 57% non-canonical, 2% laughing, and 5% crying, with the remaining 20% being categorized as “Don’t code”. Zooniverse data revealed a similar distribution: 15% canonical, 60% non-canonical, 4% laughing, 9% crying, 12% junk. Next, we inspected the relationship between age and child-level derived metrics, of which we had two: i) Linguistic proportion = (“Canonical”+“Non-Canonical”)/“All vocalizations” (i.e., we remove junk), and ii) Canonical proportion = “Canonical”/ (“Canonical”+“Non-Canonical”) (i.e. we remove junk + non-linguistic vocalizations). See Figure XX for results.

Figure XX. Correlations between child-level descriptors and age as a function of metric (linguistic ratio in the top row, canonical ratio in the bottom row), annotation method

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)

TODO

- make margins smaller
- remove title repetition (age only at the bottom)

```
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")
mycols=c("black","red")
names(mycols)<-c("Low-RiskControl","AngelmanSyndrome")
mypch=c(4,20)
names(mypch)<-c("Low-RiskControl","AngelmanSyndrome")

jpeg("../Results/corage.jpg",width=20,height=20,units="cm",res=300)
layout(matrix(c(1:4), 2, 2, byrow = F))
for(thisvar in c("z_lr","z_cr","l_lr","l_cr")) {

  plot(ratios[,thisvar]~ratios$Age, pch=mypch[ratios$Diagnosis],xlab="Age (months)",ylab=prettynames[thisvar],
       col=mycols[ratios$Diagnosis])
  abline(lm(ratios[,thisvar]~ratios$Age,subset=c(ratios$Diagnosis=="AngelmanSyndrome")),col="black")
  myr=paste0("r=",round(cor.test(ratios[ratios$Diagnosis=="AngelmanSyndrome",thisvar],ratios$Age[ratios$Diagnosis=="AngelmanSyndrome"],method="s",p.adjust="none"))$r,2))
  text(mean(ratios$Age[ratios$Diagnosis=="AngelmanSyndrome"]),mean(ratios[ratios$Diagnosis=="AngelmanSyndrome",thisvar]),myr,col="black")
  abline(lm(ratios[,thisvar]~ratios$Age,subset=c(ratios$Diagnosis!="AngelmanSyndrome")),col="red")
  myr=paste0("r=",round(cor.test(ratios[ratios$Diagnosis!="AngelmanSyndrome",thisvar],ratios$Age[ratios$Diagnosis!="AngelmanSyndrome"],method="s",p.adjust="none"))$r,2))
  text(mean(ratios$Age[ratios$Diagnosis!="AngelmanSyndrome"]),mean(ratios[ratios$Diagnosis!="AngelmanSyndrome",thisvar]),myr,col="red")
}
dev.off()

## pdf
## 2
```

Descriptive analyses on the laboratory annotations showed that the Linguistic proportion increased non-significantly with age when all 20 children were considered together $r(18) = .36$, CI $[-.09,.69]$, $p=0.11$; with a near-zero relationship among the older children diagnosed with Angelman Syndrome $r(8) = .01$, CI $[-.62,.63]$, $p=0.96$; and a significant association among than the younger low-risk control children $r(8) = .74$, CI $[0.20,0.93]$, $p=0.014$. The Canonical proportion exhibited non-significant developmental decreases found

among older children diagnosed with Angelman Syndrome $r(8) = -.55$, CI $[-0.87, .11]$, $p=0.09$; and marginal developmental increases among low-risk control $r(8) = .61$, CI $[-.04, 0.89]$, $p=.06$.

Using the Zooniverse annotations, we found that the Linguistic proportion increased non-significantly with age when all 20 children were considered together $r(18) = .38$, CI $[-.07, .70]$, $p<0.1$. As with laboratory annotations, the association with age was very weak for children diagnosed with Angelman Syndrome $r(8) = -.10$, CI $[-.68, .56]$, $p=.78$, whereas younger low-risk control children showed a significant increase with age $r(8) = .68$, CI $[0.08, 0.91]$, $p=0.03$. Similarly, there were non-significant developmental decreases in the Canonical among children with Angelman Syndrome $r(8) = -.41$, CI $[-.82, .28]$, $p=.23$; and marginal developmental increases among low-risk control children, $r(8) = .60$, CI $[-.04, 0.89]$, $p=.07$.

Given that these derived metrics are defined at the child level, there was one stage in our pre-processing that may not have been necessary, whereby we collapsed judgments across chunks associated to the same segment. We therefore repeated our analyses but deriving our proportions for the Zooniverse data not from the segment-level composite, but rather the individual chunk-level annotations. We found that the Linguistic proportion increased with age when all 20 children were considered together [$r(18) = .41$, $-.30$ $.72$, $P=.07$]. However, when each group was considered separately, Linguistic proportion was not strongly associated with showed a slight decrease with age in the Angelman Syndrome group [$r(8) = -.04$, CI $-.6$ $.6$, $p=0.91$], but increased with age an opposite pattern in the low-risk control group [$r(8) = .71$, CI $.15$ $.92$, $p=.02$]. Similarly, the Canonical proportion did not exhibit the same pattern across the groups, with developmental decreases found among children with Angelman Syndrome $r(8) = -.35$, CI $-.80$ $.35$, $p=.32$; and developmental increases among low-risk control $r(8) = .57$, CI $-.08$ 0.88 , $p=.83$.

Main analyses

Next, we discuss the correspondence between citizen science classifications and the laboratory gold standard, at the level of individual clips. Results were visualized and assessed with a confusion matrix. We report a Precision plot (Fig. 1) and a Recall plot (Fig. 2): the diagonal elements show the number of correct segment-level classifications for each class while the off-diagonal elements show non-matching classifications.

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

```
##
##      Canonical Non-Canonical      Crying      Laughing      Junk
##      1779      6423      588      186      2595
```

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

```
##
##      Canonical Non-Canonical      Crying      Laughing      Junk
##      1715      6944      1036      442      1456
```

```
gac(data = sample_data, kat = 5, weight = c("unweighted"),
    conf.level = 0.95)
```

```
## Call:
## gac(data = sample_data, kat = 5, weight = c("unweighted"), conf.level = 0.95)
##
##      Estimate      StdErr      LowerCB      UpperCB
## Const 0.5866689 0.0053816 0.5761201 0.5972
##
## Confidence level = 95%
## Sample size = 11571
```

```
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
```

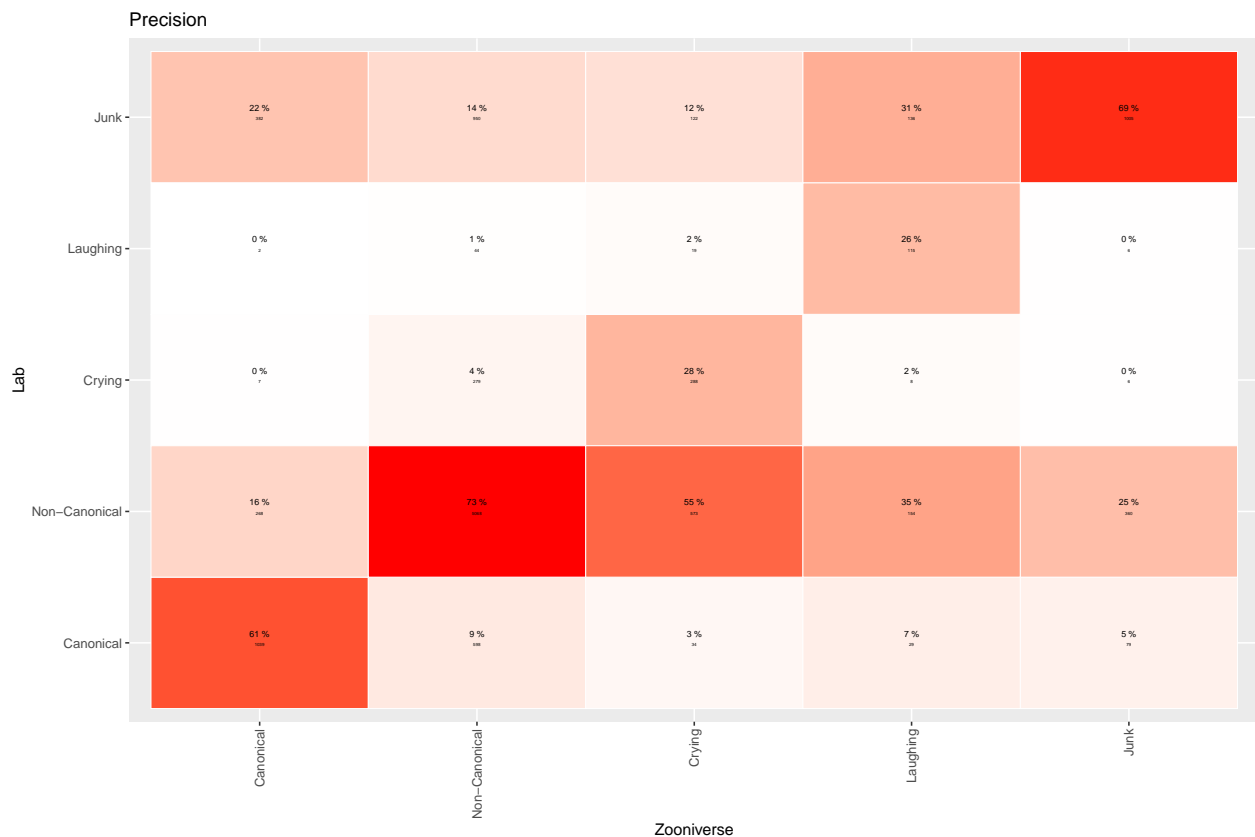
```
## Confusion Matrix and Statistics
##
##              Zooniverse
## Lab          Canonical Non-Canonical Crying Laughing Junk
## Canonical          1039           598      34       29    79
## Non-Canonical       268          5068     573      154   360
## Crying                7           279     288        8    6
## Laughing              2            44      19      115    6
## Junk                 382           950     122     136  1005
##
## Overall Statistics
##
##              Accuracy : 0.6495
##              95% CI : (0.6407, 0.6582)
##      No Information Rate : 0.5997
##      P-Value [Acc > NIR] : < 2.2e-16
##
##              Kappa : 0.4265
##
## Mcnemar's Test P-Value : < 2.2e-16
##
## Statistics by Class:
##
##              Class: Canonical Class: Non-Canonical Class: Crying
## Sensitivity              0.61190              0.7304      0.27799
## Specificity              0.92505              0.7075      0.97152
## Pos Pred Value           0.58404              0.7890      0.48980
## Neg Pred Value           0.93270              0.6366      0.93189
## Prevalence               0.14675              0.5997      0.08953
## Detection Rate           0.08979              0.4380      0.02489
## Detection Prevalence     0.15375              0.5551      0.05082
## Balanced Accuracy        0.76847              0.7189      0.62476
##
##              Class: Laughing Class: Junk
## Sensitivity              0.260181      0.69025
## Specificity              0.993620      0.84281
## Pos Pred Value           0.618280      0.38728
## Neg Pred Value           0.971278      0.94975
## Prevalence               0.038199      0.12583
## Detection Rate           0.009939      0.08686
## Detection Prevalence     0.016075      0.22427
## Balanced Accuracy        0.626901      0.76653
```

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

```
colsums=colSums(conf_tab)
my_conf_tab=conf_tab
for(i in 1:dim(conf_tab)[2]) 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=2) +
  geom_text(aes(label = Freq, vjust = 1,size=1) +
  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 means: If a segment was called X by lab coders, what proportion of the time was it called X by zooniverse coders?

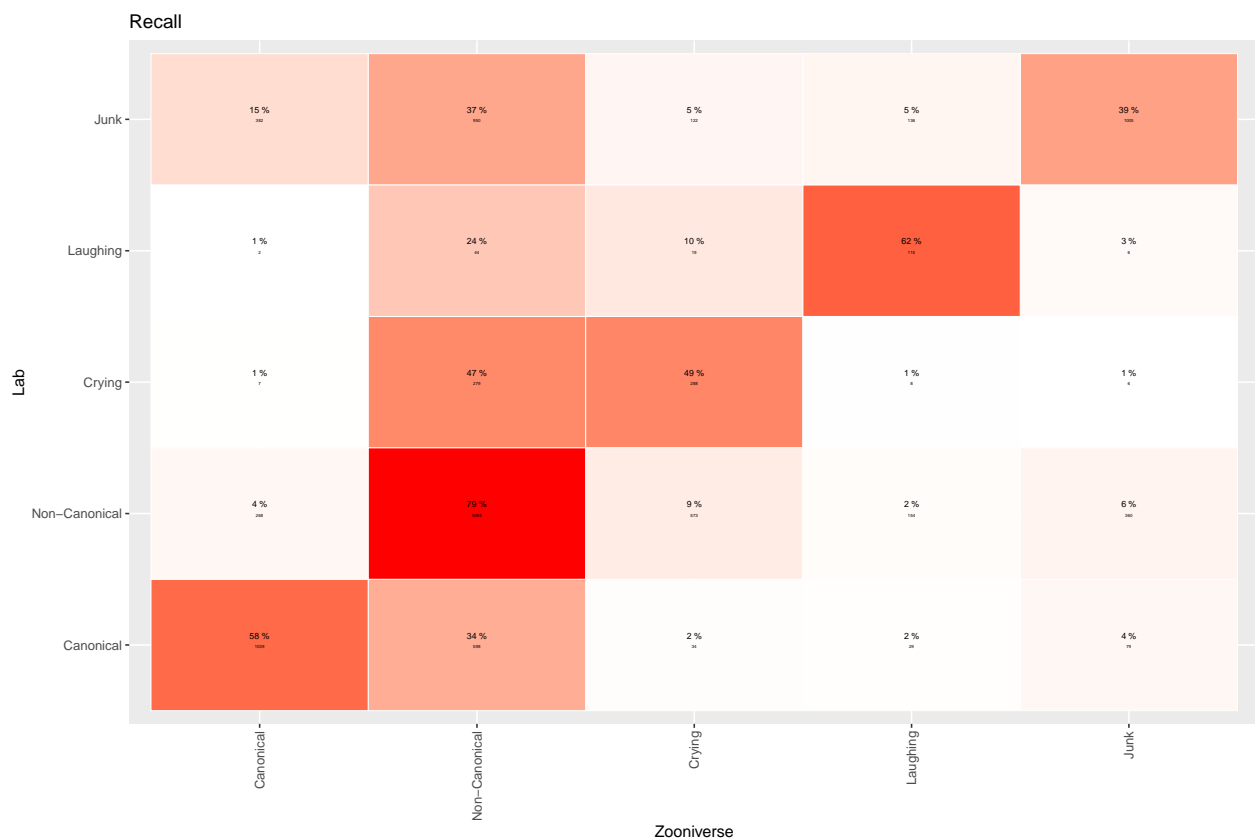
```
rowsums=rowSums(conf_tab)
my_conf_tab=conf_tab
for(i in 1:dim(conf_tab)[2]) my_conf_tab[,i]=my_conf_tab[,i]/rowsums[i]
rowSums(my_conf_tab)
```

```
## Canonical Non-Canonical Crying Laughing Junk
## 0.9213192 2.8808609 0.5824913 0.6608792 1.6885824
```

```

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=2) +
  geom_text(aes(label = Freq), vjust = 1,size=1) +
  scale_fill_gradient(low = "white", high = "red", name = "Percentage") +
  theme(legend.position = "none") +
  xlab("Zooniverse") + ylab("Lab") +
  ggtitle("Recall")+ theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))

```



From both visualizations, it appears that performance is moderate to good, with an overall accuracy of 65% (95% CI = .64-.66), a kappa of .4, and a Gwet's AC1 coefficient of .67 (95% CI = .66,.69). A closer look at the confusion matrix reveals that errors in the classification are not distributed randomly. The Non-Canonical label shows the highest agreement between Zooniverse and lab experts (Recall 79%), and it is worth noticing that a majority of segments in the dataset were assigned this classification attributed this judgment. Junk and Canonical show a moderately good agreement (Recall 62% and 58% respectively), with other classes having more variable assignments (49% for Crying and 39% for Junk).

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.

Although the classification at the clip level is only moderately accurate, what we are ultimately interested in is whether citizen scientists' classifications are able to provide a reliable snapshot of childrens' individual development. Looking at all 20 children together, we found a strong positive correlation ($r(18) = 0.811$, CI 0.58-0.92, $p < 0.001$) between Linguistic proportion by child from the Zooniverse and the lab annotators' data. We notice a trend for Linguistic Proportions from Zooniverse data to be lower than that from laboratory data (see Fig. 3). When we split by participant group, correlations remain high [Angelman Syndrome $r(8) = .88$, CI .55-.97, $p < 0.001$; low-risk control $r(8) = .82$, CI .4 - .96, $p < 0.01$].

Similarly, a strong positive correlation ($r = 0.937$, 0.84 0.97, $p < 0.001$) is found in the Canonical Proportion. Unlike the linguistic proportion, the error for Canonical Ratio is very small and does not suggest a systematic over- or under-estimation (see Fig. XX). When we split by participant group, correlations remain high although we do note they are somewhat smaller for the children with Angelman Syndrome, who are also older than the low-risk control children [Angelman Syndrome $r(8) = .86$, CI 0.5-.96, $p < 0.01$; low-risk control $r(8) = .96$, CI 0.83-0.99, $p < 0.001$]. When we use chunk-level judgments to derive the our child-level metrics, we observe very similar levels of correlation: linguistic proportion overall $r(18) = .84$, CI .63 .93, $p < 0.001$ [Angelman Syndrome $r(8) = .82$, CI .41 .95, $p < 0.01$; low-risk control $r(8) = .84$, CI .44 0.96, $p < 0.01$]; canonical proportion overall $r(18) = .96$, CI .90 .98, $p < 0.001$ [Angelman Syndrome $r(8) = .85$, CI .49 .85, $p < 0.01$; low-risk control $r(8) = .97$, CI .89 .99, $p < 0.001$].

TODO:

- change figure generation to have lines fitted to each group

```
#Ling ratio
pdf("../Results/ling_rat_z_vs_l_final.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_final.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()

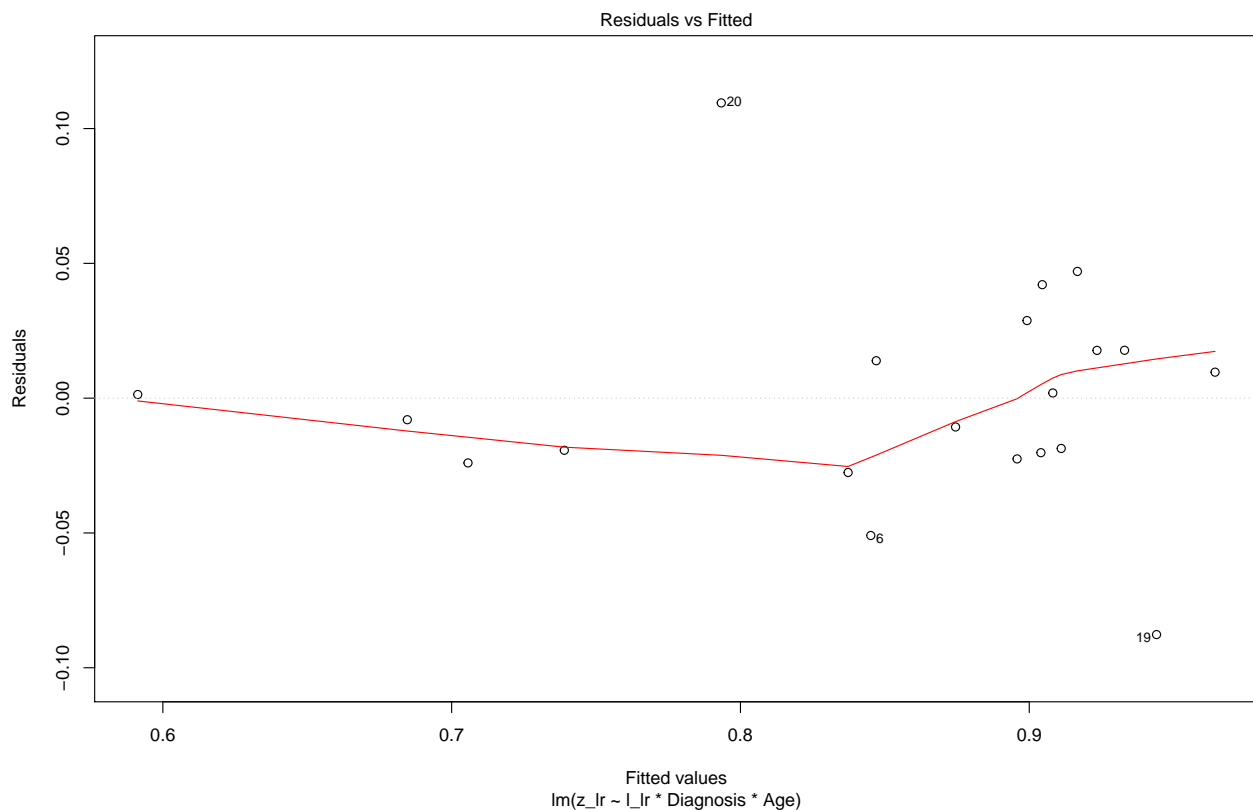
## pdf
## 2

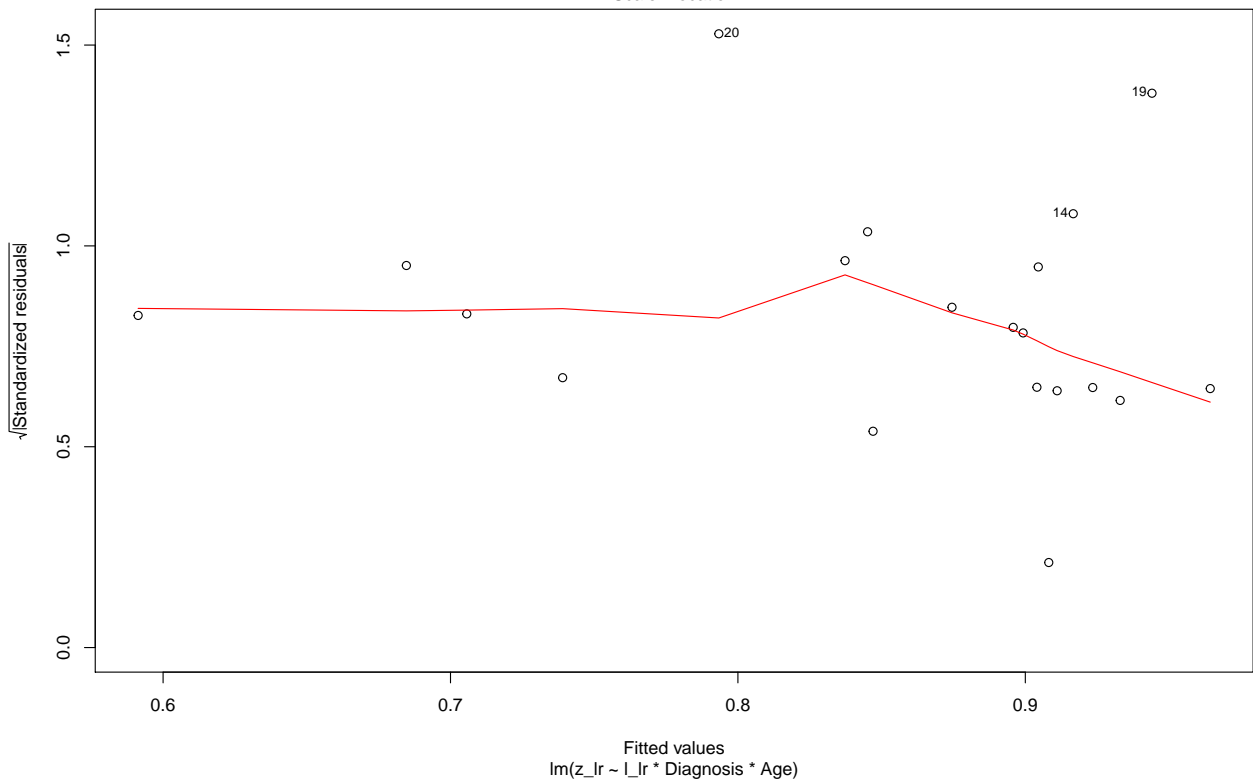
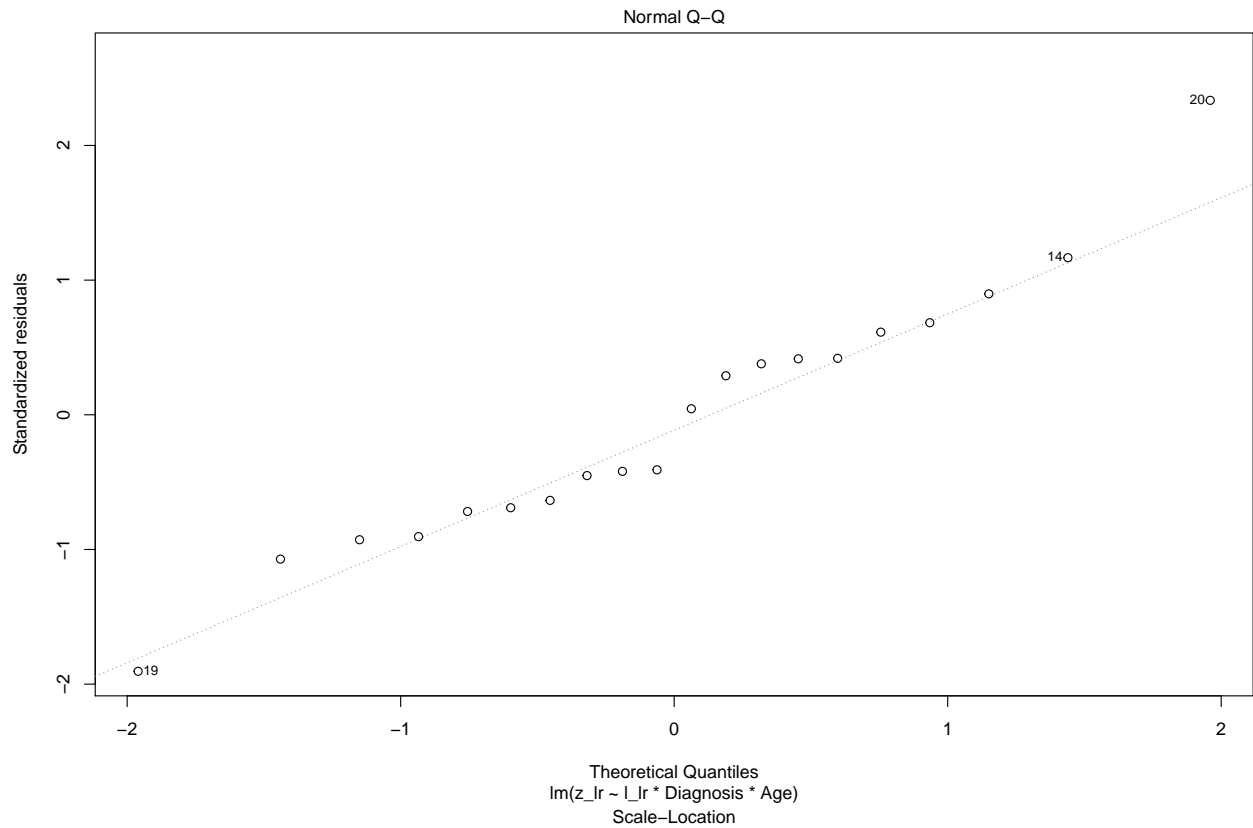
lin_mod=lm(z_lr~l_lr*Diagnosis*Age,data=ratios)
summary(lin_mod)

##
```

```
## Call:
## lm(formula = z_lr ~ l_lr * Diagnosis * Age, data = ratios)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.087697 -0.020805 -0.003327  0.017732  0.109518
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1.89796     2.53800   -0.748   0.4690
## l_lr           2.95125     2.65350    1.112   0.2878
## DiagnosisLow-RiskControl 2.84516     2.54890    1.116   0.2862
## Age            0.03583     0.05740    0.624   0.5442
## l_lr:DiagnosisLow-RiskControl -3.03307     2.66494   -1.138   0.2773
## l_lr:Age       -0.03819     0.05996   -0.637   0.5362
## DiagnosisLow-RiskControl:Age -0.15256     0.07332   -2.081   0.0595 .
## l_lr:DiagnosisLow-RiskControl:Age 0.16017     0.07535    2.126   0.0550 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05096 on 12 degrees of freedom
## Multiple R-squared:  0.8575, Adjusted R-squared:  0.7744
## F-statistic: 10.32 on 7 and 12 DF,  p-value: 0.0003014
```

```
plot(lin_mod)
```





```
## Warning in sqrt(crit * p * (1 - hh)/hh): NaNs produced
```

```
## Warning in sqrt(crit * p * (1 - hh)/hh): NaNs produced
```

