

The effect of masks on the perception of speech sounds: Supporting Information

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Introduction

A note on multimodal explanations of speech perception problems with facemasks

Lipreading is an important strategy used by all listeners, regardless of hearing impairment, to improve speech perception through visual cues telegraphed from the speaker's face, including lip and jaw movement (Jeffers & Barley, 1971; Campbell et al., 1997). Facemasks cover a portion of our face that contains important linguistic information, including place of production for consonants (closed lips suggest bilabial plosives, /p, b/), and vowel height (open jaw illustrates an open vowel, /a/). This visual information, in tandem with the speech signal, aids overall speech perception (Yi et al., 2021). Previous studies have proven that the loss of visual information caused by facemasks can inhibit speech perception, and that reintroducing visual information via a clear plastic screen can improve speech perception in hearing impaired and normal-hearing adults (Atcherson et al., 2017; Thibodeau et al 2021; Yi et al., 2021).

Thibodeau et al. (2021) tested the effects of visual information on speech perception with facemasks in noise. Two mask types were tested: a cotton mask with a transparent vinyl screen and the same mask with a piece of cotton covering the screen, therefore, the only change across mask type was the loss of visual information. Participants were presented with sentence stimuli from the Hearing in Noise Test (Nilsson et al., 1994). Listeners were tasked with transcribing a set of stimuli in both mask conditions, then accurate transcription scores were compared across mask types. Thibodeau et al. (2021) found that the use of transparent facemasks significantly facilitated speech recognition in noise, regardless of hearing ability, and

observed a mean 10 percentage-point increase in correct perception from the opaque mask to transparent mask.

Although these results provide evidence of the importance of visual information when communicating with facemasks, CDC (2021) advise that people avoid transparent plastic masks as they are not considered sufficiently breathable. Despite this, the National Association of the Deaf (NAD), a non-peer-reviewed website, suggest wearing transparent masks to aid speech perception in people who are hard-of-hearing (National Association of the Deaf, 2020). The studies cited regarding lipreading do provide one answer as to how facemasks affect speech perception; they do not, however, cover other ways facemasks may affect speech perception e.g., forms of acoustic degradation.

Jeffers, J. & Barley, M. (1971). *Speechreading (Lipreading)*. Springfield, Illinois: Charles C Thomas

Campbell, R., Zihl, J., Massaro, D., Munhall, K., Cohen, M.M. (1997) Speechreading in the akinetopsic patient. *Brain* 120 (10). pp. 1793-1803

Yi, H., Pingsterhaus, A. and Song, W. (2021) Effects of Wearing Face Masks While Using Different Speaking Styles in Noise on Speech Intelligibility During the COVID-19 Pandemic. *Front. Psychol.* 12.

Thibodeau, L.M., Thibodeau-Nielsen, R.B., Tran, C.M.Q., Jacob, R.T.S. (2021). Communicating During COVID-19: The Effect of Transparent Masks for Speech Recognition in Noise. *Ear Hear.* 42(4), pp.772-781.

Nilsson, M., Soli, S.D., Sullivan, J.A. (1994). Development of the Hearing in Noise Test for the measurement of speech reception thresholds in quiet and in noise. *J Acoust Soc Am* 95(2).

National Association of the Deaf. (2020). COVID-19: Deaf and hard of hearing communication access recommendations for the hospital. Available at: <https://www.nad.org/COVID19-communication-access-recs-for-hospital/> (accessed: 16th October 2021)

Load libraries

```
library(dplyr)
library(ggplot2)
library(lme4)
library(car)
library(sjPlot)
library(party)
library(ggpubr)
library(lattice)
```

Acoustic analysis

Make power spectrum graphs from Praat data. The function aggregates samples into bins of frequency (default is 25hz wide). The just noticeable difference data comes from Long (2014). I'm using the 5dB data since it's most conservative.

```
# Function to summarise one data file
summariseData = function(d,upperRange = 8000, samplingWindow = 25){
  # Cut data above upper range
  d = d[d$freq.Hz.<=upperRange,]

  sampleBoundaries = seq(0,upperRange,by=samplingWindow)
  sampleMidpoints = sampleBoundaries + samplingWindow/2

  d$sampleBin = cut(d$freq.Hz., sampleBoundaries)

  d.win = data.frame(
    freq.Hz. = sampleMidpoints[1:(length(sampleMidpoints))-1],
    pow.dB.Hz. = tapply(d$pow.dB.Hz., d$sampleBin,mean)
  )
  return(d.win)
}

jndHz = c(35,70,200,1000,4000,8000,10000)
# at 5db
jndDB = c(9.3,5.7,4.7,3.0,2.5,4.0,4.7)
# at 10db
jndDB10db = c(7.8, 4.2, 3.4, 2.3, 1.7, 2.8, 3.3)
jndSpline = smooth.spline(jndHz,jndDB,df = 6,all.knots = T)

makePowerDifferenceGraph = function(maskedFile, unmaskedFile,mainTitle="",plotXLAB=TRUE,plotYLAB=TRUE){
  # Load and summarise data
  d.masked = summariseData(read.csv(maskedFile))
  d.unmasked = summariseData(read.csv(unmaskedFile))

  # Plot raw power
  plot(d.unmasked$freq.Hz., d.unmasked$pow.dB.Hz., type='l',
       xlab="Frequency (Hz)", ylab="Power (dB)",
       main=mainTitle, ylim=c(-32,35))
  points(d.masked$freq.Hz., d.masked$pow.dB.Hz., type='l', col='2')
  legend(5000,32,legend=c("Unmasked", "Masked"),col=1:2,lty=1)
```

```

# Plot difference in power
d.masked$diff = d.masked$pow.dB.Hz. - d.unmasked$pow.dB.Hz.

d.masked$dbMax = predict(jndSpline, x = d.masked$freq.Hz.)$y
d.masked$dbMin = - d.masked$dbMax

attenuation = d.masked$diff - d.masked$dbMin
print(sum(attenuation[attenuation<0]))

plot(d.masked$freq.Hz., d.masked$diff, type='l',
      xlab="Frequency (Hz)", ylab= "Difference in power (dB)",
      main = mainTitle, ylim=c(-25,10))
abline(h=0,col=rgb(0,0,0,0.4))
#points(jndHzFullScale, jndDBFullScale,type = "l",col='light gray')
#points(jndHzFullScale, -jndDBFullScale,type = "l",col='light gray')

gx = ggplot(d.masked, aes(x=freq.Hz., y = diff)) +
  geom_ribbon(aes(x=freq.Hz., ymin=dbMin, ymax=dbMax),
            alpha = 0.3) +
  geom_hline(yintercept = 0,colour="dark gray") +
  geom_line(alpha=0.9) +
  ylim(c(-24,10))

if(plotXLAB){
  gx = gx + xlab("Frequency (Hz)")
} else{
  gx = gx + theme(axis.title.x = element_blank())
}
if(plotYLAB){
  gx = gx + ylab("PD (db)")
} else{
  gx = gx + theme(axis.title.y = element_blank())
}

return(gx)
}

# Apply the functions to all the files

#pdf("PowerAnalyses.pdf", width=6, height=5)
dx = summariseData(read.csv("../data/AcousticAnalysis/Masked_D.Table.csv"))
dx$dbMax = predict(jndSpline, x = dx$freq.Hz.)$y
dx$dbMin = - dx$dbMax

guideGraph = ggplot(dx,aes(x = freq.Hz., y=20)) +
  geom_ribbon(aes(x=freq.Hz., ymin=dbMin, ymax=dbMax),
            alpha = 0.3) +
  #geom_hline(yintercept = 0) +
  geom_line(alpha=0.9) +
  coord_cartesian(ylim=c(-24,10)) +
  ylab("PD (db)") + theme(axis.title.x = element_blank()) +
  annotate("text",x = 500,y=8,label="Fascemask increases intensity",hjust="left") +

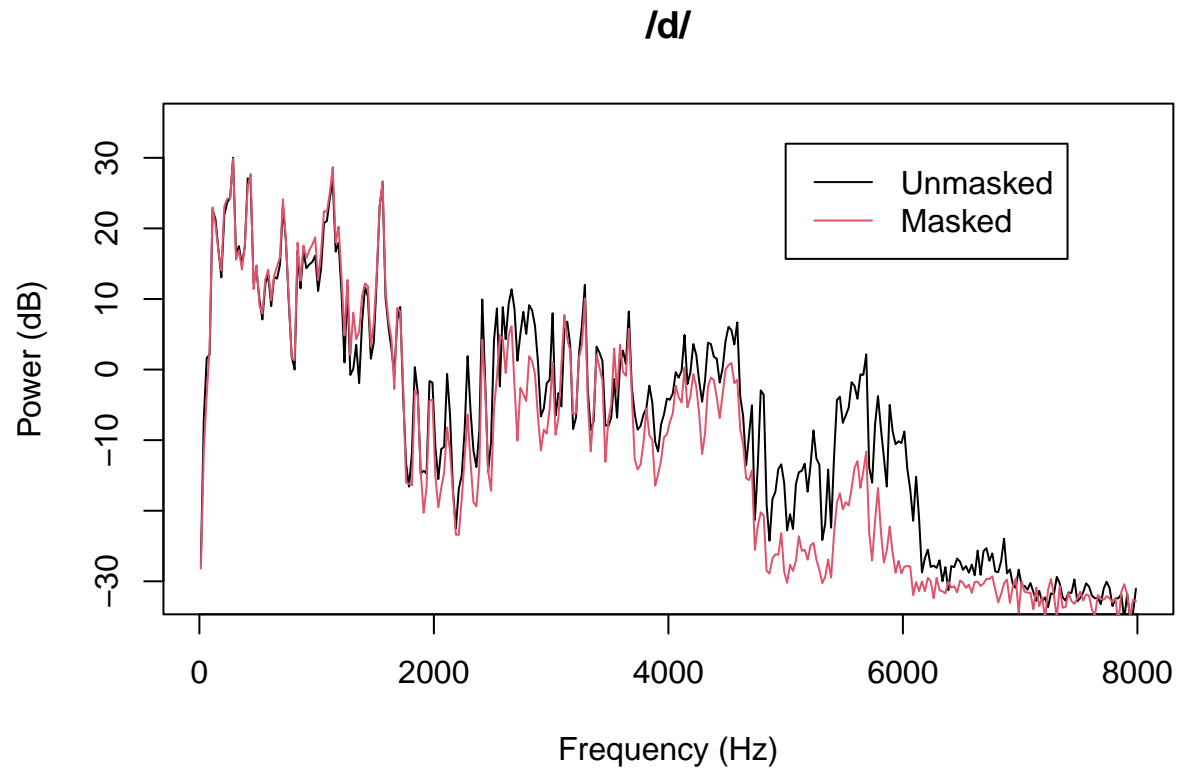
```

```

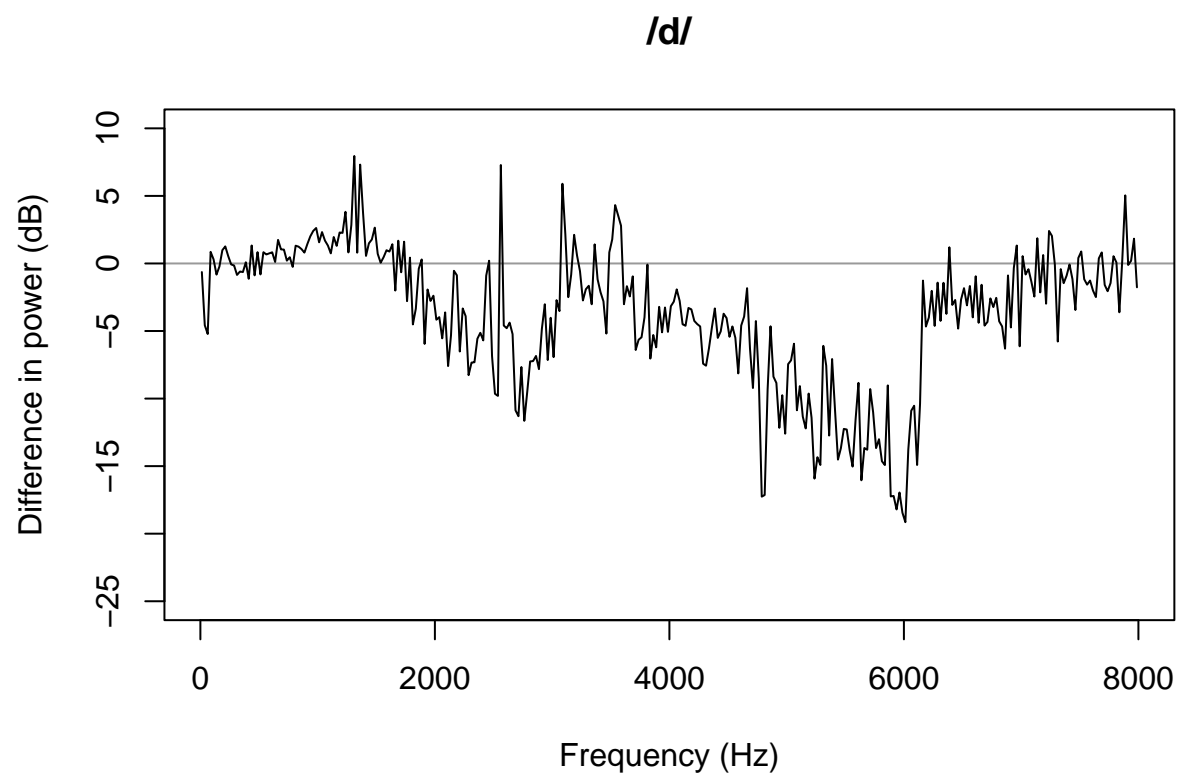
annotate("text",x = 500, y = -10, label="Fascemask decreases intensity",hjust="left") +
annotate("text",x = 500, y = 0, label="No Noticable Difference",colour="#525252",hjust="left")

gD = makePowerDifferenceGraph("../data/AcousticAnalysis/Masked_D.Table.csv", "../data/AcousticAnalysis/
annotate("text", x = 500,y=-15,label="/d/",size =8)

```

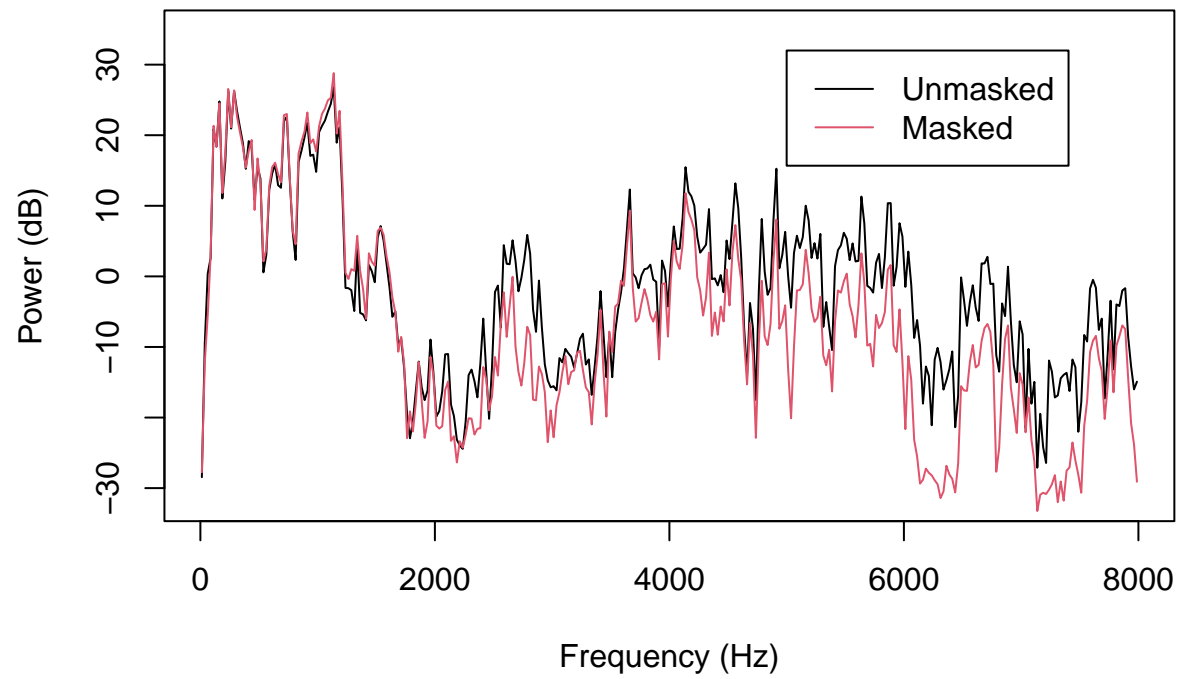


```
## [1] -779.2628
```

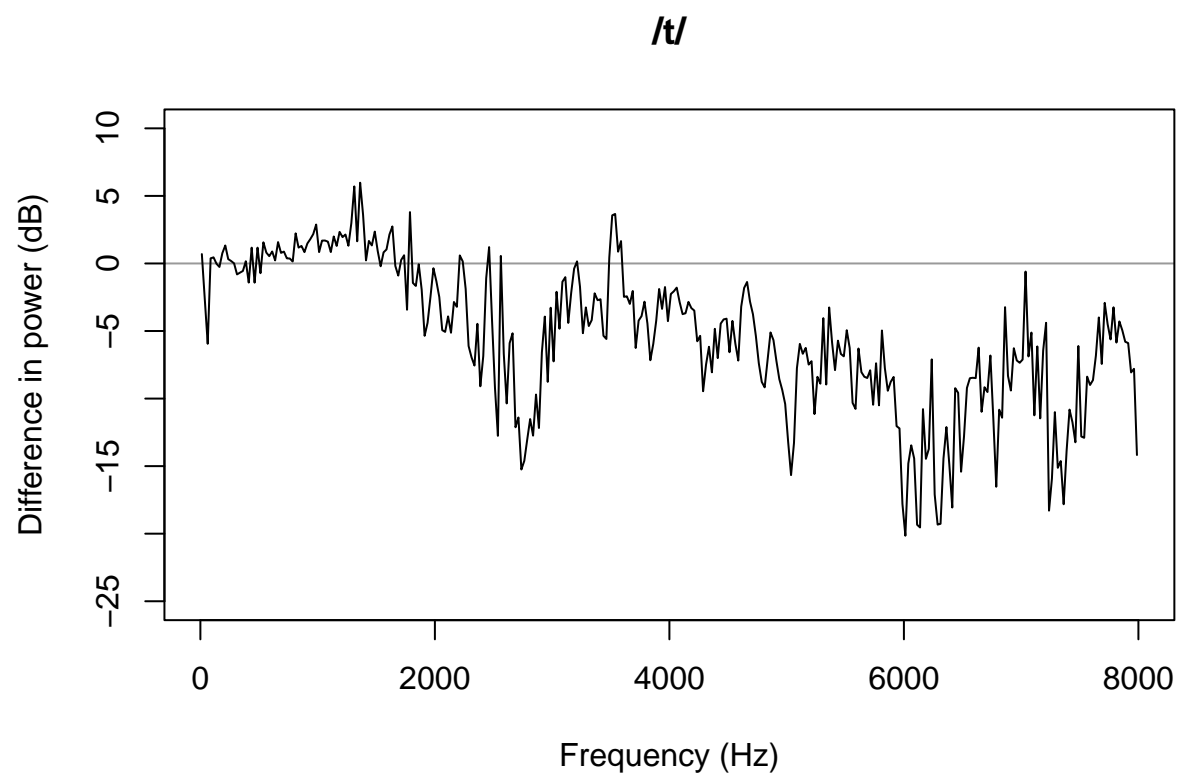


```
gT = makePowerDifferenceGraph("../data/AcousticAnalysis/Masked_T.Table.csv", "../data/AcousticAnalysis/  
    annotate("text", x = 500,y=-15,label="/t/",size =8)
```

/t/

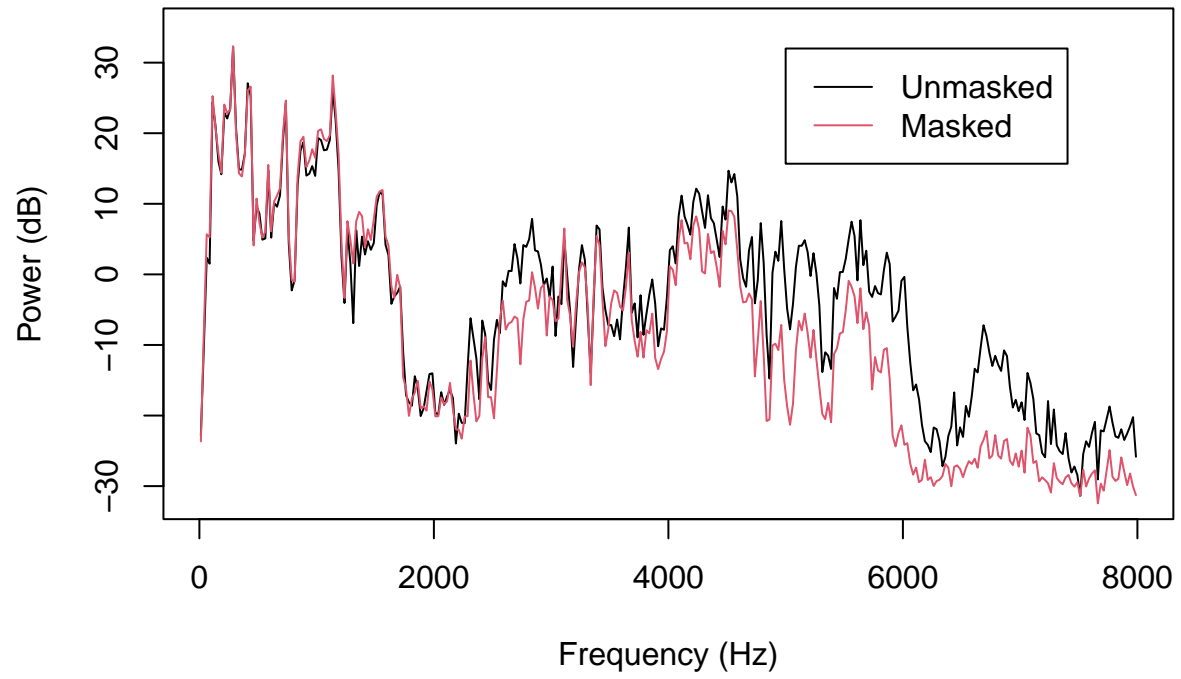


[1] -1118.167

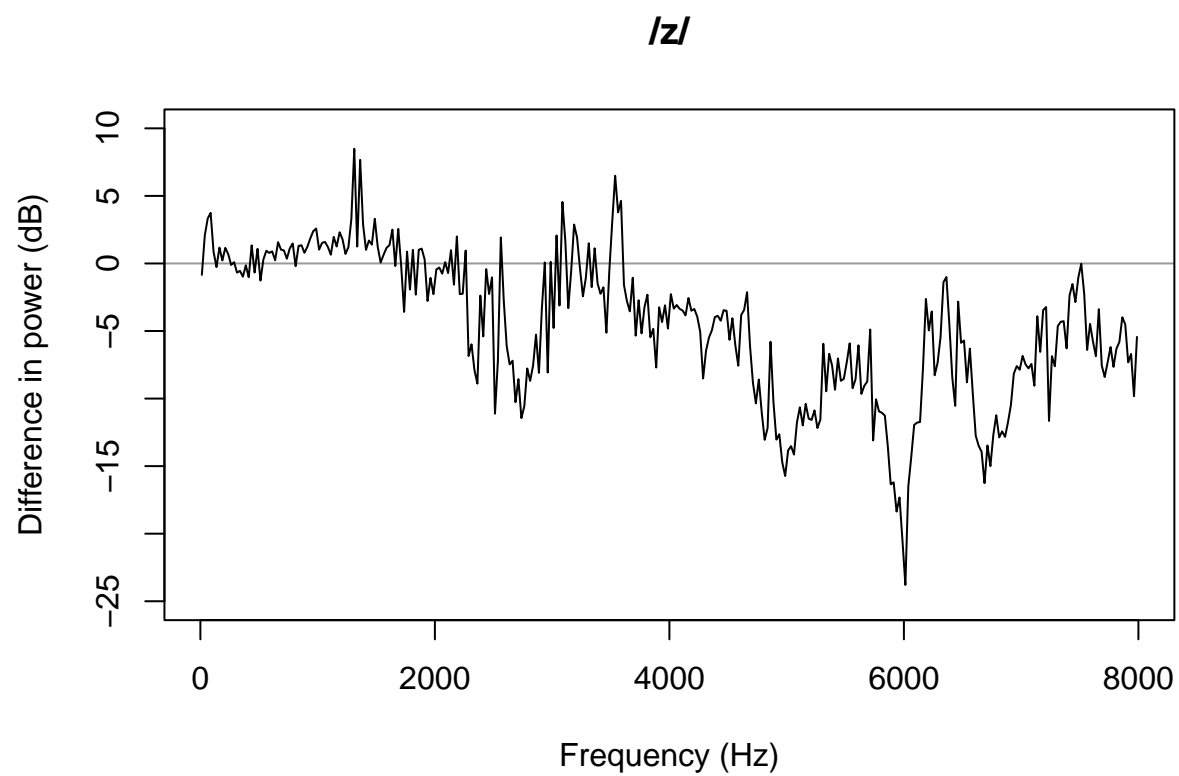


```
gZ = makePowerDifferenceGraph("../data/AcousticAnalysis/Masked_Z.Table.csv", "../data/AcousticAnalysis/  
    annotate("text", x = 500,y=-15,label="/z/",size =8)
```


/z/

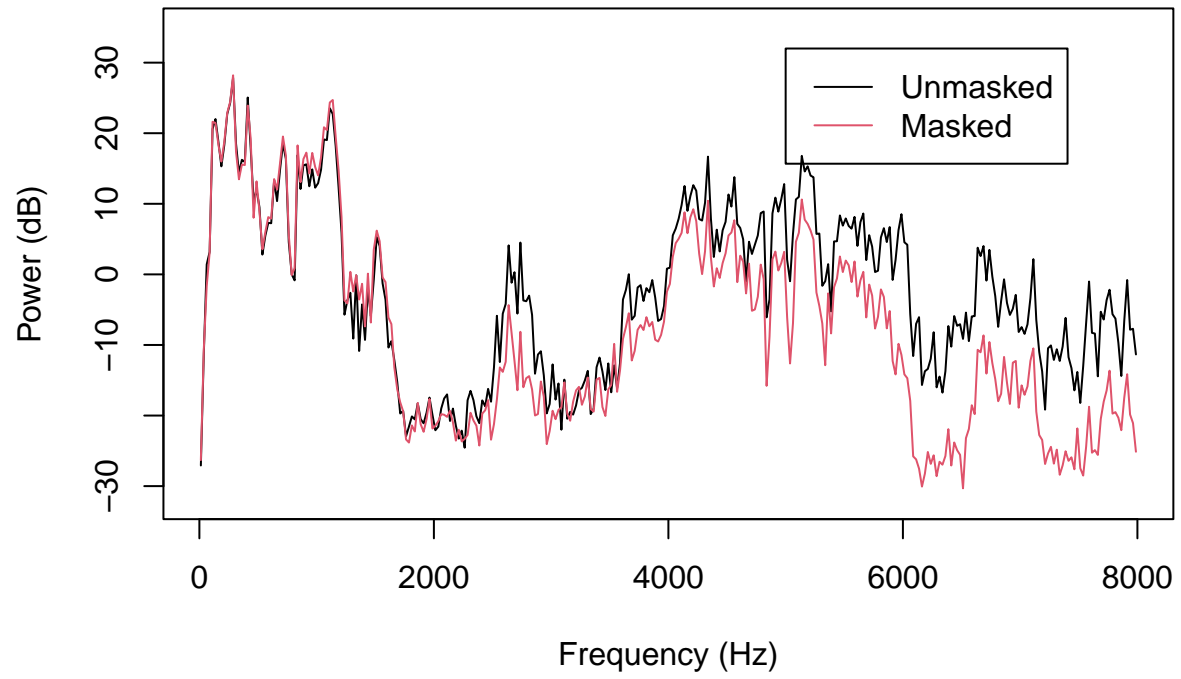


[1] -989.676

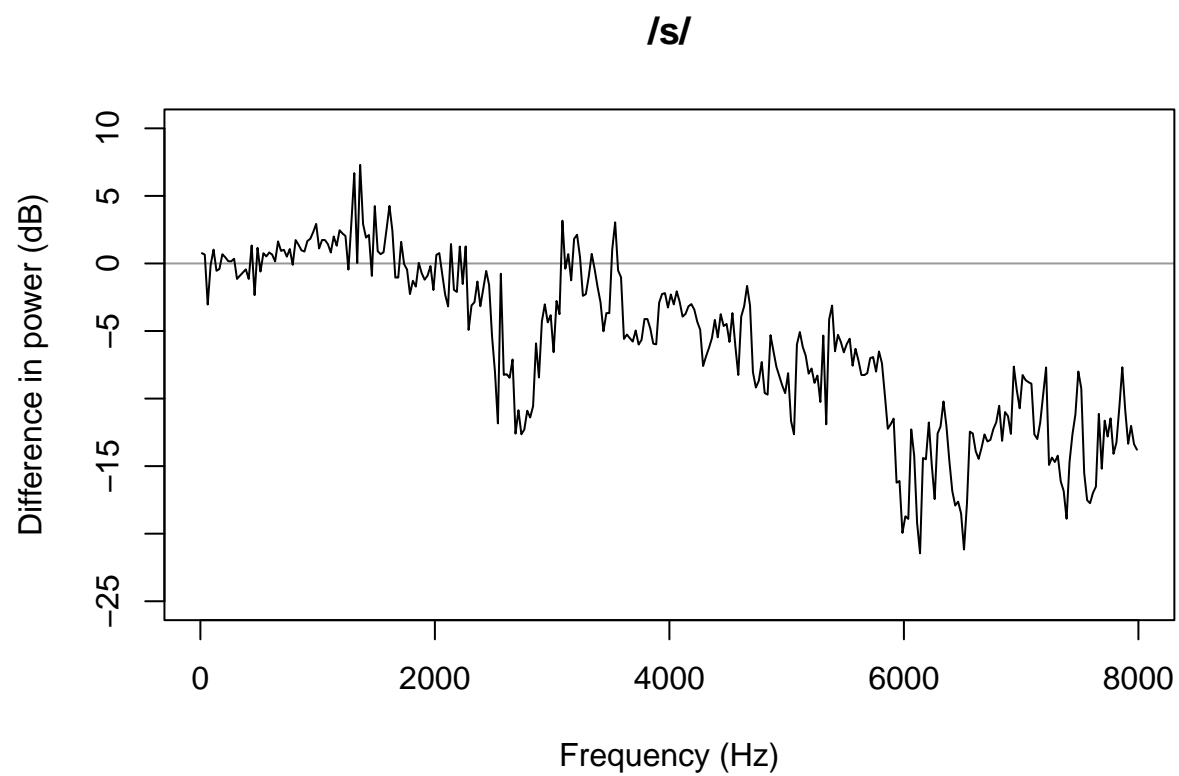


```
gS = makePowerDifferenceGraph("../data/AcousticAnalysis/Masked_S.Table.csv", "../data/AcousticAnalysis/  
    annotate("text", x = 500,y=-15,label="/s/",size =8)
```

/s/

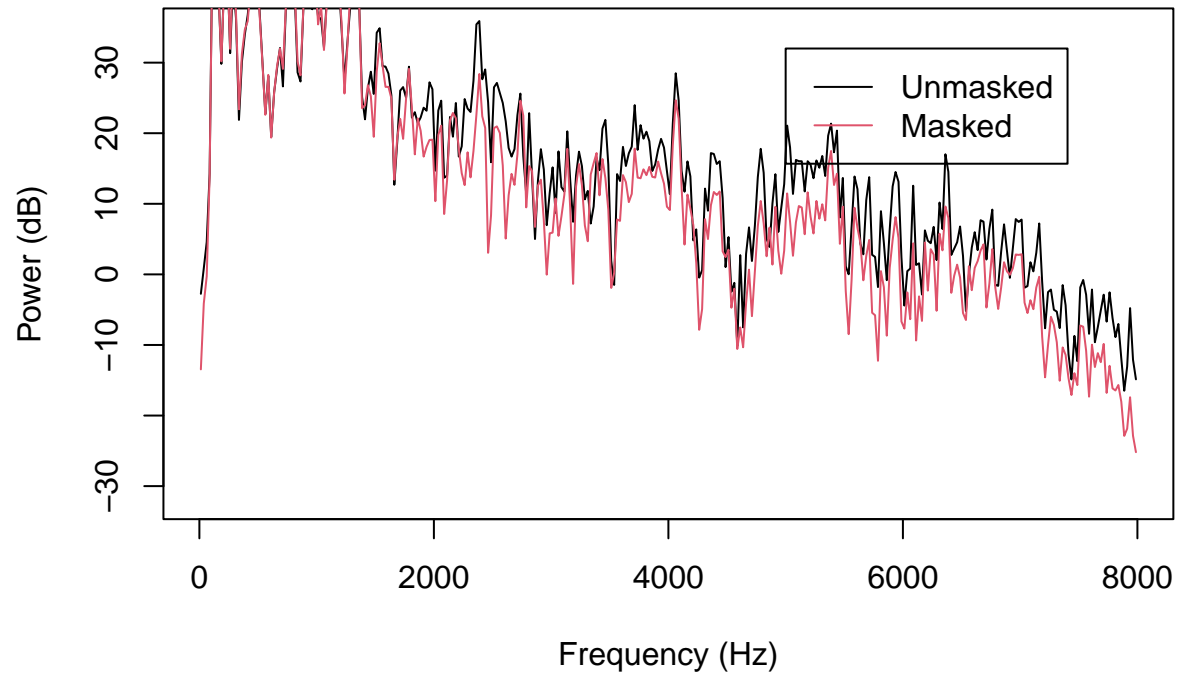


[1] -1329.152

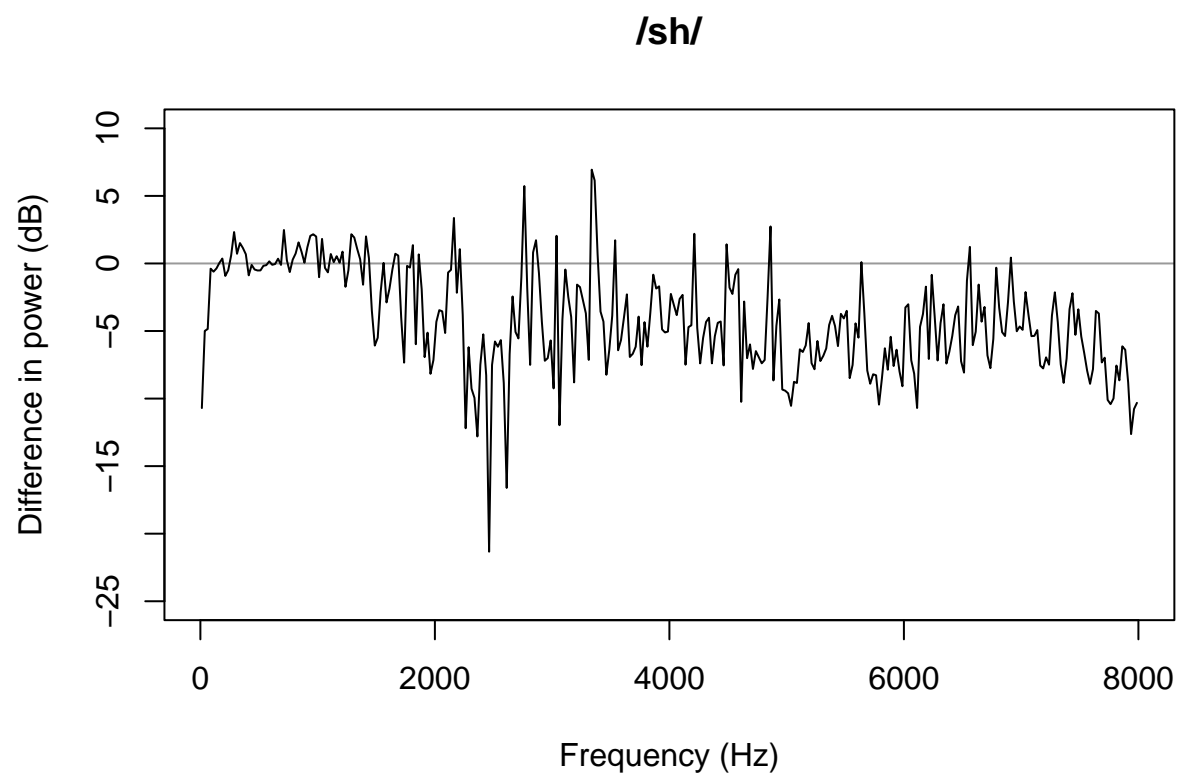


```
gSH = makePowerDifferenceGraph("../data/AcousticAnalysis/Masked_SH.Table.csv", "../data/AcousticAnalysis/Reference_SH.Table.csv")
annotate("text", x = 500,y=-15,label="/ /",size =8)
```

/sh/



[1] -684.5557



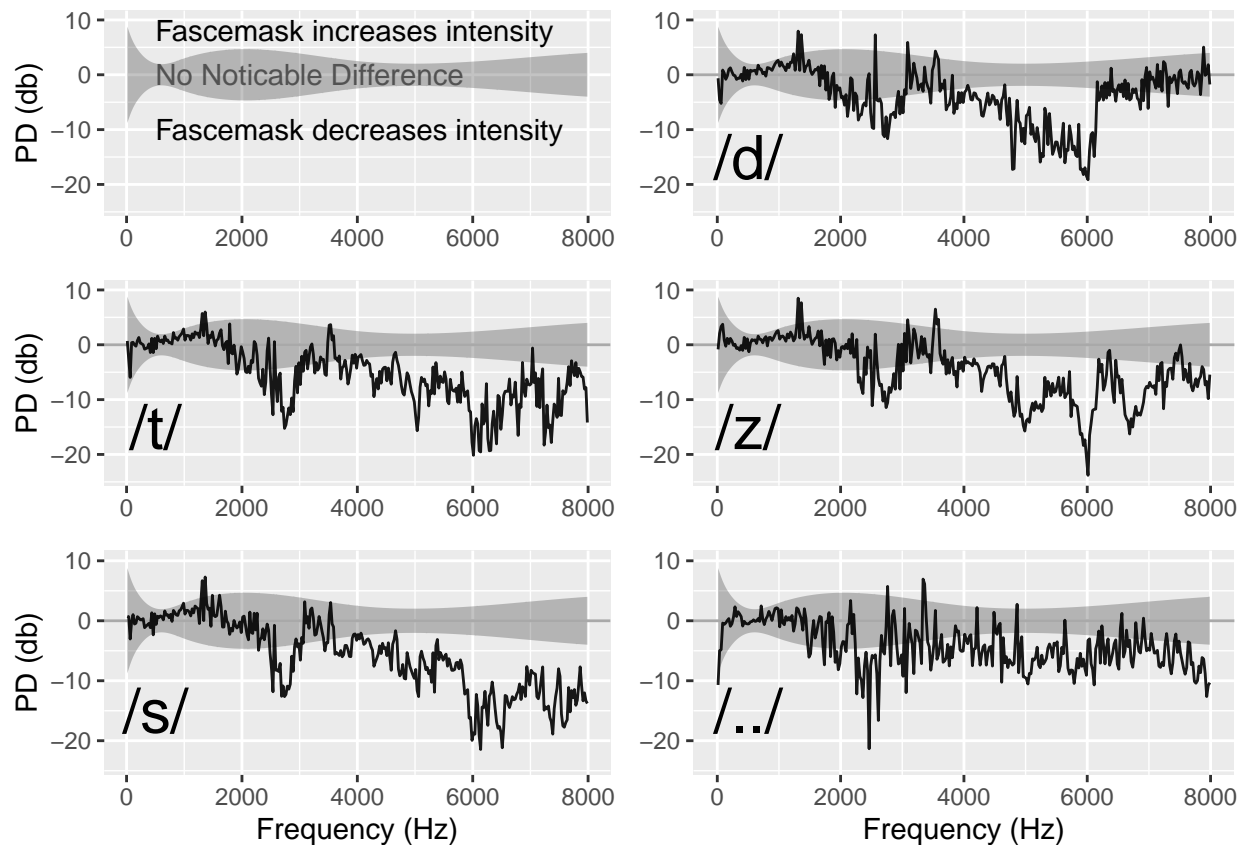
```
#dev.off()
```

```
gx = ggarrange(guideGraph, gD, gT, gZ, gS, gSH,  
              nrow = 3, ncol=2, heights = c(1,1,1.2))
```

```
gx
```

```
## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :  
## conversion failure on '/ /' in 'mbscsToSbcs': dot substituted for <ca>
```

```
## Warning in grid.Call.graphics(C_text, as.graphicsAnnot(x$label), x$x, x$y, :  
## conversion failure on '/ /' in 'mbscsToSbcs': dot substituted for <83>
```



```
grDevices::cairo_pdf("../results/AcousticAnalysis.pdf",width=6,height = 6)
gx
dev.off()
```

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

According to the area under the just noticeable difference curve, we should expect the perception accuracy to be ordered /s/ < /t/ < /z/ < /sh/ < /d/. This turns out not to agree with the experimental results below.

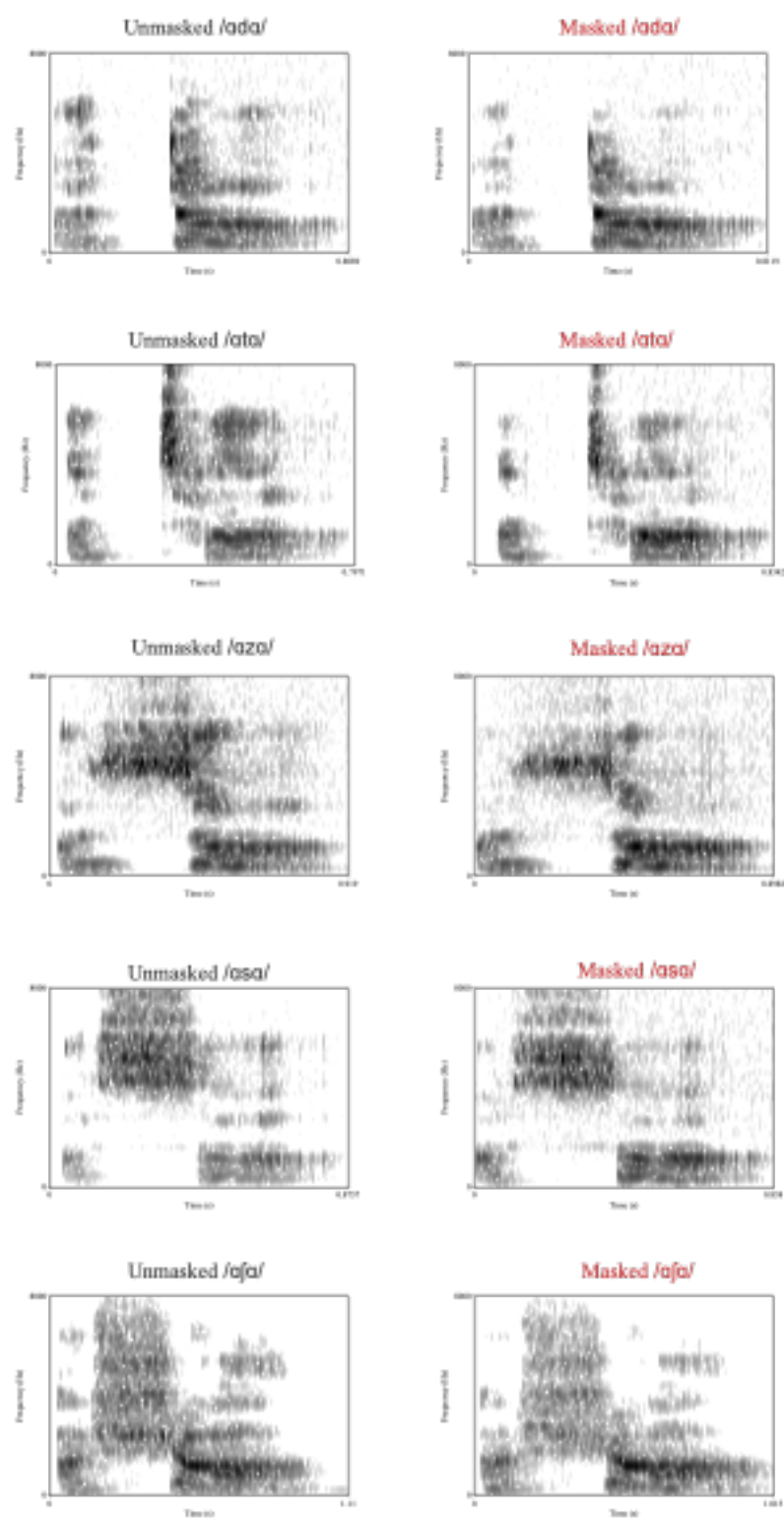


Figure 1: Spectrograms

Experiment

Load data

```
d2 = read.csv('../data/cleanedData.csv')

d2$target = factor(d2$target,
  levels=c("zoo", "sue", "to", "do", "jus", "shoe", "loo", "rue"))
```

Descriptive statistics

Number of participants:

```
length(unique(d2$IDNum))
```

```
## [1] 49
```

Number of observations (one observation has missing data due to a technical error.):

```
nrow(d2)
```

```
## [1] 1567
```

Overall percentage correct:

```
mean(d2$correct)*100
```

```
## [1] 83.66305
```

Percentage correct by condition:

```
tapply(d2$correct, d2$condition, mean)*100
```

```
##   Masked Unmasked
## 74.45722 92.85714
```

Percentage correct by target:

```
t(t(tapply(d2$correct, d2$target, mean)*100))
```

```
##           [,1]
## zoo  92.85714
## sue  52.55102
## to   95.40816
## do   83.67347
## jus  80.10204
## shoe 86.66667
## loo  89.28571
## rue  88.77551
```

Percentage correct by target for masked condition:

```
sel = d2$condition=="Masked"
t(t(tapply(d2[sel,]$correct, d2[sel,]$target, mean)*100))
```

```
##           [,1]
## zoo  91.83673
## sue  26.53061
## to   92.85714
## do   68.36735
## jus  74.48980
```

```
## shoe 74.22680
## loo 84.69388
## rue 82.65306
```

Percentage correct by target for unmasked condition:

```
sel = d2$condition=="Unmasked"
t(t(tapply(d2[sel,]$correct, d2[sel,]$target, mean)*100))
```

```
##           [,1]
## zoo  93.87755
## sue  78.57143
## to   97.95918
## do   98.97959
## jus  85.71429
## shoe 98.97959
## loo  93.87755
## rue  94.89796
```

Visualisation of raw data

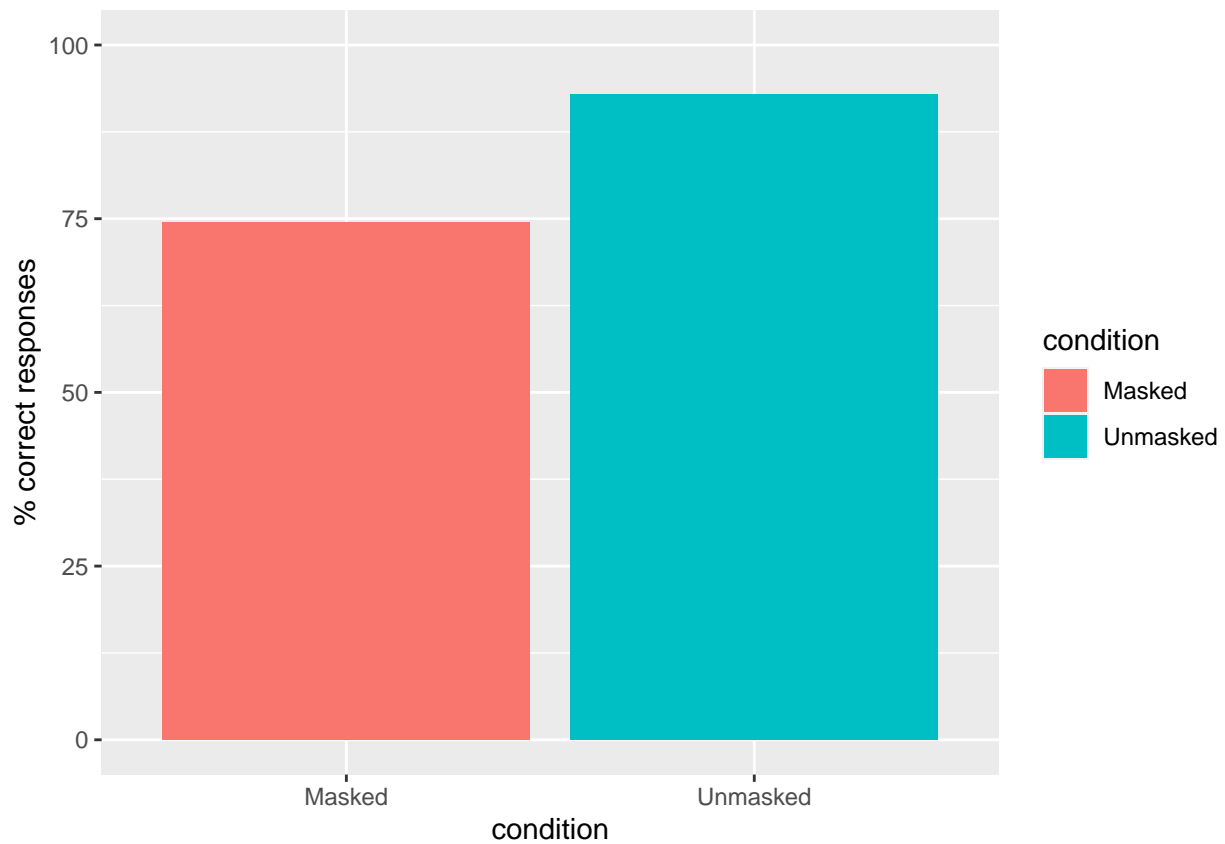
Main correct responses:

```
px1 = d2 %>% group_by(condition) %>%
  summarise(
    correct= mean(correct)*100
  ) %>% ggplot(aes(y=correct,x=condition,fill=condition)) +
  geom_bar(stat="identity") +
  ylim(c(0,100)) +
  ylab("% correct responses")
pdf("../results/RawCorrectByCondition.pdf",height=4,width=6)
px1
dev.off()
```

```
## pdf
```

```
## 2
```

```
px1
```

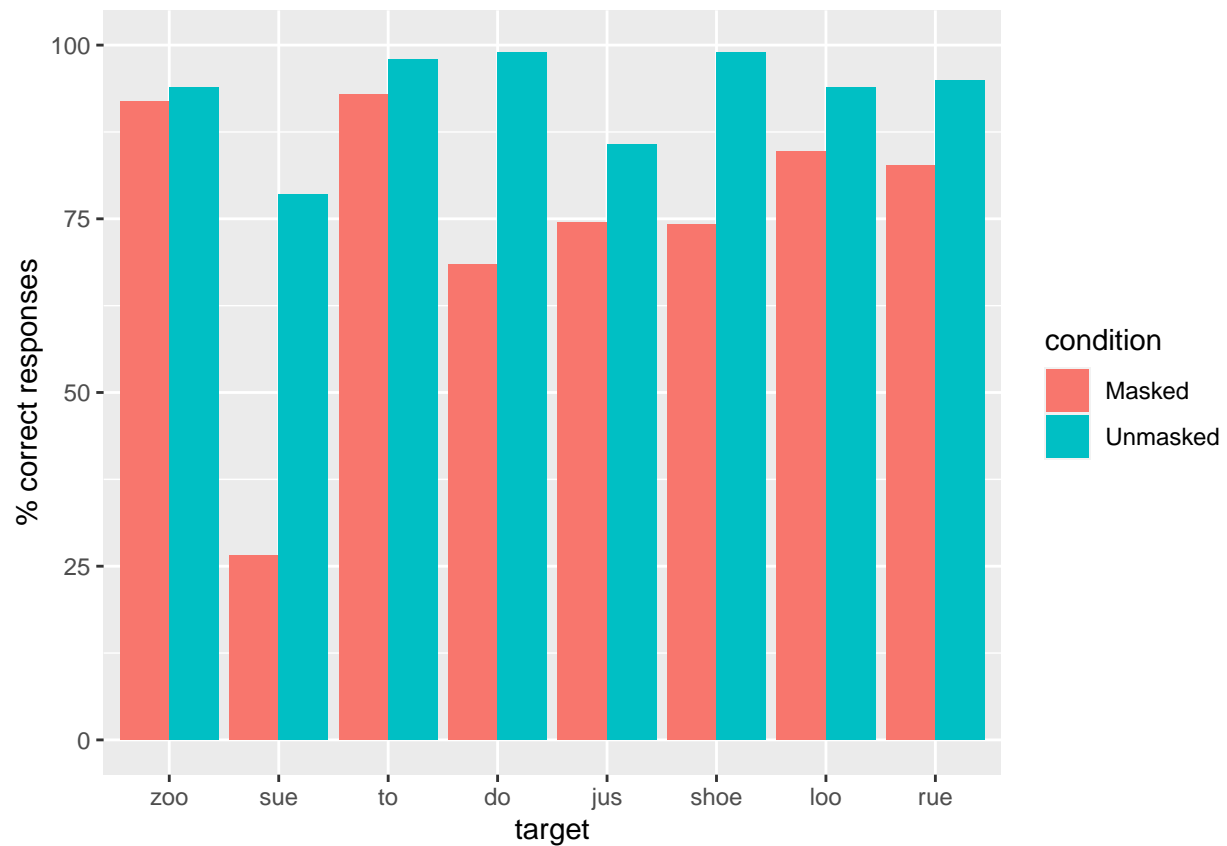


```
px2 = d2 %>% group_by(condition,target) %>%
  summarise(
    correct= mean(correct)*100
  ) %>% ggplot(aes(y=correct,x=target,fill=condition)) +
  geom_bar(stat="identity",position="dodge") +
  ylim(c(0,100)) +
  ylab("% correct responses")
pdf("../results/RawCorrectByTargetAndCondition.pdf",height=4,width=6)
```

```
px2
dev.off()
```

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

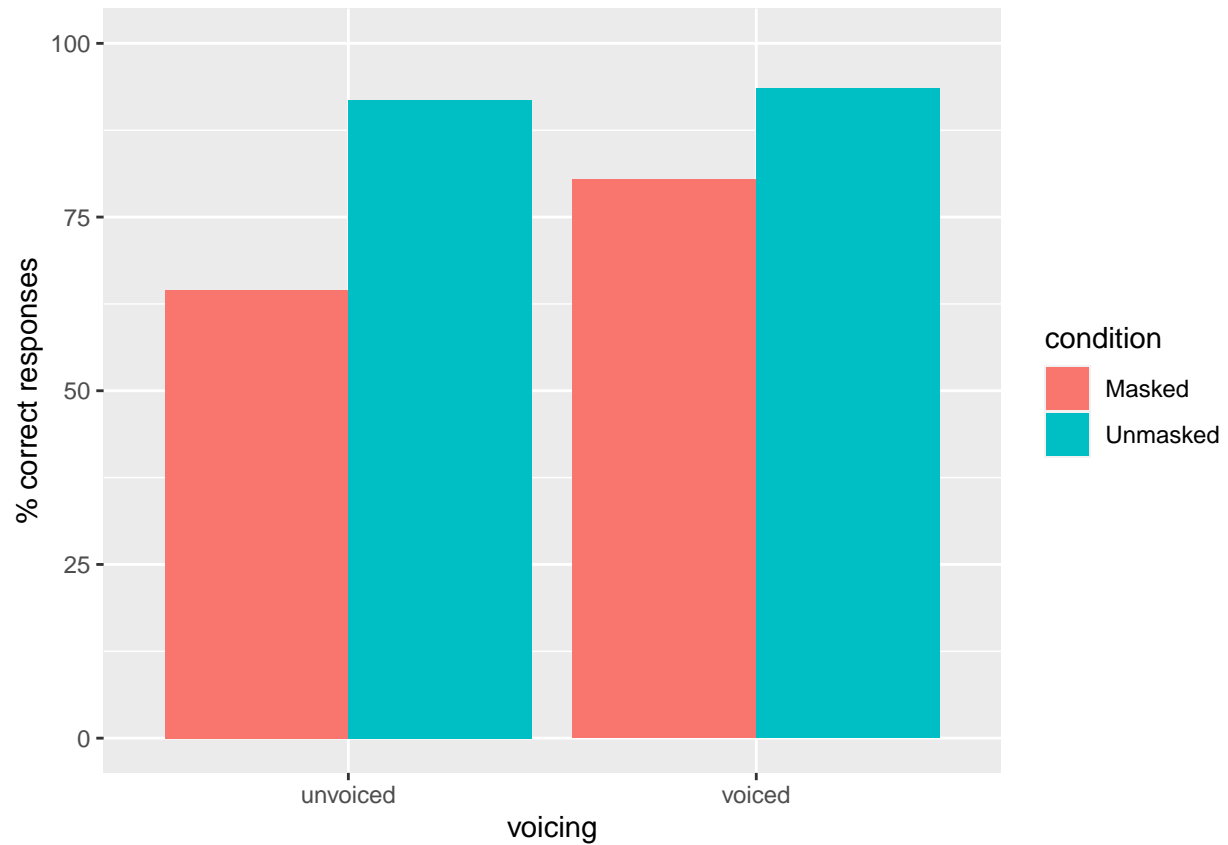
```
px2
```



```
px3 = d2 %>% group_by(condition,voicing) %>%
  summarise(
    correct= mean(correct)*100
  ) %>% ggplot(aes(y=correct,x=voicing,fill=condition)) +
  geom_bar(stat="identity",position="dodge") +
  ylim(c(0,100)) +
  ylab("% correct responses")
pdf("../results/RawCorrectByConditionAndVoicing.pdf",height=4,width=6)
px3
dev.off()
```

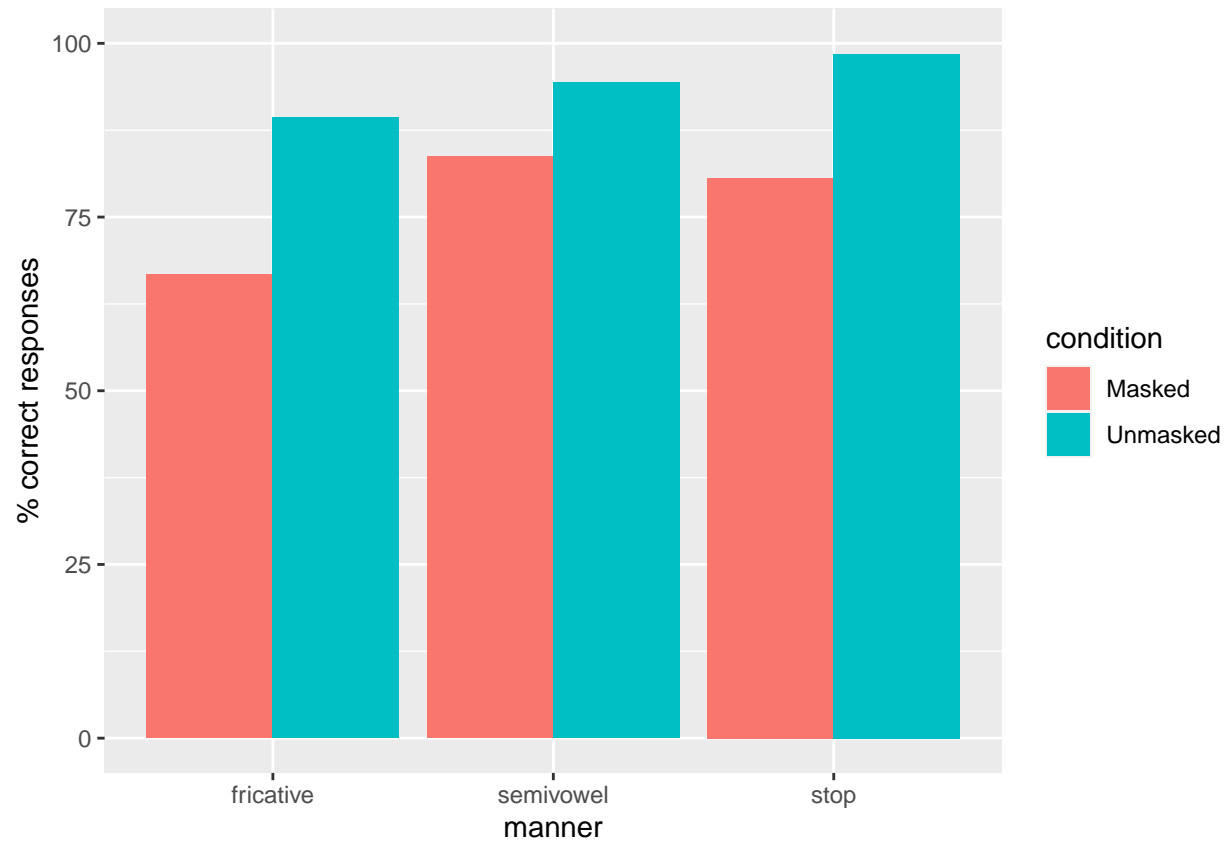
```
## pdf
## 2
```

```
px3
```



```
px4 = d2 %>% group_by(condition,manner) %>%
  summarise(
    correct= mean(correct)*100
  ) %>% ggplot(aes(y=correct,x=manner,fill=condition)) +
  geom_bar(stat="identity",position="dodge") +
  ylim(c(0,100)) +
  ylab("% correct responses")
pdf("../results/RawCorrectByConditionAndManner.pdf",height=4,width=6)
px4
dev.off()
```

```
## pdf
## 2
px4
```



```
# Combined
pdf("../results/RawCorrectByCondition_Manner_Voicing.pdf",
     width=6,height=3)
ggarrange(px3 + theme(legend.position = "none"),
          px4 + theme(axis.title.y = element_blank()),
          widths = c(1,1.4))
dev.off()
```

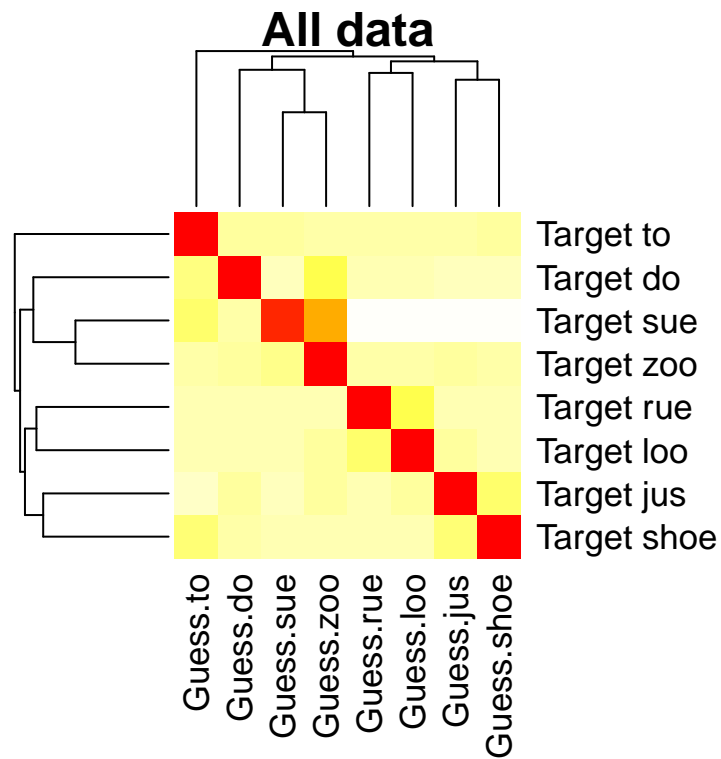
```
## pdf
## 2
```

Visualisation of confusion matrices

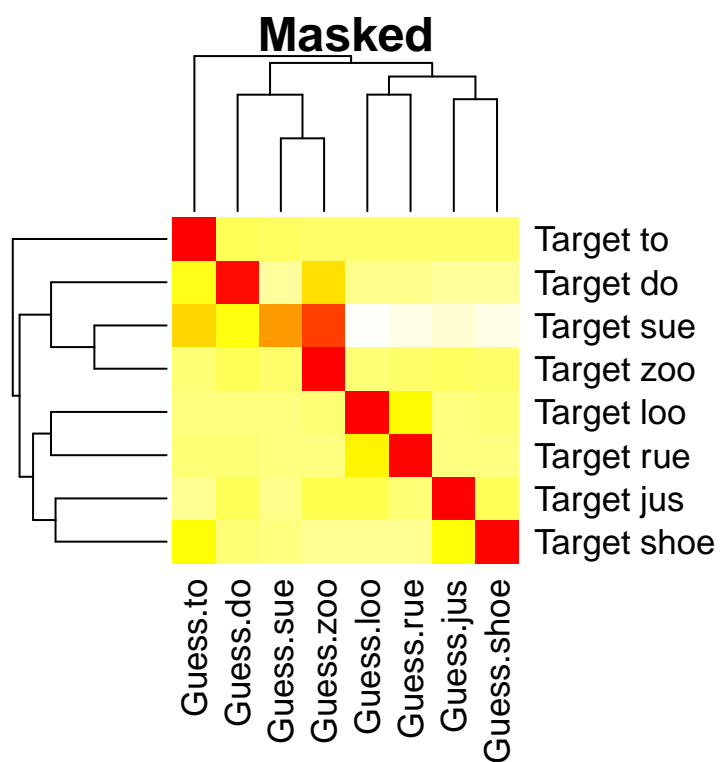
Use a heatmap to visualise the errors that participants make. Redder colours indicate more frequent decisions.

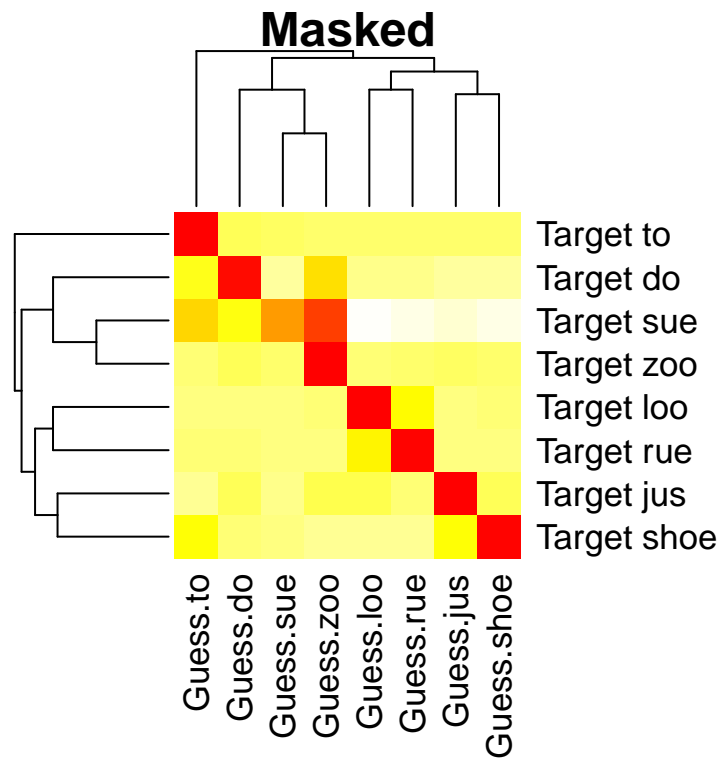
```
makeHeatmap = function(filename,label){
  confusionMatrix = read.csv(filename, stringsAsFactors = F, row.names = 1)
  confusionMatrix = as.matrix(confusionMatrix)
  confusionMatrix = 1 - (confusionMatrix/max(confusionMatrix))
  heatmap(as.matrix(confusionMatrix),Colv = "Rowv",
    margins = c(10,10),col=heat.colors(100),main = label)
  pdf(paste0("../results/Heatmap_",label,".pdf"))
  heatmap(as.matrix(confusionMatrix),Colv = "Rowv",
    margins = c(10,10),col=heat.colors(100),
    main = label)
  dev.off()
  heatmap(as.matrix(confusionMatrix),Colv = "Rowv",
    margins = c(10,10),col=heat.colors(100),
    main = label)
}
makeHeatmap("../data/confusionMatrix.csv","All data")
```





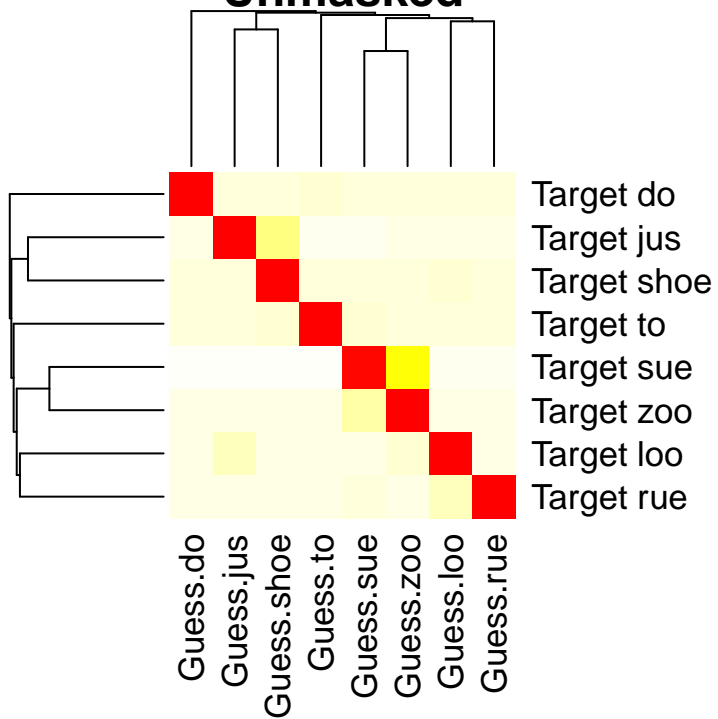
```
makeHeatmap("../data/confusionMatrix_Masked.csv", "Masked")
```

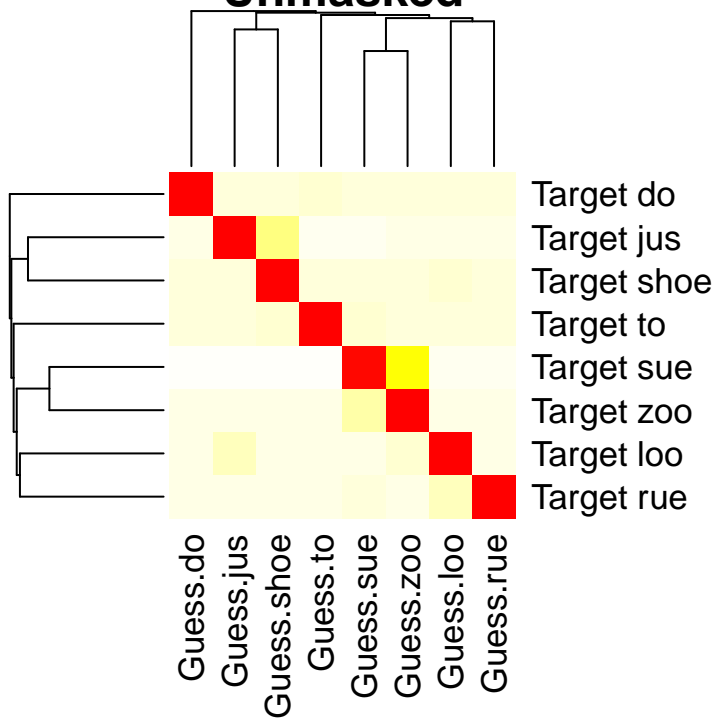


```
makeHeatmap("../data/confusionMatrix_Unmasked.csv", "Unmasked")
```

Unmasked



Unmasked



Statistical analysis

By itself, condition is a significant predictor of the proportion of correct responses:

```
chisq.test(table(d2$condition,d2$correct))
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  table(d2$condition, d2$correct)
## X-squared = 95.695, df = 1, p-value < 2.2e-16
```

The different targets also have different proportions of correct responses:

```
chisq.test(table(d2$target,d2$correct))
```

```
##
## Pearson's Chi-squared test
##
## data:  table(d2$target, d2$correct)
## X-squared = 182.1, df = 7, p-value < 2.2e-16
```

However, this is only part of the story. We use a binomial regression, predicting whether each trial is correct according to the target, the masked/unmasked condition and the interaction between the two. We also include a random intercept for participant. A random effect for condition is not used because that is a factor we are manipulating, and is operationally defined to have finite categories.

```
mBase0 = glmer(correct~ condition +
  (1 | IDNum),
  data=d2, family = "binomial",
  control = glmerControl(optimizer = "bobyqa"))
mBase1 = update(mBase0, ~. + target)
mBase2 = update(mBase1, ~. + condition:target)
m0 = glmer(correct~target*condition +
  (1 | IDNum),
  data=d2, family = "binomial",
  control = glmerControl(optimizer = "bobyqa"))
m0Summary = summary(m0)
m0Summary
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: correct ~ target * condition + (1 | IDNum)
## Data: d2
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC    logLik deviance df.resid
##  1058.9   1150.0   -512.5   1024.9     1550
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -6.2878  0.0821  0.2130  0.3742  3.1396
##
## Random effects:
##  Groups Name            Variance Std.Dev.
##  IDNum   (Intercept) 0.8842    0.9403
## Number of obs: 1567, groups:  IDNum, 49
```

```
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      2.7668    0.4117   6.720 1.81e-11 ***
## targetsue        -3.9638    0.4675  -8.478 < 2e-16 ***
## targetto          0.1608    0.5593   0.288 0.773719
## targetdo         -1.8729    0.4503  -4.160 3.19e-05 ***
## targetjus        -1.5255    0.4570  -3.338 0.000843 ***
## targetshoe       -1.5441    0.4574  -3.376 0.000736 ***
## targetloo        -0.7967    0.4839  -1.646 0.099680 .
## targettrue       -0.9662    0.4758  -2.031 0.042290 *
## conditionUnmasked  0.3437    0.5807   0.592 0.553929
## targetsue:conditionUnmasked 2.3556    0.6865   3.431 0.000601 ***
## targetto:conditionUnmasked  1.0765    1.0153   1.060 0.289016
## targetdo:conditionUnmasked  3.8475    1.1913   3.230 0.001239 **
## targetjus:conditionUnmasked  0.4766    0.6995   0.681 0.495624
## targetshoe:conditionUnmasked 3.5187    1.1939   2.947 0.003207 **
## targetloo:conditionUnmasked  0.7967    0.7839   1.016 0.309474
## targettrue:conditionUnmasked 1.1791    0.8009   1.472 0.140987
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it

write.csv(m0Summary$coefficients,"../results/ModelCoefficients.csv")

# LR Chisq tests for main effects
car::Anova(m0)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: correct
##
##              Chisq Df Pr(>Chisq)
## target          136.582  7 < 2.2e-16 ***
## condition         70.949  1 < 2.2e-16 ***
## target:condition  29.172  7 0.0001346 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Model comparisons for main effects
anova(mBase0,mBase1,mBase2)

## Data: d2
## Models:
## mBase0: correct ~ condition + (1 | IDNum)
## mBase1: correct ~ condition + (1 | IDNum) + target
## mBase2: correct ~ condition + (1 | IDNum) + target + condition:target
##      npar    AIC    BIC logLik deviance  Chisq Df Pr(>Chisq)
## mBase0     3 1255.1 1271.2 -624.55  1249.1
## mBase1    10 1080.5 1134.1 -530.26  1060.5 188.577  7 < 2.2e-16 ***
## mBase2    17 1058.9 1150.0 -512.46  1024.9  35.603  7 8.613e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Plot the output of the model:

```
pts = plot_model(m0,"pred")
pm1 = pts[[1]] + theme(panel.grid.minor.x=element_blank()) +
  ylim(c(0,1))
```

```
## Scale for 'y' is already present. Adding another scale for 'y', which will
## replace the existing scale.
```

```
pm2 = pts[[2]] + theme(panel.grid.minor.x=element_blank()) +
  ylim(c(0,1))
```

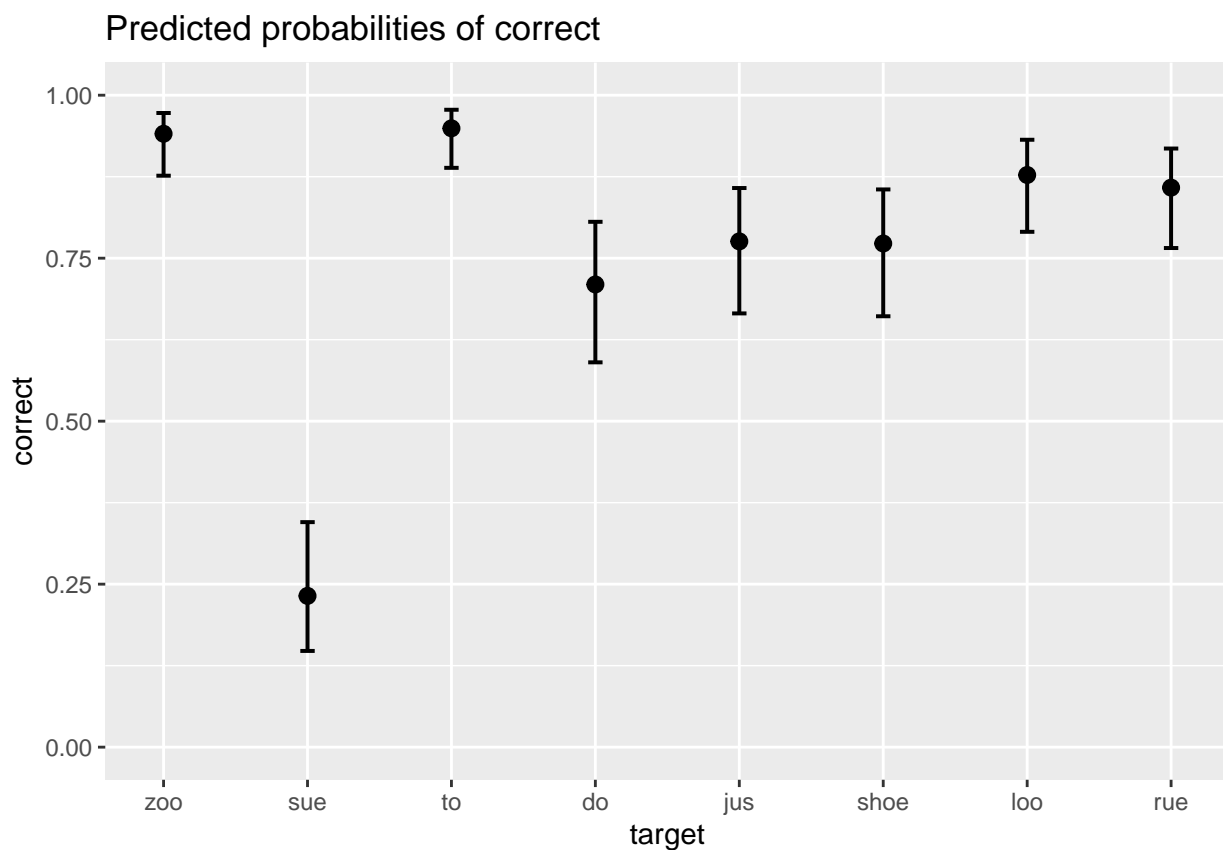
```
## Scale for 'y' is already present. Adding another scale for 'y', which will
## replace the existing scale.
```

```
pm3 = plot_model(m0,"int", axis.lim = c(0,1)) +
  theme(panel.grid.minor.x = element_blank()) +
  ylim(c(0,1))
```

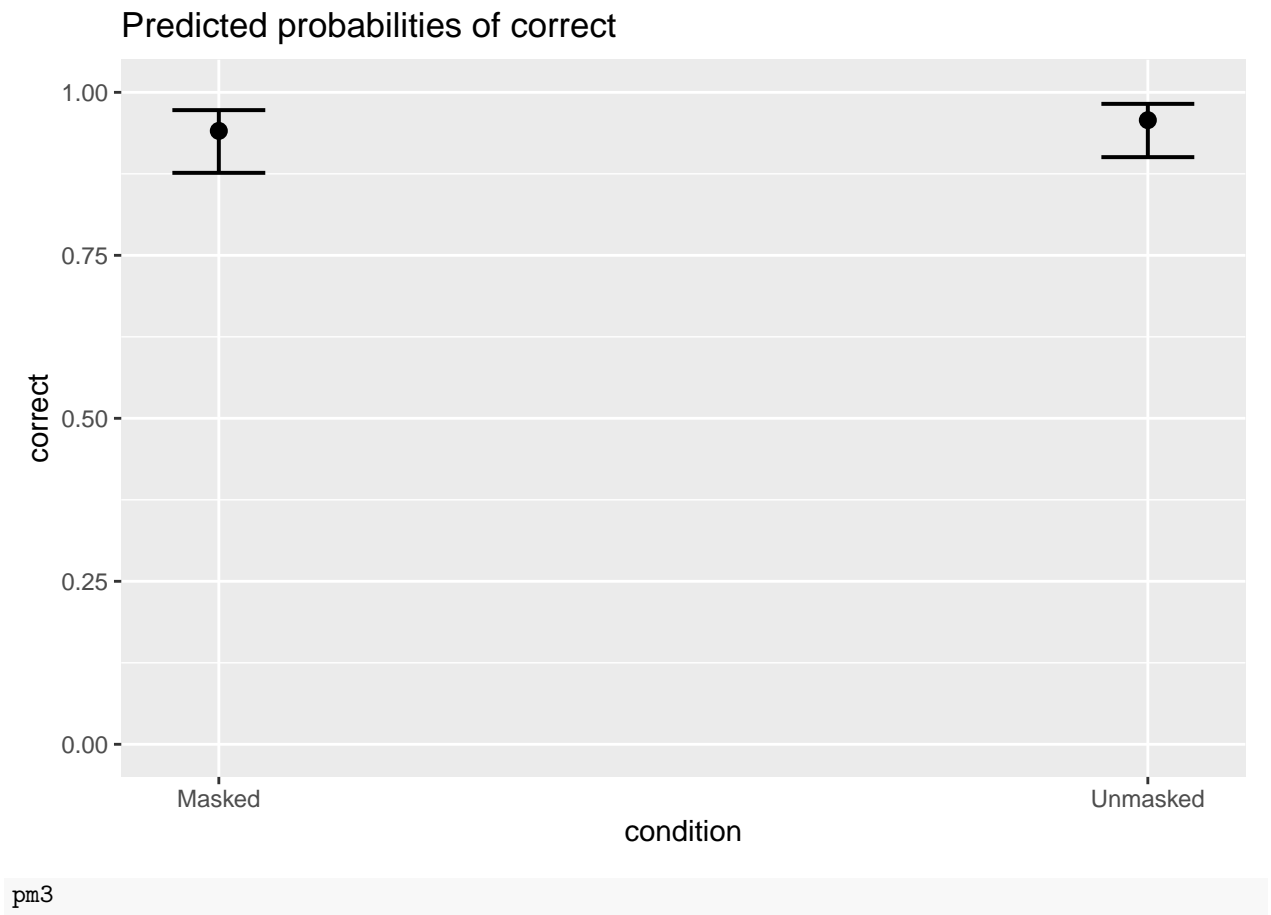
```
## Scale for 'y' is already present. Adding another scale for 'y', which will
## replace the existing scale.
```

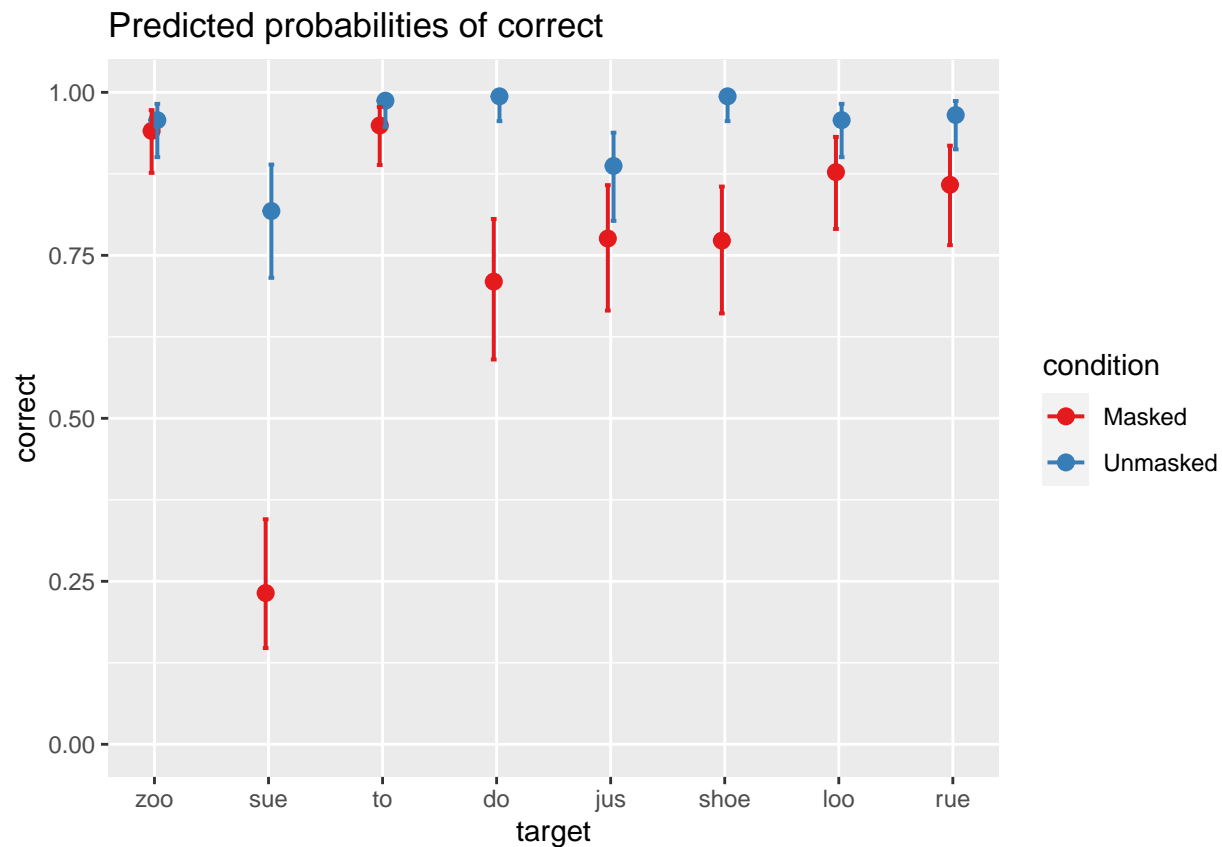
```
## Scale for 'y' is already present. Adding another scale for 'y', which will
## replace the existing scale.
```

```
pm1
```



```
pm2
```





```
pdf("../results/ModelPredictions_Target.pdf",height=4,width=6)
pm1
dev.off()
```

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

```
pdf("../results/ModelPredictions_Condition.pdf",height=4,width=6)
pm2
dev.off()
```

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

```
pdf("../results/ModelPredictions_Interaction.pdf",height=4,width=6)
pm3
dev.off()
```

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

Bayesian estimation model

The mixed effects model above converges well, but only when using the bobyqa method. Additionally, when adding a random effect for target, the glmer model above does not converge well. To check whether the estimation framework is biasing our results, we run a model using Bayesian estimation of coefficients. The implementation below uses uninformative priors. The point is simply to check whether the same qualitative results are reached using a different estimation algorithm.

```
library(brms)
m0B = brm(correct~target*condition +
           (1 | IDNum) + (0 + target | IDNum),
           iter = 10000, warmup = 1000,
           data=d2, family = "bernoulli", silent = T)
```

FALSE
FALSE SAMPLING FOR MODEL 'a5eaf40ddba7a02df4dd5993d9374247' NOW (CHAIN 1).
FALSE Chain 1:
FALSE Chain 1: Gradient evaluation took 0.000489 seconds
FALSE Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 4.89 seconds.
FALSE Chain 1: Adjust your expectations accordingly!
FALSE Chain 1:
FALSE Chain 1:
FALSE Chain 1: Iteration: 1 / 10000 [0%] (Warmup)
FALSE Chain 1: Iteration: 1000 / 10000 [10%] (Warmup)
FALSE Chain 1: Iteration: 1001 / 10000 [10%] (Sampling)
FALSE Chain 1: Iteration: 2000 / 10000 [20%] (Sampling)
FALSE Chain 1: Iteration: 3000 / 10000 [30%] (Sampling)
FALSE Chain 1: Iteration: 4000 / 10000 [40%] (Sampling)
FALSE Chain 1: Iteration: 5000 / 10000 [50%] (Sampling)
FALSE Chain 1: Iteration: 6000 / 10000 [60%] (Sampling)
FALSE Chain 1: Iteration: 7000 / 10000 [70%] (Sampling)
FALSE Chain 1: Iteration: 8000 / 10000 [80%] (Sampling)
FALSE Chain 1: Iteration: 9000 / 10000 [90%] (Sampling)
FALSE Chain 1: Iteration: 10000 / 10000 [100%] (Sampling)
FALSE Chain 1:
FALSE Chain 1: Elapsed Time: 16.5972 seconds (Warm-up)
FALSE Chain 1: 113.73 seconds (Sampling)
FALSE Chain 1: 130.327 seconds (Total)
FALSE Chain 1:
FALSE
FALSE SAMPLING FOR MODEL 'a5eaf40ddba7a02df4dd5993d9374247' NOW (CHAIN 2).
FALSE Chain 2:
FALSE Chain 2: Gradient evaluation took 0.000335 seconds
FALSE Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 3.35 seconds.
FALSE Chain 2: Adjust your expectations accordingly!
FALSE Chain 2:
FALSE Chain 2:
FALSE Chain 2: Iteration: 1 / 10000 [0%] (Warmup)
FALSE Chain 2: Iteration: 1000 / 10000 [10%] (Warmup)
FALSE Chain 2: Iteration: 1001 / 10000 [10%] (Sampling)
FALSE Chain 2: Iteration: 2000 / 10000 [20%] (Sampling)
FALSE Chain 2: Iteration: 3000 / 10000 [30%] (Sampling)
FALSE Chain 2: Iteration: 4000 / 10000 [40%] (Sampling)
FALSE Chain 2: Iteration: 5000 / 10000 [50%] (Sampling)
FALSE Chain 2: Iteration: 6000 / 10000 [60%] (Sampling)

```

FALSE Chain 2: Iteration: 7000 / 10000 [ 70%] (Sampling)
FALSE Chain 2: Iteration: 8000 / 10000 [ 80%] (Sampling)
FALSE Chain 2: Iteration: 9000 / 10000 [ 90%] (Sampling)
FALSE Chain 2: Iteration: 10000 / 10000 [100%] (Sampling)
FALSE Chain 2:
FALSE Chain 2: Elapsed Time: 20.5842 seconds (Warm-up)
FALSE Chain 2: 188.813 seconds (Sampling)
FALSE Chain 2: 209.397 seconds (Total)
FALSE Chain 2:
FALSE
FALSE SAMPLING FOR MODEL 'a5eaf40ddba7a02df4dd5993d9374247' NOW (CHAIN 3).
FALSE Chain 3:
FALSE Chain 3: Gradient evaluation took 0.000343 seconds
FALSE Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 3.43 seconds.
FALSE Chain 3: Adjust your expectations accordingly!
FALSE Chain 3:
FALSE Chain 3:
FALSE Chain 3: Iteration: 1 / 10000 [ 0%] (Warmup)
FALSE Chain 3: Iteration: 1000 / 10000 [ 10%] (Warmup)
FALSE Chain 3: Iteration: 1001 / 10000 [ 10%] (Sampling)
FALSE Chain 3: Iteration: 2000 / 10000 [ 20%] (Sampling)
FALSE Chain 3: Iteration: 3000 / 10000 [ 30%] (Sampling)
FALSE Chain 3: Iteration: 4000 / 10000 [ 40%] (Sampling)
FALSE Chain 3: Iteration: 5000 / 10000 [ 50%] (Sampling)
FALSE Chain 3: Iteration: 6000 / 10000 [ 60%] (Sampling)
FALSE Chain 3: Iteration: 7000 / 10000 [ 70%] (Sampling)
FALSE Chain 3: Iteration: 8000 / 10000 [ 80%] (Sampling)
FALSE Chain 3: Iteration: 9000 / 10000 [ 90%] (Sampling)
FALSE Chain 3: Iteration: 10000 / 10000 [100%] (Sampling)
FALSE Chain 3:
FALSE Chain 3: Elapsed Time: 18.1773 seconds (Warm-up)
FALSE Chain 3: 189.882 seconds (Sampling)
FALSE Chain 3: 208.059 seconds (Total)
FALSE Chain 3:
FALSE
FALSE SAMPLING FOR MODEL 'a5eaf40ddba7a02df4dd5993d9374247' NOW (CHAIN 4).
FALSE Chain 4:
FALSE Chain 4: Gradient evaluation took 0.000355 seconds
FALSE Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 3.55 seconds.
FALSE Chain 4: Adjust your expectations accordingly!
FALSE Chain 4:
FALSE Chain 4:
FALSE Chain 4: Iteration: 1 / 10000 [ 0%] (Warmup)
FALSE Chain 4: Iteration: 1000 / 10000 [ 10%] (Warmup)
FALSE Chain 4: Iteration: 1001 / 10000 [ 10%] (Sampling)
FALSE Chain 4: Iteration: 2000 / 10000 [ 20%] (Sampling)
FALSE Chain 4: Iteration: 3000 / 10000 [ 30%] (Sampling)
FALSE Chain 4: Iteration: 4000 / 10000 [ 40%] (Sampling)
FALSE Chain 4: Iteration: 5000 / 10000 [ 50%] (Sampling)
FALSE Chain 4: Iteration: 6000 / 10000 [ 60%] (Sampling)
FALSE Chain 4: Iteration: 7000 / 10000 [ 70%] (Sampling)
FALSE Chain 4: Iteration: 8000 / 10000 [ 80%] (Sampling)
FALSE Chain 4: Iteration: 9000 / 10000 [ 90%] (Sampling)
FALSE Chain 4: Iteration: 10000 / 10000 [100%] (Sampling)

```

```
FALSE Chain 4:
FALSE Chain 4: Elapsed Time: 17.9233 seconds (Warm-up)
FALSE Chain 4:      190.211 seconds (Sampling)
FALSE Chain 4:      208.134 seconds (Total)
FALSE Chain 4:
```

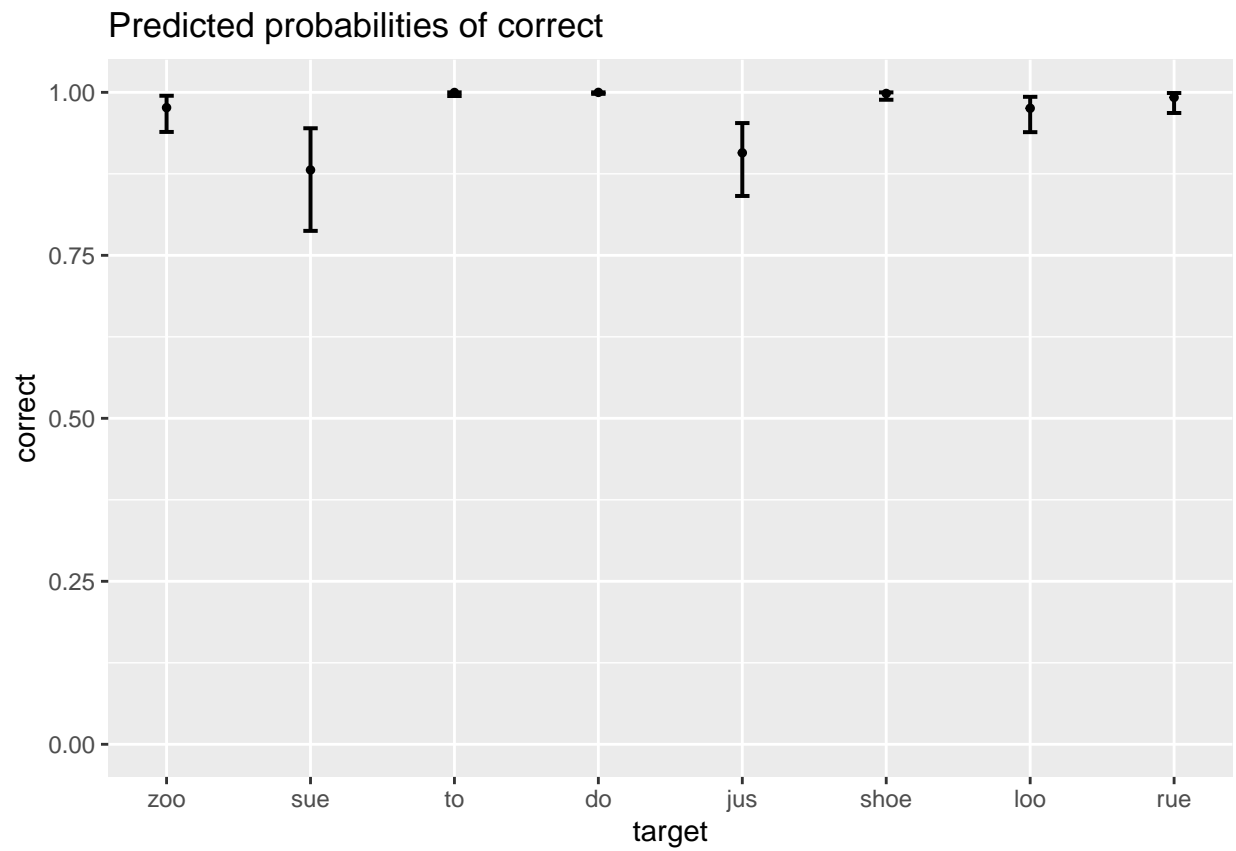
```
knitr::kable(summary(m0B)$fixed,digits = 4)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
Intercept	3.4206	0.7409	2.2644	5.1724	1.0012	7301.342	7804.246
targetsue	-5.0282	0.8350	-6.9387	-3.6344	1.0007	8045.762	9188.771
targetto	2.9981	2.5330	-0.7024	9.3701	1.0002	10212.596	11627.688
targetdo	-1.6453	1.0282	-3.6670	0.4559	1.0008	9777.880	9966.633
targetjus	-2.0137	0.7736	-3.8274	-0.7539	1.0010	7773.215	7956.954
targetshoe	-1.7647	0.8570	-3.6267	-0.1966	1.0011	8227.086	9000.866
targetloo	-1.0021	0.8779	-2.9244	0.5898	1.0010	8486.601	8723.904
targettrue	-0.6591	1.0461	-2.7609	1.4544	1.0009	7607.607	8632.152
conditionUnmasked	0.4089	0.6364	-0.8181	1.6758	1.0002	14660.333	19249.978
targetsue:conditionUnmasked	3.2281	0.8741	1.5610	4.9867	1.0002	13676.274	21761.018
targetto:conditionUnmasked	2.1591	1.4512	-0.4426	5.2905	1.0002	25221.475	24549.739
targetdo:conditionUnmasked	7.6687	2.7301	3.5646	14.1619	1.0000	14089.712	16394.296
targetjus:conditionUnmasked	0.4882	0.7589	-0.9950	1.9637	1.0001	16438.888	23650.816
targetshoe:conditionUnmasked	4.4959	1.5633	1.8772	8.0104	1.0002	20639.658	19631.498
targetloo:conditionUnmasked	0.9254	0.8710	-0.7688	2.6554	1.0001	18689.019	23175.010
targettrue:conditionUnmasked	1.7942	0.9918	-0.0828	3.8150	1.0001	19002.089	25181.147

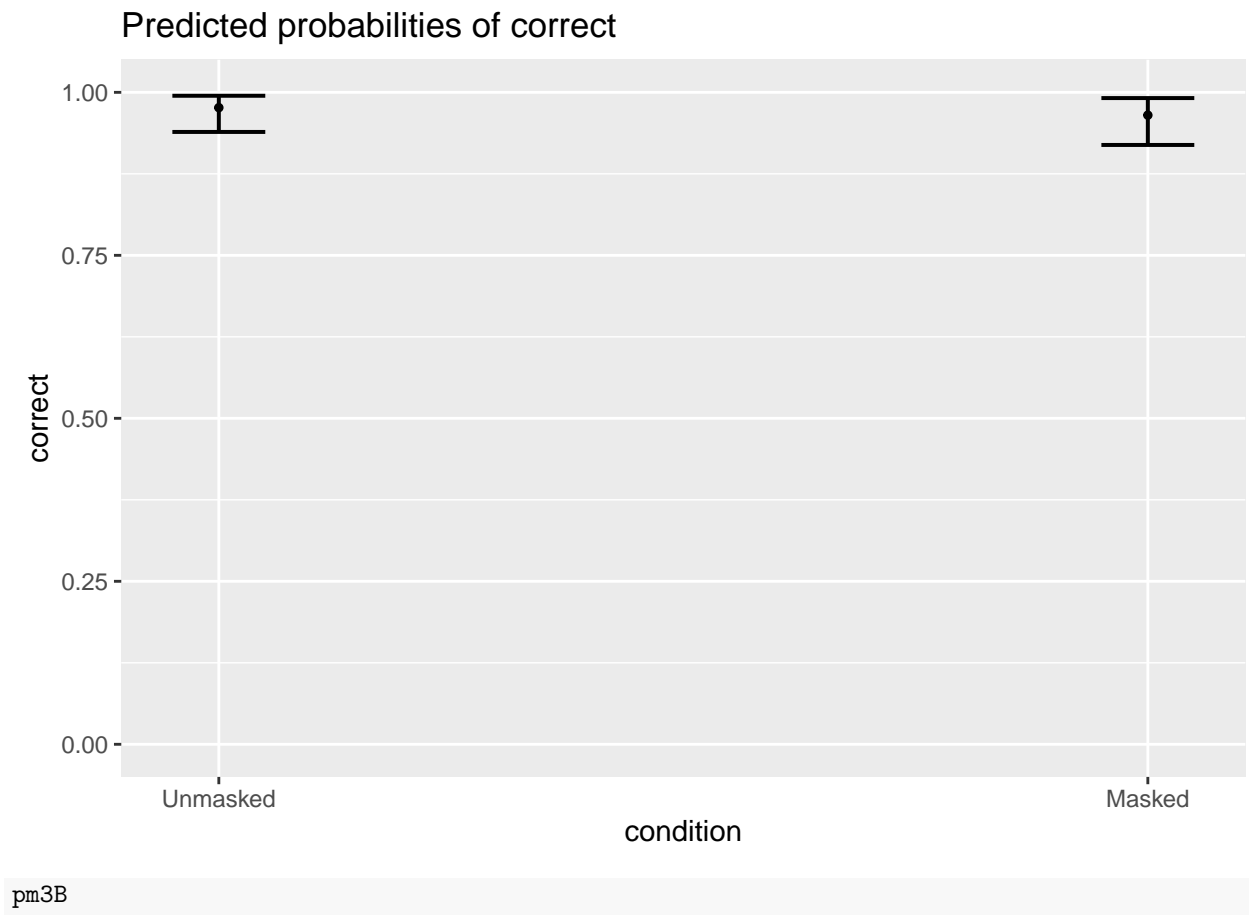
Plot the results. The effects are qualitatively the same as for the mixed effects model above.

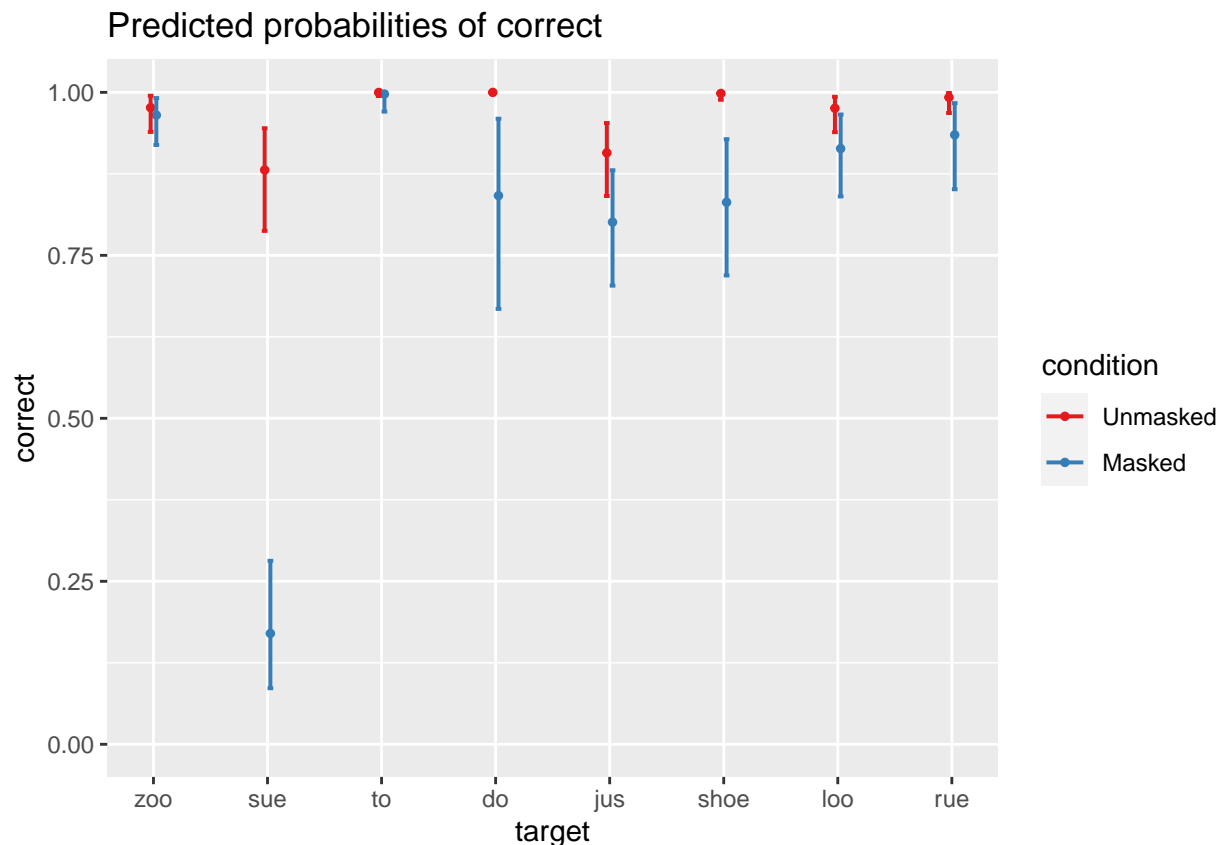
```
ptsB = plot_model(m0B,"pred")
pm1B = ptsB[[1]] + theme(panel.grid.minor.x=element_blank()) +
  ylim(c(0,1))
pm2B = ptsB[[2]] + theme(panel.grid.minor.x=element_blank()) +
  ylim(c(0,1))
pm3B = plot_model(m0B,"int", axis.lim = c(0,1)) +
  theme(panel.grid.minor.x = element_blank()) +
  ylim(c(0,1))

pm1B
```



pm2B





Coefficients are highly correlated between implementations:

```
cor(summary(m0B)$fixed[, "Estimate"],
     summary(m0)$coefficients[, "Estimate"])
```

```
## Warning: There were 4 divergent transitions after warmup. Increasing adapt_delta
## above 0.8 may help. See http://mc-stan.org/misc/warnings.html#divergent-
## transitions-after-warmup
## [1] 0.955099
```

The differences between estimates are shown below. In cases where there are sizable differences, the Bayesian estimates are more extreme.

```
diffx = data.frame(
  MixedEffects = summary(m0)$coefficients[, "Estimate"],
  Bayesian = summary(m0B)$fixed[, "Estimate"])
```

```
## Warning: There were 4 divergent transitions after warmup. Increasing adapt_delta
## above 0.8 may help. See http://mc-stan.org/misc/warnings.html#divergent-
## transitions-after-warmup
```

```
diffx$Difference = diffx$Bayesian - diffx$MixedEffects
diffx
```

	MixedEffects	Bayesian	Difference
## (Intercept)	2.7667764	3.4205626	0.65378628
## targetsue	-3.9638021	-5.0282282	-1.06442613
## targetto	0.1608094	2.9981152	2.83730581

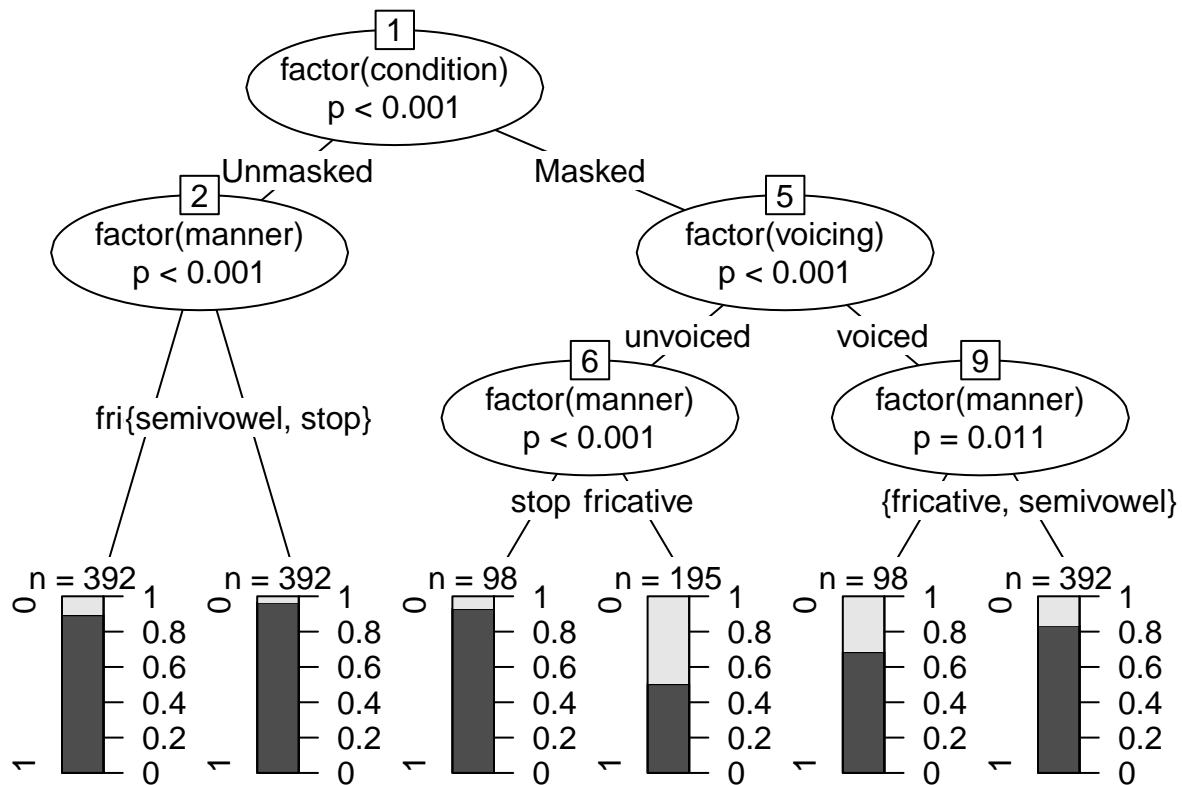
## targetdo	-1.8728562	-1.6452999	0.22755628
## targetjus	-1.5255055	-2.0136693	-0.48816381
## targetshoe	-1.5441157	-1.7647313	-0.22061565
## targetloo	-0.7967040	-1.0020709	-0.20536694
## targettrue	-0.9661874	-0.6590993	0.30708810
## conditionUnmasked	0.3437024	0.4088592	0.06515684
## targetsue:conditionUnmasked	2.3555754	3.2280631	0.87248778
## targetto:conditionUnmasked	1.0764995	2.1590577	1.08255829
## targetdo:conditionUnmasked	3.8474815	7.6686548	3.82117324
## targetjus:conditionUnmasked	0.4766201	0.4881909	0.01157082
## targetshoe:conditionUnmasked	3.5187468	4.4959268	0.97718001
## targetloo:conditionUnmasked	0.7966986	0.9254324	0.12873374
## targettrue:conditionUnmasked	1.1790669	1.7941805	0.61511359

Binary decision tree

The figure below shows a decision tree, the product of a machine learning algorithm that represents a series of yes/no questions to ask about the data to guess whether a subject got a trial correct or incorrect (Hothorn et al., 2006). This shows us how each condition, and the cumulative effects of conditions present across stimuli, affect the probability of a correct response.

The tree confirms that the probability of correct responses is predicted by a complex interaction between target properties and conditions. The first split in the tree is for masked and unmasked. In the masked branch on the right, the data is further divided into four groups. The poorest performance is for unvoiced fricatives, then voiced fricatives and semivowels, and the best performance is for unvoiced stops.

```
ct = ctree(factor(correct)~
  factor(condition)+
  factor(voicing)+
  factor(manner),
  data=d2)
plot(ct,terminal_panel=node_barplot(ct,id=FALSE))
```



```
pdf("../results/DecisionTree.pdf",width=12,height=6)
plot(ct,terminal_panel=node_barplot(ct,id=FALSE))
dev.off()
```

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

Use a random forest to compare the relative variable importance:

```

cf = cforest(factor(correct)~
              factor(condition)+
              factor(voicing)+
              factor(manner),
              data=d2)

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imp = varimp(cf)  
dotplot(sort(imp))
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