FLO replication - Preprocessing + analysis + results summary

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Contents

clean WS, set WD

```r
rm(list = ls());
```

Set your local working directory. This should be (and is assumed to be in the rest of the code) the highest point in your local folder:

```r
localGitDir <- 'C:/Users/eva_v/Documents/GitHub/leverhulmeNDL'
#setwd(localGitDir);
```

```r
fribbleSet <- read.csv(paste(localGitDir, "/exp1/stimuli/stimuli.csv", sep = ""),
                       header = T,
                       colClasses=c("cueID"="factor",
                        "bodyShape"="factor",
                        "label"="factor",
                        "fribbleID"="factor"
                        ));
```

Load functions from the lab repo

```r
urlFolder <- 'https://api.github.com/repos/n400peanuts/languagelearninglab/git/trees/master?recursive=1
urlRaw <- 'https://raw.githubusercontent.com/n400peanuts/languagelearninglab/master/tools/'

loadFunctionsGithub <-function(urlFolder, urlRaw){
  if (!require(httr)) {
    stop("httr not installed")
  }
  else if (!require(RCurl)){
    stop("RCurl not installed")
  }
  else {
    print('----loading. Please wait----')
  };
  httr::GET(urlFolder)-> req
  stop_for_status(req)
  filelist <- unlist(lapply(content(req)$tree, "[", "path"), use.names = F)
  urlFunctions <- grep("docs/tools/", filelist, value = TRUE, fixed = TRUE)
  gsub("docs/tools/", "", urlFunctions) -> functions
  for (i in 1:length(functions)){
    RCurl::getURL(paste0(urlRaw, functions[i]), ssl.verifypeer = FALSE)-> temp
    eval(parse(text = temp), envir = .GlobalEnv)
  };
}

loadFunctionsGithub(urlFolder = urlFolder, urlRaw = urlRaw);
```

```
## [1] "----loading. Please wait----"
```

```
rm(urlFolder, urlRaw)
```

Check stimuli set

It's important to check that every fribble is unique in the way its features are assembled within each category. Feature position and identity are coded into cueID.

I'm going to check whether the combination of cues used to build the fribble is unique by filtering for n > 1:

```
fribbleSet %>%
  group_by(category, cueID) %>%
  count() %>%
  filter(n > 1);
```

```
## Warning: Factor `cueID` contains implicit NA, consider using
## `forcats::fct_explicit_na`
```

```
## # A tibble: 0 x 3
## # Groups:   category, cueID [1]
## # ... with 3 variables: category <int>, cueID <fct>, n <int>
```

Great, each Fribble is unique!

Load data

List the files present in the folder, and load them.

```
df <- list.files(paste(localGitDir, "/exp1/data/", sep = ""));
```

We have 6 files.

```
for (i in 1:length(df)){
  gsub(".csv$", "", df[i]) -> id
  assign(id, data.frame())
  read.csv(paste(localGitDir, "/exp1/data/", df[i], sep = ""),
           na.strings=c("","NA"),
           colClasses=c("presentedLabel"="factor",
                        "presentedImage"="factor",
                        "learningType"="factor",
                        "Trial.Type"="factor",
                        "Test.Part"="factor",
                        "Key.Press"="factor"
                        ))-> temp
  assign(paste0(id), temp)
};

rm(temp, df, i, id);
```

The dataset name is decided autonomously by Gorilla. Importantly, Gorilla produces a different file per condition, and codes the conditions by the last 4 letters.

- 2yjh is the FL learning
- q8hp is the LF learning

I'm going to rename them for clarity.

```
dataFL<-`data_exp_15519-v13_task-2yjh`
dataFL$Experiment.Version <- c(14)
dataFL2<-`data_exp_15519-v14_task-2yjh`
dataFL3<-`data_exp_15519-v15_task-2yjh`

rm(`data_exp_15519-v13_task-2yjh`)
rm(`data_exp_15519-v14_task-2yjh`)
rm(`data_exp_15519-v15_task-2yjh`)

dataLF <- `data_exp_15519-v13_task-q8hp`
dataLF$Experiment.Version <- c(14)
dataLF2 <- `data_exp_15519-v14_task-q8hp`
dataLF3 <- `data_exp_15519-v15_task-q8hp`

rm(`data_exp_15519-v13_task-q8hp`)
rm(`data_exp_15519-v14_task-q8hp`)
rm(`data_exp_15519-v15_task-q8hp`)
```

```
rbind(dataFL, dataFL2, dataFL3)-> dataFL
rbind(dataLF, dataLF2, dataLF3)-> dataLF

rm(dataFL2, dataFL3, dataLF2, dataLF3)
```

Gorilla's output is extremely messy. Each row is a screen event. However, we want only the events related to 1. the presentations of the fribbles and the labels 2. participants' response and 3. what type of tasks.

I have coded these info in some columns and rows that I'm going to select:

```
raw_dataFL<- dataFL[c('Participant.Private.ID', 'learningType', 'Test.Part' ,
         'presentedImage', 'presentedLabel', 'Reaction.Time', "Key.Press",
          'Trial.Type', 'Trial.Index', 'Correct', 'Experiment.Version')]

raw_dataLF<- dataLF[c('Participant.Private.ID', 'learningType', 'Test.Part' ,
         'presentedImage', 'presentedLabel', 'Reaction.Time', "Key.Press",
          'Trial.Type', 'Trial.Index', 'Correct', 'Experiment.Version')]
```

Select rows:

```
rowsIwantTokeep <- c("learningBlock1", "learningBlock2", "learningBlock3",
                        "learningBlock4", "generalizationPL", "generalizationLP",
                        "randomDot", "contingencyJudgement")

raw_dataFL <- raw_dataFL %>%
  filter(Test.Part %in% rowsIwantTokeep ) %>%
  rename(subjID = Participant.Private.ID,
         learning = learningType,
         task = Test.Part,
         fribbleID = presentedImage,
         label = presentedLabel,
         rt = Reaction.Time,
         resp = Key.Press,
         trialType = Trial.Type,
         trialIndex = Trial.Index,
         acc = Correct)

raw_dataLF <- raw_dataLF %>%
  filter(Test.Part %in% rowsIwantTokeep ) %>%
  rename(subjID = Participant.Private.ID,
         learning = learningType,
         task = Test.Part,
         fribbleID = presentedImage,
         label = presentedLabel,
         rt = Reaction.Time,
         resp = Key.Press,
         trialType = Trial.Type,
         trialIndex = Trial.Index,
         acc = Correct)

rm(rowsIwantTokeep, dataFL, dataLF);
```

I'm going to merge both datasets, FL and LF, because we have anyway a column "learning" that can tell us which one is which.

```
rbind(raw_dataFL, raw_dataLF)-> raw_data;
rm(raw_dataFL, raw_dataLF);
```

Check learning

Let's filter and check learning trials:

```
learningBlocks <- c("learningBlock1", "learningBlock2", "learningBlock3", "learningBlock4");

learning <- raw_data %>%
  filter(task %in% learningBlocks)

learning <- droplevels(learning);
rm(learningBlocks)
```

How many trials per participant?

```
learning %>%
  group_by(subjID, learning) %>%
  count()
```

```
## # A tibble: 120 x 3
## # Groups:   subjID, learning [120]
##     subjID learning     n
##      <int> <fct>    <int>
##  1 1414932 LF         120
##  2 1414933 LF         120
##  3 1414937 FL         120
##  4 1414945 FL         120
##  5 1414957 FL         120
##  6 1415040 FL         120
##  7 1420163 FL         120
##  8 1420165 FL         120
##  9 1420169 LF         120
## 10 1420171 LF         120
## # ... with 110 more rows
```

Great, 120 trials per participant, per learning.

Let's check whether the blocks' length varied across participants:

```
learning %>%
  group_by(subjID, task) %>%
  count()
```

```
## # A tibble: 480 x 3
## # Groups:   subjID, task [480]
##     subjID task               n
##      <int> <fct>          <int>
##  1 1414932 learningBlock1    21
##  2 1414932 learningBlock2    28
##  3 1414932 learningBlock3    47
##  4 1414932 learningBlock4    24
##  5 1414933 learningBlock1    26
##  6 1414933 learningBlock2    22
##  7 1414933 learningBlock3    44
##  8 1414933 learningBlock4    28
##  9 1414937 learningBlock1    27
## 10 1414937 learningBlock2    47
## # ... with 470 more rows
```

Great! Each participant had a different amount of trials distributed across blocks. That's important because our random dot task was presented at the end of each block, and we wanted its presentation to be unpredictable. Anyway, the sum of all the learning trials was always 120.

Did we assign our learning randomly every couple of people?

```
table(learning$subjID, learning$learning)
```

```
##
##             FL  LF
##   1414932    0 120
##    1414933   0 120
##    1414937 120   0
##    1414945 120   0
##    1414957 120   0
##    1415040 120   0
##    1420163 120   0
##    1420165 120   0
##    1420169   0 120
##    1420171   0 120
##    1420177 120   0
##    1420180 120   0
##    1420185   0 120
##    1420199 120   0
##    1420204   0 120
##    1420552   0 120
##    1420573   0 120
##    1420577   0 120
##    1420580 120   0
##    1420622 120   0
##    1422463 120   0
##    1422465 120   0
##    1422466 120   0
##    1422467   0 120
##    1422470   0 120
##    1422472 120   0
##    1422473   0 120
##    1422475   0 120
##    1422476   0 120
##    1422477 120   0
##    1422675 120   0
##    1422676   0 120
##    1422677 120   0
##    1422678   0 120
##    1422679 120   0
##    1422680   0 120
##    1422681   0 120
##    1422689 120   0
##    1422715   0 120
##    1422716 120   0
##    1431942   0 120
##    1431944 120   0
##    1431946 120   0
##    1431948   0 120
##    1431949 120   0
##    1431952   0 120
##    1431953 120   0
##    1431954   0 120
##    1431956   0 120
##    1431957 120   0
##    1431958 120   0
##    1431959   0 120
##    1431960   0 120
##    1431961 120   0
##    1431963   0 120
##    1431965 120   0
##    1431966   0 120
##    1431968   0 120
##    1431969 120   0
##    1431970   0 120
##    1431972 120   0
##    1431974 120   0
##    1431978 120   0
##    1431979 120   0
##    1431981   0 120
##    1431984 120   0
##    1431989   0 120
##    1431992 120   0
##    1431997 120   0
##    1431998   0 120
##    1431999   0 120
##    1432003   0 120
##    1432007   0 120
##    1432009 120   0
##    1432011 120   0
##    1432030   0 120
##    1432052 120   0
##    1432075 120   0
##    1432301   0 120
##    1432323   0 120
##    1457883   0 120
##    1458992 120   0
##    1458996   0 120
##    1458997   0 120
##    1458998   0 120
##    1459001 120   0
##    1459002 120   0
##    1459003 120   0
##    1459007 120   0
##    1459009 120   0
##    1459013 120   0
##    1459015   0 120
##    1459018 120   0
##    1459020   0 120
##    1459024 120   0
##    1459025   0 120
##    1459029 120   0
##    1459036   0 120
##    1459039   0 120
##    1459043   0 120
##    1459046   0 120
##    1459047 120   0
##    1459048 120   0
##    1459052 120   0
##    1459057 120   0
##    1459064 120   0
##    1459067   0 120
##    1459078   0 120
##    1459109   0 120
##   1459696 116   0
##   1459697 120   0
##   1459699   0 120
##   1459700   0 120
##   1459701   0 120
##   1459702 120   0
##   1459703 120   0
##   1459706 120   0
##   1459708 120   0
##   1459709   0 120
##   1459767 120   0
```

Kind of. After chicking with Gorilla's suppoert: apparently, if a participant access Gorilla, but it's not allowed to start the experiment (e.g., the browser is not suitable), or leaves the session, this counts anyway for the randomisation.

The rows related to the presentation of fribbles and labels, inherit Gorilla's http address of where they are stored. Nothing I can do to change this in Gorilla, but we can clean the rows by those info like this:

```
as.factor(gsub("/task/70033/56/asset/|/task/70033/57/asset/|/task/70033/58/asset/", "", learning$fribbl
as.factor(gsub(".jpg$", "", learning$fribbleID))-> learning$fribbleID

as.factor(gsub("/task/70033/56/asset/|/task/70033/57/asset/|/task/70033/58/asset/", "", learning$label))
as.factor(gsub(".mp3$", "", learning$label))-> learning$label
learning$resp <- as.factor('NA')
```

This is how the learning dataframe looks like now:

```
head(learning);
```

```
##    subjID learning           task fribbleID label rt resp
## 1 1414937       FL learningBlock1     20375 FLbim NA   NA
## 2 1414937       FL learningBlock1     31075 FLtob NA   NA
## 3 1414937       FL learningBlock1     32775 FLtob NA   NA
## 4 1414937       FL learningBlock1     32875 FLtob NA   NA
## 5 1414937       FL learningBlock1     22025 FLbim NA   NA
## 6 1414937       FL learningBlock1     10425 FLdep NA   NA
##                  trialType trialIndex acc Experiment.Version
## 1 audio-keyboard-response         22  NA                 14
## 2 audio-keyboard-response         25  NA                 14
## 3 audio-keyboard-response         28  NA                 14
## 4 audio-keyboard-response         31  NA                 14
## 5 audio-keyboard-response         34  NA                 14
## 6 audio-keyboard-response         37  NA                 14
```

```
summary(learning);
```

```
##      subjID        learning              task        fribbleID       label
##  Min.   :1414932   FL:7556   learningBlock1:3529   10475  :  124   FLbim:2519
##  1st Qu.:1422477   LF:6840   learningBlock2:3773   31675  :  124   FLdep:2517
##  Median :1431970             learningBlock3:3595   13375  :  121   FLtob:2520
##  Mean   :1437270             learningBlock4:3499   22775  :  120   LFbim:2280
##  3rd Qu.:1459009                                   30375  :  120   LFdep:2280
##  Max.   :1459767                                   32475  :  120   LFtob:2280
##                                                    (Other):13667
##       rt          resp                          trialType       trialIndex
##  Min.   : 12.36   NA:14396   audio-keyboard-response:7556   Min.   : 22.0
##  1st Qu.: 52.50              image-keyboard-response:6840   1st Qu.:115.0
##  Median : 88.00                                             Median :211.0
##  Mean   :126.25                                             Mean   :210.8
##  3rd Qu.:214.71                                             3rd Qu.:307.0
##  Max.   :249.00                                             Max.   :400.0
##  NA's   :14389
##       acc        Experiment.Version
##  Min.   : NA     Min.   :14.00
##  1st Qu.: NA     1st Qu.:14.00
##  Median : NA     Median :14.00
##  Mean   :NaN     Mean   :14.33
##  3rd Qu.: NA     3rd Qu.:15.00
##  Max.   : NA     Max.   :15.00
##  NA's   :14396
```

Our fribbles were presented two times during learning.

Check if fribbles are presented > 2 times:

```
learning %>%
  group_by(subjID, fribbleID) %>%
  count() %>%
  filter(n >2)
```

```
## Warning: Factor `fribbleID` contains implicit NA, consider using
## `forcats::fct_explicit_na`
```

```
## # A tibble: 0 x 3
## # Groups:   subjID, fribbleID [1]
## # ... with 3 variables: subjID <int>, fribbleID <fct>, n <int>
```

None, perfect.

Check whether there are fribbles presented only once:

```
learning %>%
  group_by(subjID, fribbleID) %>%
  count() %>%
  filter(n < 2)
```

```
## # A tibble: 4 x 3
## # Groups:   subjID, fribbleID [4]
##    subjID fribbleID     n
##     <int> <fct>     <int>
## 1 1459696 12075         1
## 2 1459696 12675         1
## 3 1459696 13375         1
## 4 1459696 22125         1
```

Perfect.

Check the association between the fribbles and the labels (high and low frequency with the correct labels)

Fribbles ID are coded in this way: e.g., 10175-> [1] is the category [01] is the number of the fribble [75] is the frequency.

In the column fribbleID we have the fribble presented, in the column label we have the sound played.

Association between fribbles and labels are fixed:

- category 1, regardless of the frequency, has the label: dep
- category 2, regardless of the frequency, has the label: bim
- category 3, regardless of the frequency, has the label: tob

I'm going to add a column for category, fribble number, and frequency, in order to check whether everything is okay:

We should have only 3 categories, presented twice per participant. Each category is made of 20 exemplars.

```r
learning$category <- 0
learning[substr(as.character(learning$fribbleID), 1, 1)==1,]$category <- 1
learning[substr(as.character(learning$fribbleID), 1, 1)==2,]$category <- 2
learning[substr(as.character(learning$fribbleID), 1, 1)==3,]$category <- 3

(nrow(learning[learning$category==1,]) / length(unique(learning$subjID))) / 2
```

```
## [1] 19.9875
```

```r
(nrow(learning[learning$category==2,]) / length(unique(learning$subjID))) / 2
```

```
## [1] 19.99583
```

```r
(nrow(learning[learning$category==3,]) / length(unique(learning$subjID))) / 2
```

```
## [1] 20
```

We have 15 high frequency and 5 low frequency exemplars x category:

```r
learning$frequency <- 25
learning[substr(as.character(learning$fribbleID), 4, 5)==75,]$frequency <- 75

(nrow(learning[learning$frequency==25,]) / length(unique(learning$subjID))) / 2
```

```
## [1] 14.99583
```

```
(nrow(learning[learning$frequency==75,]) / length(unique(learning$subjID))) / 2
```

```
## [1] 44.9875
```

Now let's check the fribble-label association:

```
table(learning$category, learning$label, learning$frequency)
```

```
## , ,  = 25
##
##
##     FLbim FLdep FLtob LFbim LFdep LFtob
##   1     0   630     0     0   570     0
##   2   629     0     0   570     0     0
##   3     0     0   630     0     0   570
##
## , ,  = 75
##
##
##     FLbim FLdep FLtob LFbim LFdep LFtob
##   1     0  1887     0     0  1710     0
##   2  1890     0     0  1710     0     0
##   3     0     0  1890     0     0  1710
```

Okay, each label was associated to its correct fribble (coded here as category).

Check Testing

I'm going to select the tests and clean the rows from Gorilla's http address:

```
tests <- c("generalizationPL", "generalizationLP", "contingencyJudgement", "randomDot");

testing <- raw_data %>%
  filter(task %in% tests)


testing <- droplevels(testing);
rm(tests);

as.factor(gsub("/task/70033/56/asset/|/task/70033/57/asset/|/task/70033/58/asset/", "", testing$fribble
as.factor(gsub(".jpg$", "", testing$fribbleID))-> testing$fribbleID

as.factor(gsub("/task/70033/56/asset/|/task/70033/57/asset/|/task/70033/58/asset/", "", testing$label))
as.factor(gsub(".mp3$", "", testing$label))-> testing$label
```

Check test 1: Generalization from picture to labels

We filter the rows for this task, and clean both the resp and fribble columns.

```
generalizationPL <- testing %>%
  filter(task == 'generalizationPL')
generalizationPL <- droplevels(generalizationPL);

as.factor(gsub("/task/70033/56/asset/|/task/70033/57/asset/|/task/70033/58/asset/", "", generalizationPl
as.factor(gsub(".mp3$", "", generalizationPL$resp))-> generalizationPL$resp
as.factor(gsub(".jpg", "", generalizationPL$resp))-> generalizationPL$resp

gsub('[[:punct:]]|"', "", generalizationPL$label)-> generalizationPL$label

as.factor(gsub('mp3', "_", generalizationPL$label))-> generalizationPL$label
```

Check how many trials participants

```
generalizationPL %>%
  group_by(subjID) %>%
  count()
```

```
## # A tibble: 120 x 2
## # Groups:   subjID [120]
##     subjID     n
##      <int> <int>
##  1 1414932    24
##  2 1414933    24
##  3 1414937    24
##  4 1414945    24
##  5 1414957    24
##  6 1415040    24
##  7 1420163    24
##  8 1420165    24
##  9 1420169    24
## 10 1420171    24
## # ... with 110 more rows
```

Great, 24 trials per participant.

Check whether participants saw a unique fribble:

```
generalizationPL %>%
  group_by(subjID, fribbleID) %>%
  count() %>%
  filter(n > 1)
```

```
## Warning: Factor `fribbleID` contains implicit NA, consider using
## `forcats::fct_explicit_na`
```

```
## # A tibble: 0 x 3
## # Groups:   subjID, fribbleID [1]
## # ... with 3 variables: subjID <int>, fribbleID <fct>, n <int>
```

Great!

Integrate stimuli info. In the file "fribbleSet" I have listed all the fribbles ID and their category, along with their cueIDs and body shape. I'm going to add those columns by merging the test file with the fribbleSet by fribbleID. The rest of the file is left untouched.

```r
merge(generalizationPL, fribbleSet, by = 'fribbleID')-> generalizationPL;
generalizationPL$label.y <- NULL;

generalizationPL <- rename(generalizationPL, label = label.x);
```

Let's check the responses they made, just to see if they make sense.

For example, we want the resp column to be one of the labels.

```r
generalizationPL %>%
  group_by(subjID, resp) %>%
  count()
```

```
## Warning: Factor `resp` contains implicit NA, consider using
## `forcats::fct_explicit_na`

## Warning: Factor `resp` contains implicit NA, consider using
## `forcats::fct_explicit_na`

## Warning: Factor `resp` contains implicit NA, consider using
## `forcats::fct_explicit_na`
```

```
## # A tibble: 434 x 3
## # Groups:   subjID, resp [434]
##     subjID resp      n
##      <int> <fct> <int>
##  1 1414932 bim       6
##  2 1414932 dep       5
##  3 1414932 tob       9
##  4 1414932 <NA>      4
##  5 1414933 bim       8
##  6 1414933 dep       8
##  7 1414933 tob       8
##  8 1414937 bim       8
##  9 1414937 dep       7
## 10 1414937 tob       8
## # ... with 424 more rows
```

Great, some participant missed some trials (coded as NA), but that's okay.

So far, so good.

Check trial/stimuli per category, per frequency, per subject

We have 24 trials per participant, but within those trials we *should* have 8 trials per category, 4 low frequency and 4 high frequency trials.

```
head(table(generalizationPL$subjID, generalizationPL$category, generalizationPL$frequency))
```

```
## , ,  = 25
##
##
##           1 2 3
##   1414932 4 4 4
##   1414933 4 4 4
##   1414937 4 4 4
##   1414945 4 4 4
##   1414957 4 4 4
##   1415040 4 4 4
##
## , ,  = 75
##
##
##           1 2 3
##   1414932 4 4 4
##   1414933 4 4 4
##   1414937 4 4 4
##   1414945 4 4 4
##   1414957 4 4 4
##   1415040 4 4 4
```

Let's check the second task.

Check test 2: Generalization from label to pictures

```
generalizationLP <- testing %>%
  filter(task == 'generalizationLP')
generalizationLP <- droplevels(generalizationLP)
```

How many trials per participant?

```
generalizationLP %>%
  group_by(subjID) %>%
  count()
```

```
## # A tibble: 120 x 2
## # Groups:   subjID [120]
##     subjID     n
##      <int> <int>
##  1 1414932    24
##  2 1414933    24
##  3 1414937    24
##  4 1414945    24
##  5 1414957    24
##  6 1415040    24
##  7 1420163    24
##  8 1420165    24
##  9 1420169    24
## 10 1420171    24
## # ... with 110 more rows
```

24 trials, great.

Check whether participants saw a unique fribble

First let's clean the rows from Gorilla gibberish.

```
as.factor(gsub('[[:punct:]]|"', "", generalizationLP$fribbleID))-> generalizationLP$fribbleID

as.factor(gsub('jpg', "_", generalizationLP$fribbleID))-> generalizationLP$fribbleID

as.factor(gsub("/task/70033/56/asset/|/task/70033/57/asset/|/task/70033/58/asset/", "", generalizationL

as.factor(gsub(".jpg", "", generalizationLP$resp))-> generalizationLP$resp
```

Then check for duplicates:

```
substr(as.character(generalizationLP$fribbleID), 1, 5)-> temp
substr(as.character(generalizationLP$fribbleID), 7, 11)-> temp2
substr(as.character(generalizationLP$fribbleID), 13, 17)-> temp3

fribblePresented <- c(temp,temp2,temp3)
unique(generalizationLP$subjID)-> subj

duplicatedFribbles <- NA;
for (i in 1:length(subj)){
  substr(as.character(generalizationLP[generalizationLP$subjID==subj[i],]$fribbleID), 1, 5)-> temp
  substr(as.character(generalizationLP[generalizationLP$subjID==subj[i],]$fribbleID), 7, 11)-> temp2
  substr(as.character(generalizationLP[generalizationLP$subjID==subj[i],]$fribbleID), 13, 17)-> temp3
  fribblePresented <- c(temp,temp2,temp3)
  dup <- fribblePresented[duplicated(fribblePresented)] #extract duplicated elements
  print(subj[i])

  if (length(dup)>0){
    print(dup)
  } else {
    print(length(dup))
  }

};
```

```
## [1] 1414937
## [1] 0
## [1] 1414945
## [1] 0
## [1] 1414957
## [1] 0
## [1] 1415040
## [1] 0
## [1] 1431949
## [1] 0
## [1] 1431944
## [1] 0
## [1] 1431953
## [1] 0
## [1] 1431958
## [1] 0
## [1] 1431965
## [1] 0
## [1] 1431946
## [1] 0
## [1] 1431957
## [1] 0
## [1] 1431961
## [1] 0
## [1] 1431969
## [1] 0
## [1] 1431978
## [1] 0
## [1] 1431979
## [1] 0
## [1] 1422477
## [1] 0
## [1] 1422675
## [1] 0
## [1] 1422677
## [1] 0
## [1] 1422679
## [1] 0
## [1] 1422689
## [1] 0
## [1] 1422716
## [1] 0
## [1] 1431972
## [1] 0
## [1] 1431974
## [1] 0
## [1] 1431984
## [1] 0
## [1] 1431992
## [1] 0
## [1] 1431997
## [1] 0
## [1] 1432009
## [1] 0
## [1] 1432011
## [1] 0
## [1] 1432052
## [1] 0
## [1] 1432075
## [1] 0
## [1] 1420163
## [1] 0
## [1] 1420165
## [1] 0
## [1] 1420177
## [1] 0
## [1] 1420180
## [1] 0
## [1] 1420199
## [1] 0
## [1] 1420580
## [1] 0
## [1] 1420622
## [1] 0
## [1] 1422463
## [1] 0
## [1] 1422465
## [1] 0
## [1] 1422466
## [1] 0
## [1] 1422472
## [1] 0
## [1] 1459007
## [1] 0
## [1] 1459002
## [1] 0
## [1] 1459009
## [1] 0
## [1] 1459001
## [1] 0
## [1] 1459003
## [1] 0
## [1] 1459013
## [1] 0
## [1] 1459029
## [1] 0
## [1] 1458992
## [1] 0
## [1] 1459018
## [1] 0
## [1] 1459024
## [1] 0
## [1] 1459047
## [1] 0
## [1] 1459052
## [1] 0
## [1] 1459064
## [1] 0
## [1] 1459048
## [1] 0
## [1] 1459057
## [1] 0
## [1] 1459697
## [1] 0
## [1] 1459696
## [1] 0
## [1] 1459706
## [1] 0
## [1] 1459702
## [1] 0
## [1] 1459708
## [1] 0
## [1] 1459703
## [1] 0
## [1] 1459767
## [1] 0
## [1] 1414933
## [1] 0
## [1] 1414932
## [1] 0
## [1] 1420169
## [1] 0
## [1] 1420171
## [1] 0
## [1] 1420577
## [1] 0
## [1] 1422467
## [1] 0
## [1] 1422475
## [1] 0
## [1] 1422678
## [1] 0
## [1] 1422680
## [1] 0
## [1] 1422681
## [1] 0
## [1] 1431942
## [1] 0
## [1] 1431948
## [1] 0
## [1] 1431966
## [1] 0
## [1] 1431968
## [1] 0
## [1] 1431952
## [1] 0
## [1] 1431954
## [1] 0
## [1] 1431956
## [1] 0
## [1] 1431959
## [1] 0
## [1] 1431960
## [1] 0
## [1] 1431963
## [1] 0
## [1] 1431970
## [1] 0
## [1] 1431981
## [1] 0
## [1] 1431989
## [1] 0
## [1] 1431998
## [1] 0
## [1] 1431999
## [1] 0
## [1] 1432003
## [1] 0
## [1] 1432007
## [1] 0
## [1] 1432030
## [1] 0
## [1] 1420185
## [1] 0
## [1] 1420204
## [1] 0
## [1] 1420552
## [1] 0
## [1] 1420573
## [1] 0
## [1] 1422470
## [1] 0
## [1] 1422473
## [1] 0
## [1] 1422476
## [1] 0
## [1] 1422676
## [1] 0
## [1] 1422715
## [1] 0
## [1] 1432301
## [1] 0
## [1] 1432323
## [1] 0
## [1] 1457883
## [1] 0
## [1] 1458997
## [1] 0
## [1] 1459015
## [1] 0
## [1] 1459025
## [1] 0
## [1] 1458998
## [1] 0
## [1] 1458996
## [1] 0
## [1] 1459043
## [1] 0
## [1] 1459036
## [1] 0
## [1] 1459039
## [1] 0
## [1] 1459046
## [1] 0
## [1] 1459067
## [1] 0
## [1] 1459020
## [1] 0
## [1] 1459078
## [1] 0
## [1] 1459109
## [1] 0
## [1] 1459701
## [1] 0
## [1] 1459700
## [1] 0
## [1] 1459709
## [1] 0
## [1] 1459699
## [1] 0
```

```
rm(subj, temp, temp2, temp3, i, fribblePresented, duplicatedFribbles, dup)
```

Great! participants saw always different fribble.

Check whether fribbles presented were either high or low frequency within trials

In this task we have three pictures and one label pronounced. This means that the fribbleID column contains 3 images. I'm going to cycle over the dataset, and break the fribbleID column in three, then I'm going to print the fribble that within the same trial has a different frequency. I'm going to print the fribbles that are presented wrongly, e.g., "low high low" etc. If all fribbles are presented correctly: , e.g., "low low low" and "high high high", then the output is empty.

```
unique(generalizationLP$subjID)-> subj;

trials <- NULL;
task <- NULL;

for (i in 1:length(subj)){
  as.integer(substr(as.character(generalizationLP[generalizationLP$subjID==subj[i],]$fribbleID), 4, 5))
  as.integer(substr(as.character(generalizationLP[generalizationLP$subjID==subj[i],]$fribbleID), 10, 11
  as.integer(substr(as.character(generalizationLP[generalizationLP$subjID==subj[i],]$fribbleID), 16, 17
trials <- cbind(temp, temp2, temp3, as.integer(subj[i])) # store it in columns along with subj info
task <- rbind(task, trials) #store all subjs
};

for (i in 1:nrow(task)){ #check by rows whether there is a unique number, print the row if wrong
  if ((task[i,1] == task[i,2] & task[i,3])== FALSE) {
    print('wrong frequency fribble:')
    print(task[i,1], task[i,2], task[i,3])
  }
};

frequency <- ifelse(substr(as.character(task[,1]), 1, 1)==2, 'low', 'high')
cbind(task, frequency)->task
```

```
as.data.frame(task)-> task
rm(trials, i, subj, temp, temp2, temp3);
```

Great, fribbles presented were either low or high frequency. Check whether participants saw 4 trials with low and 4 trials with high frequency:

Check trial distribution per frequency:

```
head(table(task$V4, task$frequency))
```

```
##
##           high low
##   1414932   12  12
##   1414933   12  12
##   1414937   12  12
##   1414945   12  12
##   1414957   12  12
##   1415040   12  12
```

I'm going to merge the stimuli set now.

When we do it, this time we need to merge by resp and not by fribbleID, because our fribble selected is coded in this column:

```
fribbleSet$resp <- fribbleSet$fribbleID # column's name needs to be the same in order to merge
merge(generalizationLP, fribbleSet, by = 'resp', all.x = T)-> generalizationLP;
fribbleSet$resp <- NULL;
generalizationLP$fribbleID.y <- NULL;
generalizationLP$label.y <- NULL;
generalizationLP <- rename(generalizationLP, label = label.x);
generalizationLP <- rename(generalizationLP, fribbleID = fribbleID.x);
```

Check responses distribution by category:

```
generalizationLP %>%
  group_by(subjID, category) %>%
  count()
```

```
## # A tibble: 427 x 3
## # Groups:   subjID, category [427]
##     subjID category     n
##      <int>    <int> <int>
##  1 1414932        1     7
##  2 1414932        2    11
##  3 1414932        3     2
##  4 1414932       NA     4
##  5 1414933        1     8
##  6 1414933        2     5
##  7 1414933        3    10
##  8 1414933       NA     1
##  9 1414937        1     7
## 10 1414937        2     7
## # ... with 417 more rows
```

Cool.

Check responses distribution by frequency:

```
generalizationLP %>%
  group_by(subjID, label, frequency) %>%
  count()
```

```
## # A tibble: 837 x 4
## # Groups:   subjID, label, frequency [837]
##     subjID label frequency     n
##      <int> <fct>     <int> <int>
##  1 1414932 bim          25     3
##  2 1414932 bim          75     4
##  3 1414932 bim          NA     1
##  4 1414932 dep          25     3
##  5 1414932 dep          75     3
##  6 1414932 dep          NA     2
##  7 1414932 tob          25     3
##  8 1414932 tob          75     4
##  9 1414932 tob          NA     1
## 10 1414933 bim          25     4
## # ... with 827 more rows
```

Check test 3: Contingency Judgement task

```
contingencyJudgement <- testing %>%
  filter(task == 'contingencyJudgement')
contingencyJudgement <- droplevels(contingencyJudgement)
```

How many trials per participant?

```
contingencyJudgement %>%
  group_by(subjID) %>%
  count()
```

```
## # A tibble: 120 x 2
## # Groups:   subjID [120]
##     subjID     n
##      <int> <int>
##  1 1414932    24
##   2 1414933    24
##   3 1414937    24
##   4 1414945    24
##   5 1414957    24
##   6 1415040    24
##   7 1420163    24
##   8 1420165    24
##   9 1420169    24
##  10 1420171    24
## # ... with 110 more rows
```

Very good.

Did participants see a fribble more than once?

```
droplevels(contingencyJudgement) %>%
  group_by(subjID, fribbleID) %>%
  count() %>%
  filter( n > 1)
```

```
## Warning: Factor `fribbleID` contains implicit NA, consider using
## `forcats::fct_explicit_na`
```

```
## # A tibble: 0 x 3
## # Groups:   subjID, fribbleID [1]
## # ... with 3 variables: subjID <int>, fribbleID <fct>, n <int>
```

No! that's great.

Are labels repeated equally?

```
table(contingencyJudgement$subjID, contingencyJudgement$label)
```

```
##
##            bim dep tob
##   1414932    8   8   8
##   1414933    8   8   8
##   1414937    8   8   8
##   1414945    8   8   8
##   1414957    8   8   8
##   1415040    8   8   8
##   1420163    8   8   8
##   1420165    8   8   8
##   1420169    8   8   8
##   1420171    8   8   8
##   1420177    8   8   8
##   1420180    8   8   8
##   1420185    8   8   8
##   1420199    8   8   8
##    1420204    8    8    8
##    1420552    8    8    8
##    1420573    8    8    8
##    1420577    8    8    8
##    1420580    8    8    8
##    1420622    8    8    8
##    1422463    8    8    8
##    1422465    8    8    8
##    1422466    8    8    8
##    1422467    8    8    8
##    1422470    8    8    8
##    1422472    8    8    8
##    1422473    8    8    8
##    1422475    8    8    8
##    1422476    8    8    8
##    1422477    8    8    8
##    1422675    8    8    8
##    1422676    8    8    8
##    1422677    8    8    8
##    1422678    8    8    8
##    1422679    8    8    8
##    1422680    8    8    8
##    1422681    8    8    8
##    1422689    8    8    8
##    1422715    8    8    8
##    1422716    8    8    8
##    1431942    8    8    8
##    1431944    8    8    8
##    1431946    8    8    8
##    1431948    8    8    8
##    1431949    8    8    8
##    1431952    8    8    8
##    1431953    8    8    8
##    1431954    8    8    8
##    1431956    8    8    8
##    1431957    8    8    8
##    1431958    8    8    8
##    1431959    8    8    8
##    1431960    8    8    8
##    1431961    8    8    8
##    1431963    8    8    8
##    1431965    8    8    8
##    1431966    8    8    8
##    1431968    8    8    8
##    1431969    8    8    8
##    1431970    8    8    8
##    1431972    8    8    8
##    1431974    8    8    8
##    1431978    8    8    8
##    1431979    8    8    8
##    1431981    8    8    8
##    1431984    8    8    8
##    1431989    8    8    8
##    1431992    8    8    8
##    1431997    8    8    8
##    1431998    8    8    8
##    1431999    8    8    8
##    1432003    8    8    8
##    1432007    8    8    8
##    1432009    8    8    8
##    1432011    8    8    8
##    1432030    8    8    8
##    1432052    8    8    8
##    1432075    8    8    8
##    1432301    8    8    8
##    1432323    8    8    8
##    1457883    8    8    8
##    1458992    8    8    8
##    1458996    8    8    8
##    1458997    8    8    8
##    1458998    8    8    8
##    1459001    8    8    8
##    1459002    8    8    8
##    1459003    8    8    8
##    1459007    8    8    8
##    1459009    8    8    8
##    1459013    8    8    8
##    1459015    8    8    8
##    1459018    8    8    8
##    1459020    8    8    8
##    1459024    8    8    8
##    1459025    8    8    8
##    1459029    8    8    8
##    1459036    8    8    8
##    1459039    8    8    8
##    1459043    8    8    8
##    1459046    8    8    8
##    1459047    8    8    8
##    1459048    8    8    8
##    1459052    8    8    8
##    1459057    8    8    8
##    1459064    8    8    8
##    1459067    8    8    8
##    1459078    8    8    8
##    1459109    8    8    8
##    1459696    8    8    8
##    1459697    8    8    8
##    1459699    8    8    8
##    1459700    8    8    8
##    1459701    8    8    8
##    1459702    8    8    8
##    1459703    8    8    8
##    1459706    8    8    8
##    1459708    8    8    8
##    1459709    8    8    8
##    1459767    8    8    8
```

good

```
merge(contingencyJudgement, fribbleSet, by = 'fribbleID')-> contingencyJudgement
contingencyJudgement$label.y <- NULL;
contingencyJudgement <- rename(contingencyJudgement, label = label.x)
```

Check category presentation:

```
contingencyJudgement %>%
  group_by(subjID, category) %>%
  count()
```

```
## # A tibble: 360 x 3
## # Groups:   subjID, category [360]
##     subjID category     n
##      <int>    <int> <int>
##  1 1414932        1     8
##  2 1414932        2     8
##  3 1414932        3     8
##  4 1414933        1     8
##  5 1414933        2     8
##  6 1414933        3     8
##  7 1414937        1     8
##  8 1414937        2     8
##  9 1414937        3     8
## 10 1414945        1     8
## # ... with 350 more rows
```

```
table(contingencyJudgement$category, contingencyJudgement$label)
```

```
##
##     bim dep tob
##   1 312 312 336
##   2 384 288 288
##   3 264 360 336
```

Check test 4: Random dot task

Let's check our random dot task. This was inserted randomly during trials 4 times. 5 trials each time, plus 4 practice trials.

```
randomDot <- testing %>%
  filter(task == 'randomDot')
```

How many trials per participant?

```
randomDot %>%
  group_by(subjID) %>%
  count()
```

```
## # A tibble: 120 x 2
## # Groups:   subjID [120]
##     subjID     n
##      <int> <int>
##   1 1414932    26
##   2 1414933    26
##   3 1414937    26
##   4 1414945    26
##   5 1414957    26
##   6 1415040    26
##   7 1420163    26
##   8 1420165    26
##   9 1420169    26
## 10 1420171    26
## # ... with 110 more rows
```

we have 5 trials repeated during learning four times (20) plus 4 practice trials.

How was accuracy distributed across participants?

First, let's consider that when we have a timeout, the output is -1

```
randomDot %>%
  group_by(subjID, resp) %>%
  filter(rt == -1) %>%
  count()
```

```
## # A tibble: 83 x 3
## # Groups:   subjID, resp [83]
##     subjID resp      n
##      <int> <fct> <int>
##   1 1414932 -1       10
##   2 1414933 -1        1
##   3 1414945 -1        3
##   4 1415040 -1        1
##   5 1420163 -1        2
##   6 1420165 -1        1
##   7 1420180 -1        2
##   8 1420185 -1        1
##   9 1420204 -1        1
## 10 1420552 -1        3
## # ... with 73 more rows
```

Here we can see that some participant missed some trials.

Let's see how accuracy is coded when response is -1:

```
head(randomDot[randomDot$rt == -1,]$acc)
```

```
## [1] NA NA NA NA NA NA
```

So it is coded as "NA", great. However:

```
nrow(randomDot[is.na(randomDot$acc),]) #total of NA
```

```
## [1] 325
```

```
nrow(randomDot[randomDot$resp == -1,]) # total of timeouts
```

```
## [1] 196
```

There are more NA's in acc than can be explained by timeouts. This means that also wrong responses are coded as NA. We need to recode those.

```
randomDot[is.na(randomDot$acc),]$acc <- 0 #recode everything that is wrong or timeout as 0
```

Check the overall accuracy of participants, filtering by timeouts:

```
aggregate(acc ~ subjID, data = randomDot[!(randomDot$resp == -1),], FUN = mean)# without timeouts
```

```
##     subjID       acc
## 1   1414932 0.6875000
## 2   1414933 1.0000000
## 3   1414937 1.0000000
## 4   1414945 1.0000000
## 5   1414957 1.0000000
## 6   1415040 1.0000000
## 7   1420163 0.9583333
## 8   1420165 0.9600000
## 9   1420169 1.0000000
## 10  1420171 1.0000000
## 11  1420177 1.0000000
## 12  1420180 0.9583333
## 13  1420185 1.0000000
## 14  1420199 1.0000000
## 15  1420204 1.0000000
## 16  1420552 1.0000000
## 17  1420573 1.0000000
## 18  1420577 0.9583333
## 19  1420580 1.0000000
## 20  1420622 1.0000000
## 21  1422463 1.0000000
## 22  1422465 1.0000000
## 23  1422466 0.9565217
## 24  1422467 1.0000000
## 25  1422470 0.7600000
## 26  1422472 1.0000000
## 27  1422473 1.0000000
## 28  1422475 0.5200000
## 29  1422476 0.9600000
## 30  1422477 1.0000000
## 31  1422675 1.0000000
## 32  1422676 0.9615385
## 33  1422677 0.9047619
## 34  1422678 0.9600000
## 35  1422679 0.9565217
## 36  1422680 1.0000000
## 37  1422681 1.0000000
## 38  1422689 0.6000000
## 39  1422715 1.0000000
## 40  1422716 1.0000000
## 41  1431942 0.8461538
## 42  1431944 0.7619048
## 43  1431946 1.0000000
## 44  1431948 0.9600000
## 45  1431949 1.0000000
## 46  1431952 0.9565217
## 47  1431953 0.9615385
## 48  1431954 1.0000000
## 49  1431956 0.9166667
## 50  1431957 1.0000000
## 51  1431958 0.9615385
## 52  1431959 1.0000000
## 53  1431960 1.0000000
## 54  1431961 1.0000000
## 55  1431963 1.0000000
## 56  1431965 1.0000000
## 57  1431966 0.9600000
## 58  1431968 1.0000000
## 59  1431969 1.0000000
## 60  1431970 0.9565217
## 61  1431972 0.9600000
## 62  1431974 1.0000000
## 63  1431978 1.0000000
## 64  1431979 1.0000000
## 65  1431981 1.0000000
## 66  1431984 0.9600000
## 67  1431989 1.0000000
## 68  1431992 1.0000000
## 69  1431997 1.0000000
## 70  1431998 1.0000000
## 71  1431999 1.0000000
## 72  1432003 0.9130435
## 73  1432007 1.0000000
## 74  1432009 0.9600000
## 75  1432011 0.9090909
## 76  1432030 1.0000000
## 77  1432052 0.9166667
## 78  1432075 0.9600000
## 79  1432301 1.0000000
## 80  1432323 1.0000000
## 81  1457883 1.0000000
## 82  1458992 1.0000000
## 83  1458996 1.0000000
## 84  1458997 1.0000000
## 85  1458998 1.0000000
## 86  1459001 0.6521739
## 87  1459002 1.0000000
## 88  1459003 0.9600000
## 89  1459007 1.0000000
## 90  1459009 0.2916667
## 91  1459013 0.9600000
## 92  1459015 0.9565217
## 93  1459018 1.0000000
## 94  1459020 1.0000000
## 95  1459024 1.0000000
## 96  1459025 1.0000000
## 97  1459029 1.0000000
## 98  1459036 0.5652174
## 99  1459039 1.0000000
## 100 1459043 1.0000000
## 101 1459046 1.0000000
## 102 1459047 1.0000000
## 103 1459048 0.9523810
## 104 1459052 1.0000000
## 105 1459057 0.9166667
## 106 1459064 1.0000000
## 107 1459067 1.0000000
## 108 1459078 0.8800000
## 109 1459109 0.9583333
## 110 1459696 0.8333333
## 111 1459697 1.0000000
## 112 1459699 1.0000000
## 113 1459700 0.9600000
## 114 1459701 0.9615385
## 115 1459702 1.0000000
## 116 1459703 0.6956522
## 117 1459706 0.9565217
## 118 1459708 1.0000000
## 119 1459709 1.0000000
## 120 1459767 1.0000000
```

Now that we have all tests separated, better to remove this file:

Data visualization

Okay, from the sanity checks done above we can draw two conclusions:

1. Learning and Testing was presented as it was supposed to be and
2. data was stored correctly

Let's see now if data makes sense.

Select the version of the experiment

Select the version of the experiment you want:

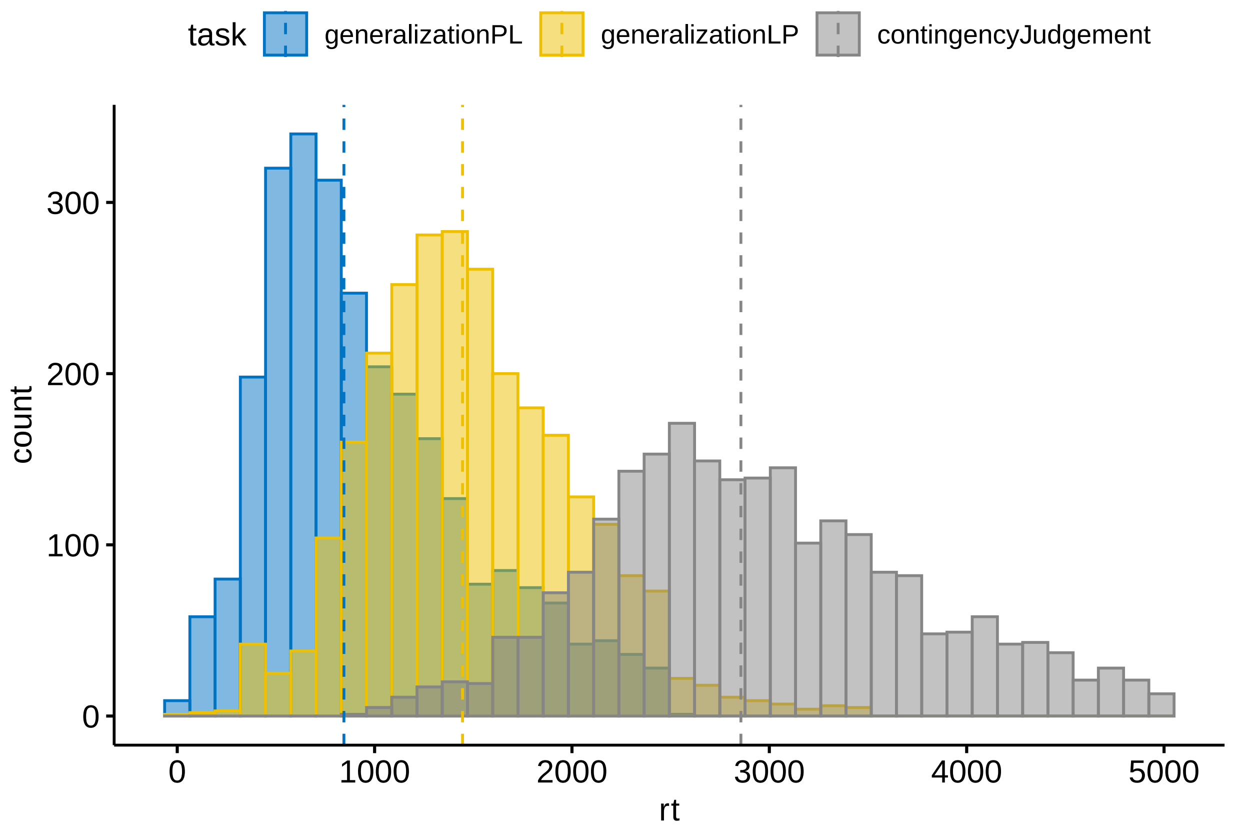
- Version 14 has 80 subjects, label picture task has 2500ms as timeout
- Version 15 has 42 subjects, label picture task has 3500ms as timeout

Reaction times

```r
rbind(generalizationPL, generalizationLP, contingencyJudgement)-> alltasks
alltasks <- droplevels(alltasks)
```

```r
gghistogram(alltasks,
       x = "rt",
       y = "..count..",
       xlab = "rt",
       color = "task",
       fill = "task",
       bins = 40,
       palette = "jco",
       add = "median"
)
```

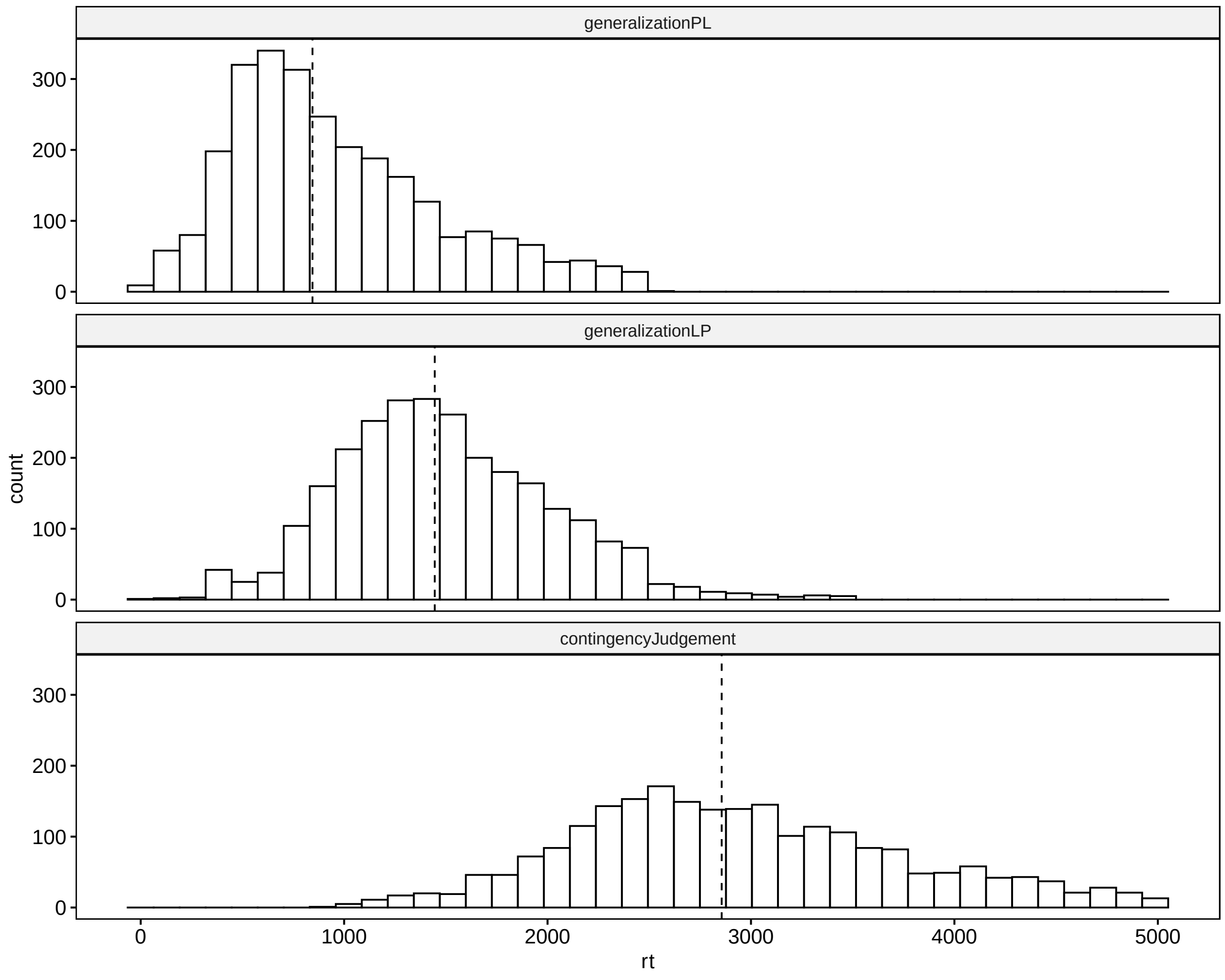
```
## Warning: Removed 934 rows containing non-finite values (stat_bin).
```



The two generalization tasks looks quite different. I'm going to plot it separately for a better inspection:

```r
p<- gghistogram(alltasks, #will throw warnings related to non responses but that's okay, ggplot simply
        x = "rt",
        y = "..count..",
        xlab = "rt",
        facet.by = "task",
        add = "median",
        bins = 40
)

facet(p, facet.by = "task",
      nrow = 3,
      ncol = 1)
```

```
## Warning: Removed 934 rows containing non-finite values (stat_bin).
```



The tails of the first two tasks don’t end smoothly, especially in task 2.

accuracy

RandomDot

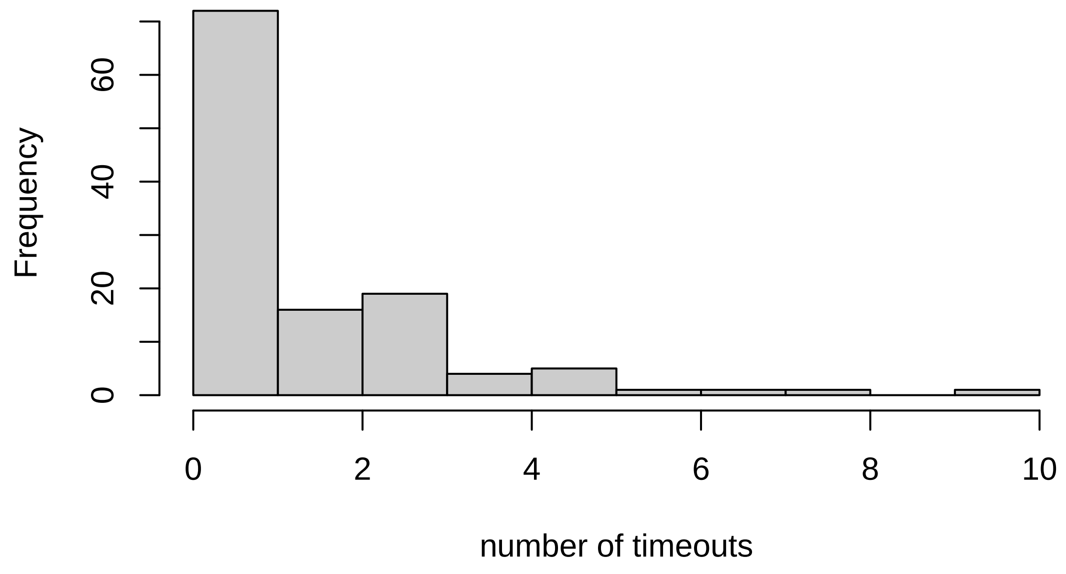
```r
unique(randomDot$subjID)-> subj;
randomDot-> randomTask

trials <- c(rep('0', 6), rep('1', 5),
              rep('2', 5), rep('3', 5),
              rep('4', 5))

trialstot <- as.factor(rep(trials, length(subj)))

randomTask$blocks <- trialstot
```

```r
randomTask$timeout <- ifelse(randomTask$resp== -1, 1, 0)
```

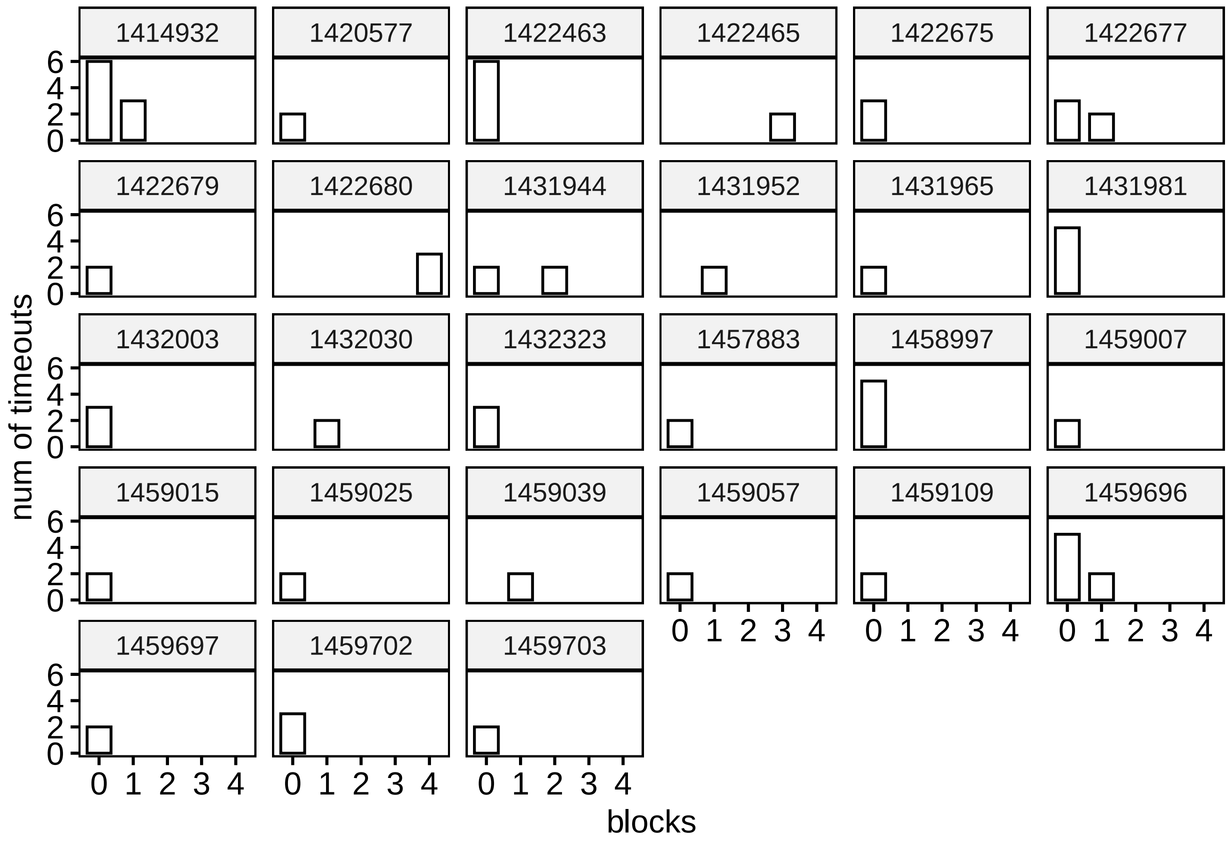
```r
temp<-randomTask %>%
  count(timeout, subjID) %>%
  filter(timeout == 1)

unique(temp$subjID)-> subjs

temp2<-randomTask[!(randomTask$subjID %in% subjs),] %>%
  count(timeout, subjID,  ) %>%
  filter(timeout == 0)

temp2[temp2$timeout==0,]$n <- 0

rbind(temp,temp2)-> timeout
```

How many timeouts by participant? Histrogram by participant:

```r
hist(timeout$n, xlab = 'number of timeouts',
     main = '',
     col=grey(.80),
     border=grey(0),
     breaks = seq(0,max(timeout$n),1))
```



```r
timeout <- randomTask %>%
  group_by(subjID, blocks) %>%
  filter(resp == -1) %>%
  count()


ggbarplot(timeout[timeout$n>1 ,], x = "blocks", y = "n",
          facet.by = "subjID",
          sort.by.groups = TRUE,      # Sort inside each group
          ylab = "num of timeouts")
```

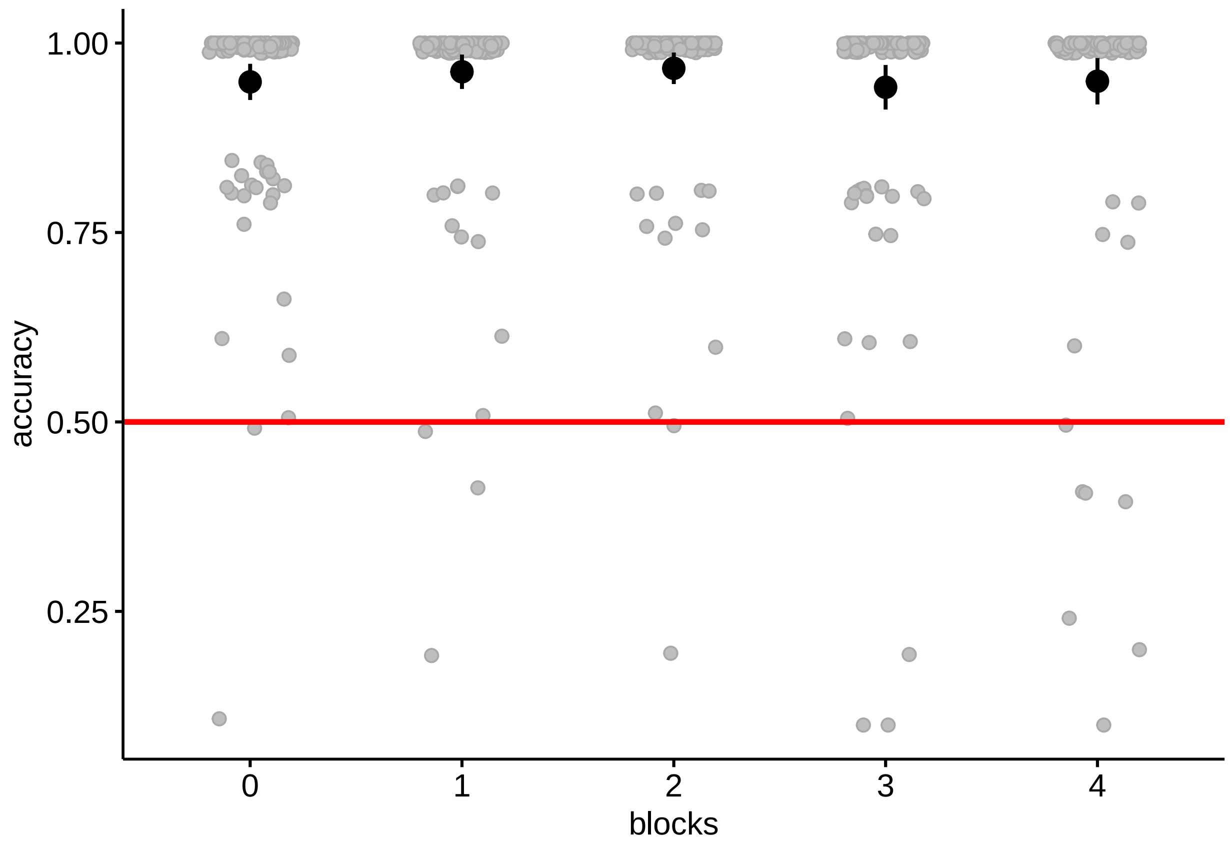


#### Subjects that made more than 3 timeouts

```
unique(timeout[timeout$n>3,]$subjID) -> problematicPeople
```

```
accdistr <- randomTask[!(randomTask$resp == -1),] %>%
  group_by(subjID, blocks,  ) %>%
  summarise(m = mean(acc))
```

```
ggstripchart(accdistr, x = "blocks", y = "m",
             xlab = "blocks",
             ylab = "accuracy",
             add = "mean_ci",
             size = 2,
             color = "darkgray",
             shape = 21,
             fill = "gray",
             error.plot = "pointrange",
             add.params = list(color = "black",
                               size = 0.7)) +
  scale_y_continuous(limits = c(0.1, 1), oob = scales::squish) + #to prevent jitter to move above 100%
  geom_hline(yintercept = .50, col='red', lwd=1);
```



```
accdistr <- randomTask[!(randomTask$resp == -1),] %>%
  group_by(subjID, blocks) %>%
  summarise(m = mean(acc))

accdistr[accdistr$m<=.5,]
```

```
## # A tibble: 21 x 3
## # Groups:   subjID [11]
##     subjID blocks     m
##      <int> <fct>  <dbl>
##  1 1414932 4       0.25
##  2 1422470 1       0.4
##  3 1422475 2       0.5
##  4 1422475 3       0.2
##  5 1422475 4       0
##  6 1422689 3       0
##  7 1422689 4       0.4
##  8 1431942 4       0.4
##  9 1459001 3       0.5
## 10 1459001 4       0.2
## # ... with 11 more rows
```

```
unique(accdistr[accdistr$m<.7,]$subjID) -> dumbPeople
```

```
setdiff(dumbPeople, problematicPeople)-> dumbPeople
```

People that scored less than 70%: Let's consider them as bad subjects.

```
c(problematicPeople, dumbPeople)->badsubjs
```

```
rm(temp, temp2, timeout, subj, subjs, trials, trialstot, accdistr)
```

Task 1: from picture to labels

The column fribbleID stores the fribble presented, while the column label stores the labels presented. Resp column in this task refers to the label selected. Category and frequency refers to the fribbleID column.

I'm going to add 1 in the accuracy column for every instance where response matches the category column, i.e., the participant correctly associated the fribble to its label.

I remove the no-response, and compute accuracy based on category and response.

```
length(unique(generalizationPL$subjID))
```

How many participants do we have per learning?

```
## [1] 120
```

```
fl<- length(unique(generalizationPL[generalizationPL$learning=='FL' &
                                    !(generalizationPL$subjID %in% badsubjs),]$subjID))
lf<- length(unique(generalizationPL[generalizationPL$learning=='LF' &
                                    !(generalizationPL$subjID %in% badsubjs),]$subjID))
fl
```

```
## [1] 55
```

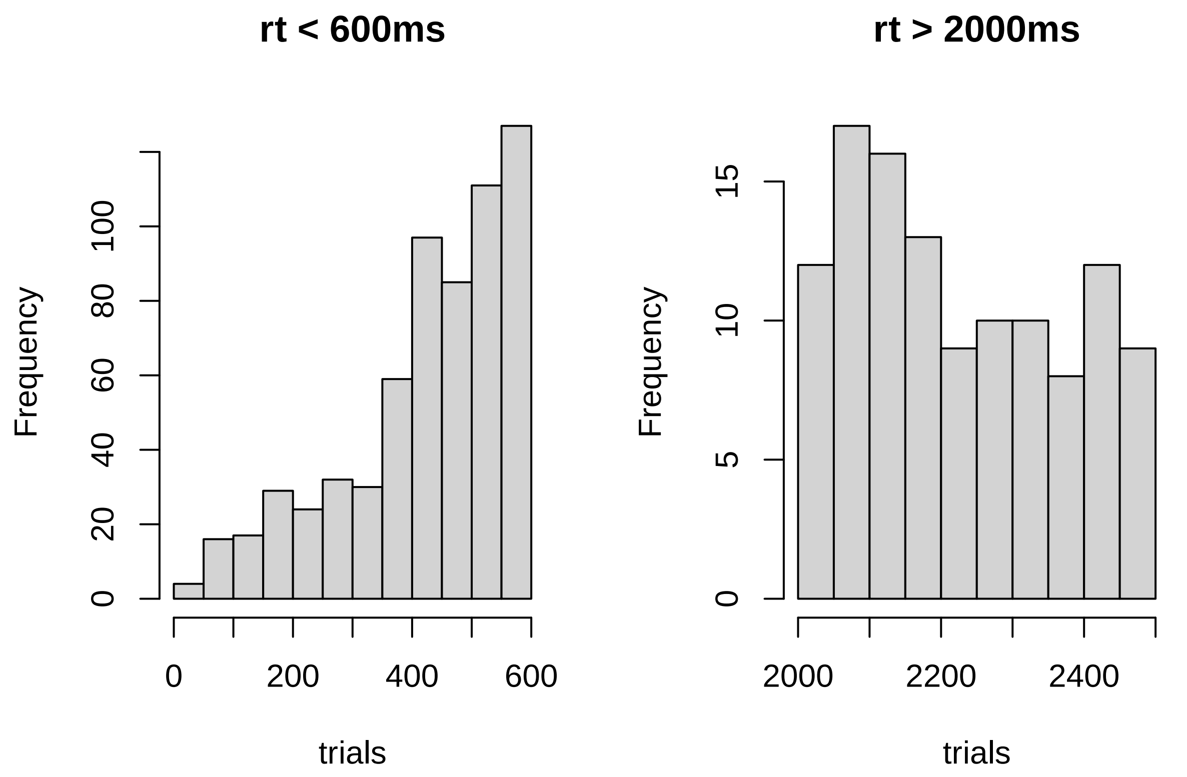
```
lf
```

```
## [1] 47
```

We have 55 for feature-label learning, and 47 for label-feature learning.

Check tails of the rt distribution The point is that we can't rely on responses made very early, because these might be simply mistakes or technical errors.

```
par(mfrow=c(1,2))
hist(generalizationPL[generalizationPL$rt<600 &
                       !(generalizationPL$subjID %in% badsubjs),]$rt, main = 'rt < 600ms', xlab = 'tri

hist(generalizationPL[generalizationPL$rt>2000 &
                       !(generalizationPL$subjID %in% badsubjs),]$rt, main = 'rt > 2000ms', xlab = 'tr
```



```
par(mfrow=c(1,1))
```

I would remove rt <100ms for all tasks.

```
round(nrow(generalizationPL[generalizationPL$rt<100 &
                            !(generalizationPL$subjID %in% badsubjs),]) / nrow(generalizationPL[!(gene
```

How many, what type of trials do we have?

```
## [1] 6.74
```

```
rm(fl,lf)
pictureLabel <- generalizationPL[!(is.na(generalizationPL$resp)),]

pictureLabel$acc <- 0;
pictureLabel[pictureLabel$category==1 & pictureLabel$resp=='dep',]$acc <- 1;

pictureLabel[pictureLabel$category==2 & pictureLabel$resp=='bim',]$acc <- 1;

pictureLabel[pictureLabel$category==3 & pictureLabel$resp=='tob',]$acc <- 1;
```

```
n <- length(unique(pictureLabel[!(pictureLabel$subjID %in% badsubjs),]$subjID))

nrows <- (nrow(generalizationPL[!(generalizationPL$subjID %in% badsubjs),])) - (nrow(pictureLabel[!(pic
```

```
sort(unique(pictureLabel[!(pictureLabel$subjID %in% badsubjs),]$subjID))-> subjs;
sort(unique(generalizationPL[!(generalizationPL$subjID %in% badsubjs),]$subjID)) ->totsubjs;

subjmissed<- setdiff(totsubjs, subjs);

rm(subjs, totsubjs);
```

We have 101 participants in this task, this is -1 compared to our total number of participants. The subject(s) that didn't answer at all the task is: 1420171. We have lost also 145 responses, that is 5.0347222 over the total: 2880.

How many trials per participant do we have now?

```
pictureLabel %>%
  group_by(subjID) %>%
  count() %>% filter(n<=18)
```

```
## # A tibble: 2 x 2
## # Groups:   subjID [2]
##    subjID     n
##     <int> <int>
## 1 1422475    18
## 2 1432075    18
```

No one had less than 18 trials, over the total (24). That's fine!

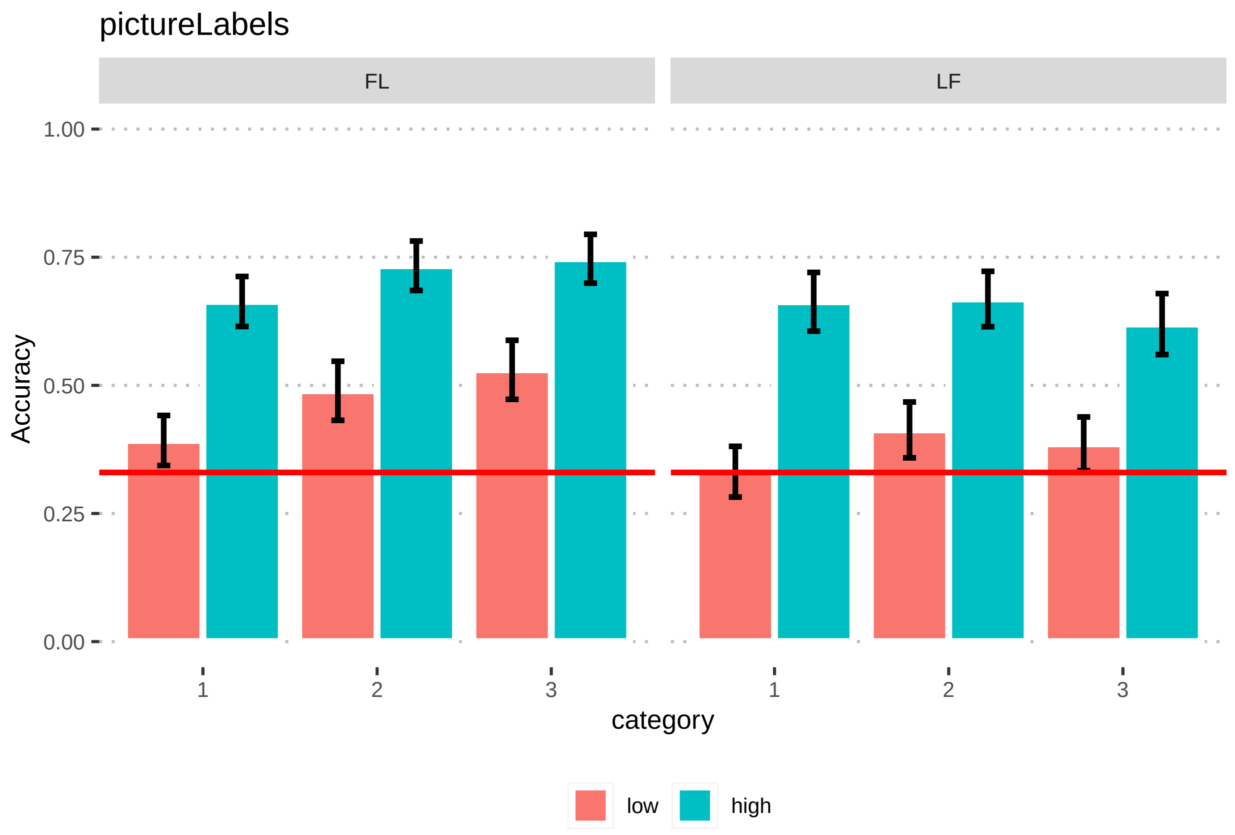
Barplot accuracy by category + frequency + learning picture label

```
c(badsubjs, subjmissed) -> badsubjs

rm(n, subjmissed, nrows)

ss_prop<-aggregate(acc ~ frequency+category+subjID+learning,
                   data = pictureLabel[pictureLabel$rt > 100 &
                                         !(pictureLabel$subjID %in% badsubjs),], FUN = mean)
```

Plot aggregated over subjs. To see accuracy distributed over categories.

```
ms <- ss_prop %>%
  group_by( category, frequency, learning) %>%
  summarise(n=n(),
    mean=mean(acc),
    sd=sd(acc)
  ) %>%
  mutate( se=sd/sqrt(n))  %>%
  mutate( ci=se * qt((1-0.05)/2 + .5, n-1))
```

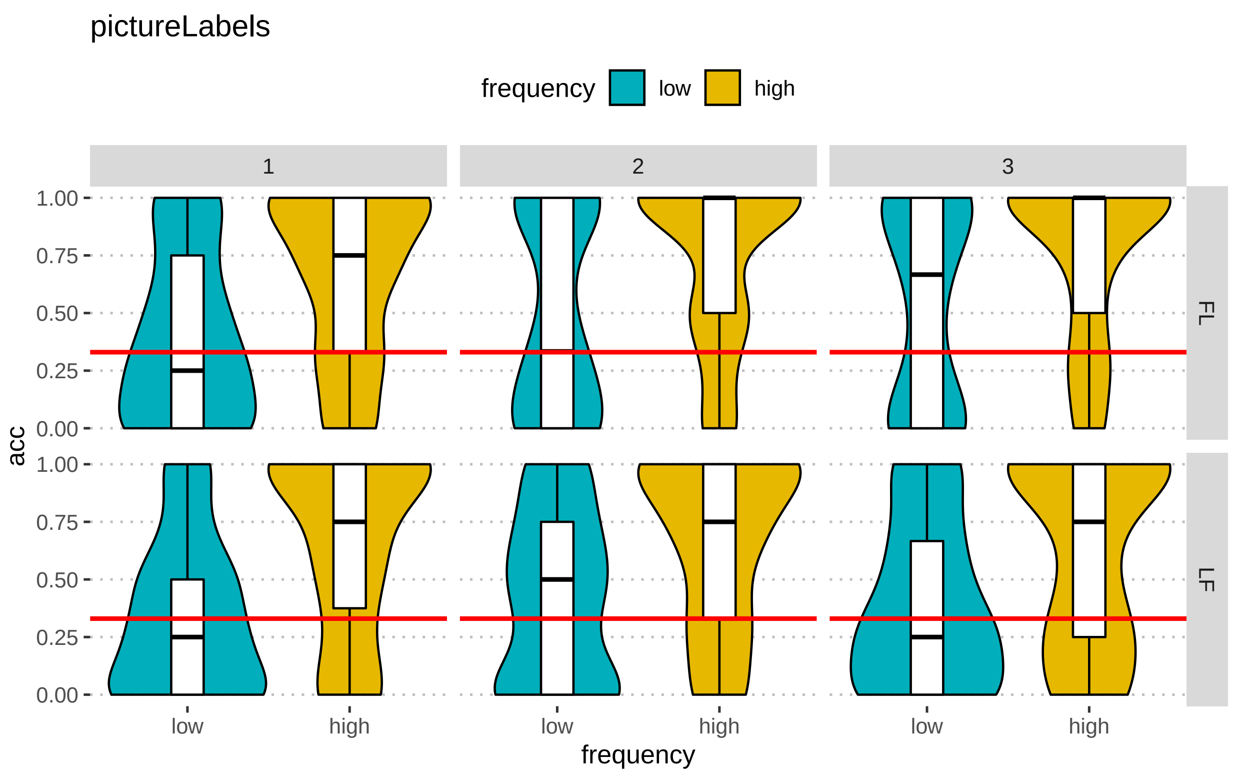
```r
ms$frequency <- as.factor(ms$frequency)
plyr::revalue(ms$frequency, c("25"="low"))-> ms$frequency;
plyr::revalue(ms$frequency, c("75"="high"))-> ms$frequency;

ggplot(aes(x = category, y = mean, fill = frequency), data = ms) +
  facet_grid( . ~ learning) +
  geom_bar(stat = "identity", color='white', position=position_dodge(), size=1.2) +
  geom_errorbar(aes(ymin=mean-se, ymax=mean+se), width=.15, size=1,position=position_dodge(.9)) +
  ylab("Accuracy ") +
  xlab("category") +
  ggtitle('pictureLabels') +
  coord_cartesian(ylim = c(0, 1))+
  ggpubr::theme_pubclean() +
  theme(legend.position="bottom", legend.title = element_blank()) +
  theme(text = element_text(size=10)) +
  geom_hline(yintercept = .33, col='red', lwd=1);
```



```r
df <- aggregate(acc ~ subjID+frequency+learning+category,
                data = pictureLabel[pictureLabel$rt > 100  &
                                        !(pictureLabel$subjID %in% badsubjs),], mean)
df$frequency <- as.factor(df$frequency)
plyr::revalue(df$frequency, c("25"="low"))-> df$frequency;
```

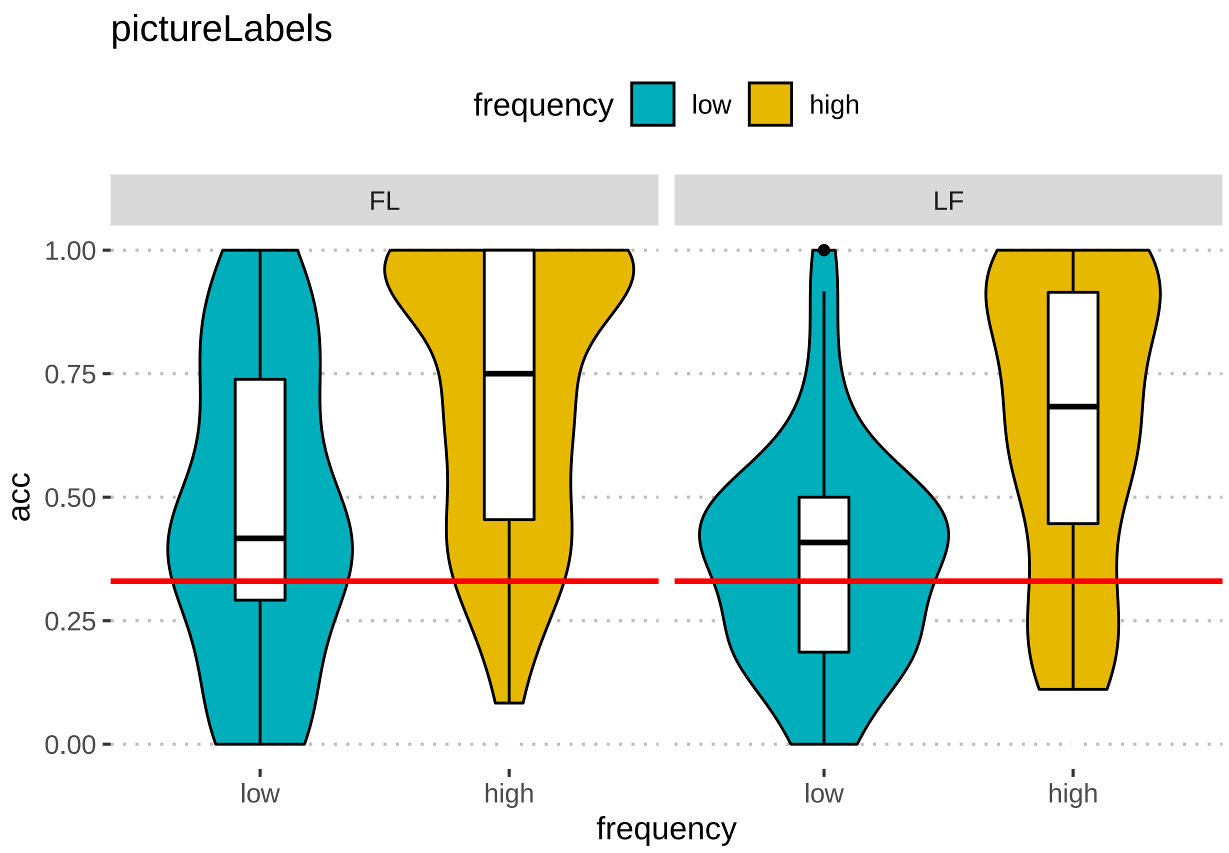
```
plyr::revalue(df$frequency, c("75"="high"))-> df$frequency;

ggviolin(df, x = "frequency", y = "acc", fill = "frequency",
         palette = c("#00AFBB", "#E7B800"),
         add = "boxplot",
         add.params = list(fill = "white"),
         trim=TRUE) +
        ggtitle('pictureLabels') +
        facet_grid( learning ~ category) +
        theme_pubclean()+
  geom_hline(yintercept = .33, col='red', lwd=1);
```

Violin plot accuracy by category + frequency + learning



Violin plot accuracy by frequency + learning Let's see how participants scored for the high/low frequency:

```
df <- aggregate(acc ~ subjID+frequency+learning,
                data = pictureLabel[pictureLabel$rt > 100  &
                                       !(pictureLabel$subjID %in% badsubjs),], mean)
df$frequency <- as.factor(df$frequency)
plyr::revalue(df$frequency, c("25"="low"))-> df$frequency;
plyr::revalue(df$frequency, c("75"="high"))-> df$frequency;

ggviolin(df, x = "frequency", y = "acc", fill = "frequency",
         palette = c("#00AFBB", "#E7B800"),
         add = "boxplot",
         add.params = list(fill = "white"),
         trim=TRUE) +
        ggtitle('pictureLabels') +
        facet_grid( . ~ learning) +
        theme_pubclean()+
  geom_hline(yintercept = .33, col='red', lwd=1);
```



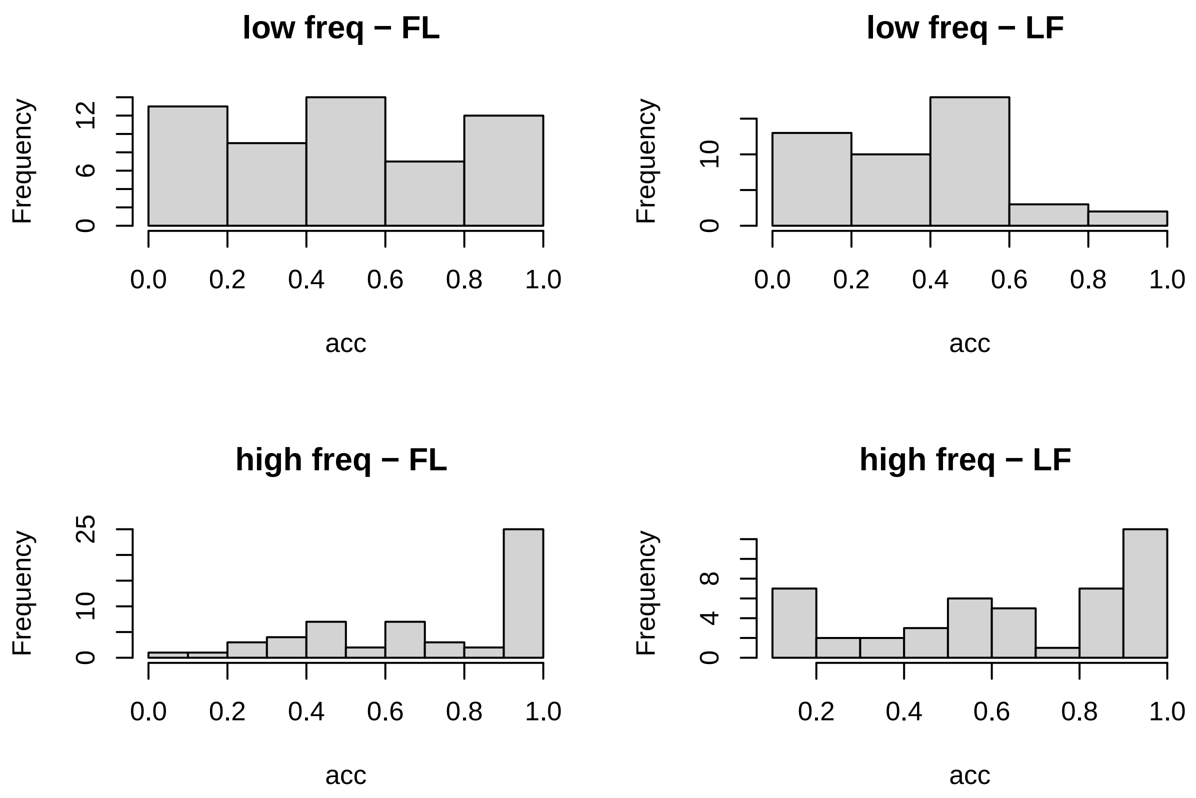
```
df %>%
  group_by(learning, frequency) %>%
  summarise(mean(acc))
```

```
## # A tibble: 4 x 3
## # Groups:   learning [2]
##   learning frequency `mean(acc)`
##   <fct>    <fct>           <dbl>
## 1 FL       low             0.474
## 2 FL       high            0.721
## 3 LF       low             0.376
## 4 LF       high            0.656
```

Closer inspection:

```
par(mfrow=c(2,2))
hist(df[df$frequency=='low' & df$learning=='FL' ,]$acc, xlab = 'acc', main = 'low freq - FL ')
```

```r
hist(df[df$frequency=='low' & df$learning=='LF',]$acc, xlab = 'acc', main = 'low freq - LF ')
hist(df[df$frequency=='high' & df$learning=='FL',]$acc, xlab = 'acc', main = 'high freq - FL ')
hist(df[df$frequency=='high' & df$learning=='LF',]$acc, xlab = 'acc', main = 'high freq - LF ')
```



```r
par(mfrow=c(1,1))
```

```r
#barPlot aggregated over categories:

ms <- aggregate(acc ~ subjID+frequency+learning,
                data=pictureLabel[pictureLabel$rt > 100 &
                                  !(pictureLabel$subjID %in% badsubjs)  ,], FUN= mean)

df<- ms %>%
  group_by(frequency, learning)%>%
  summarise(
    mean = mean(acc),
    sd = sd(acc),
    n = n()) %>%
  mutate( se=sd/sqrt(n))  %>%
  mutate( ci=se * qt((1-0.05)/2 + .5, n-1))

df$frequency <- as.factor(df$frequency)
```

```
plyr::revalue(df$frequency, c("25"="low"))-> df$frequency;
plyr::revalue(df$frequency, c("75"="high"))-> df$frequency;


pl<-ggplot(aes(x = frequency, y = mean, fill = frequency), data = df) +
  facet_grid( . ~ learning) +
  geom_bar(stat = "identity", color='white', position=position_dodge(), size=1.2) +
  geom_errorbar(aes(ymin=mean-se, ymax=mean+se), width=.15, size=1,position=position_dodge(.9)) +
  ylab("Accuracy ") +
  xlab("frequency") +
  ggtitle('pictureLabels') +
  coord_cartesian(ylim = c(0, 1))+
  ggpubr::theme_pubclean() +
  theme(legend.position = "none") +
  theme(text = element_text(size=10)) +
  geom_hline(yintercept = .33, col='red', lwd=1);
```

Barplot accuracy by frequency + learning

```
rbind(lowFreqFL, highFreqFL, lowFreqLF, highFreqLF)-> pictureLabel_respType
rm(lowFreqFL, highFreqFL, lowFreqLF, highFreqLF)
```

Response type: match, mismatch-type1, mismatch-type2

Task 2: from label to pictures

Let's check now the generalizaton from label to pictures:

```
length(unique(generalizationLP$subjID))
```

```
## [1] 120
```

```
fl<- length(unique(generalizationLP[generalizationLP$learning=='FL' &
                                      !(generalizationLP$subjID %in% badsubjs),]$subjID))

lf<- length(unique(generalizationLP[generalizationLP$learning=='LF' &
                                      !(generalizationLP$subjID %in% badsubjs),]$subjID))
fl
```

```
## [1] 55
```

```
lf
```

```
## [1] 46
```

How many participants do we have per learning? We have 55 for feature-label learning, and 46 for label-feature learning.

```r
rm(fl,lf)
labelPicture <- generalizationLP[!(is.na(generalizationLP$resp)),]
n<- length(unique(labelPicture$subjID))
nrows <- (nrow(generalizationLP)) - (nrow(labelPicture))

sort(unique(labelPicture$subjID))-> subjs;
sort(unique(generalizationLP$subjID)) ->totsubjs;

subjmissed<- setdiff(totsubjs, subjs);
```

Great, we have 120 participants in this task, so -0, and we have missed 195 over the total 2880, that is 6.7708333. The subject(s) that missed completely the task is: .

How many, what type of trials do we have? How many datapoints did we lose for no-responses?

```r
round(nrow(generalizationLP[(is.na(generalizationLP$resp)) &
                              !(generalizationLP$subjID %in% badsubjs),]) /nrow(generalizationLP[!(gene
```

```
## [1] 6.77
```

How many trials were rt < 100?

```r
round(nrow(generalizationLP[generalizationLP$rt<100 &
                              !(generalizationLP$subjID %in% badsubjs),])/ nrow(generalizationLP[!(gene
```

```
## [1] 6.81
```

Once trimmed, how many trials per participant do we have in this task?

```r
labelPicture %>%
  group_by(subjID) %>%
  count() %>%
  filter(n<=18)
```

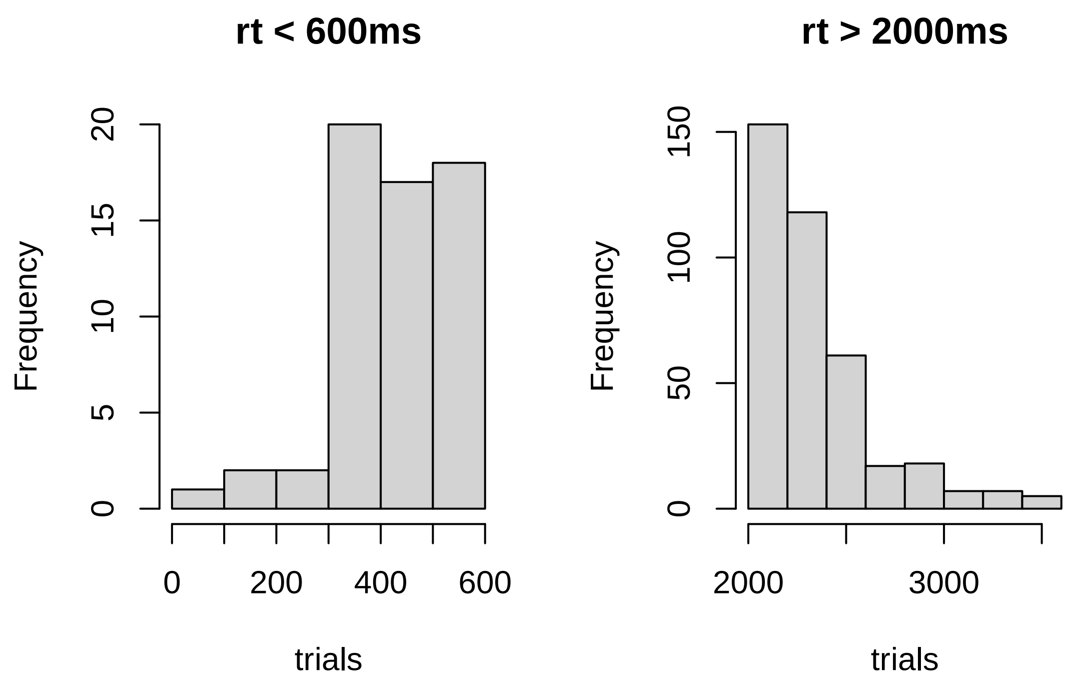
```
## # A tibble: 8 x 2
## # Groups:   subjID [8]
##    subjID     n
##     <int> <int>
## 1 1420577    18
## 2 1422475    18
## 3 1422477    17
## 4 1422677    17
## 5 1422680     9
## 6 1422689    17
## 7 1432009     8
## 8 1432075    17
```

Here we have less datapoints. For sure, 1422680 needs to be added to the black list because has few correct trials.

```
c(badsubjs, 1422680, 1432009) -> badsubjs
```

```
par(mfrow=c(1,2))
hist(generalizationLP[generalizationLP$rt<600 &
                        !(generalizationLP$subjID %in% badsubjs),]$rt, main = 'rt < 600ms', xlab = 'tri
hist(generalizationLP[generalizationLP$rt>2000 &
                        !(generalizationLP$subjID %in% badsubjs),]$rt, main = 'rt > 2000ms', xlab = 'tr
```

Check tails of the rt distribution



```
par(mfrow=c(1,1))
```

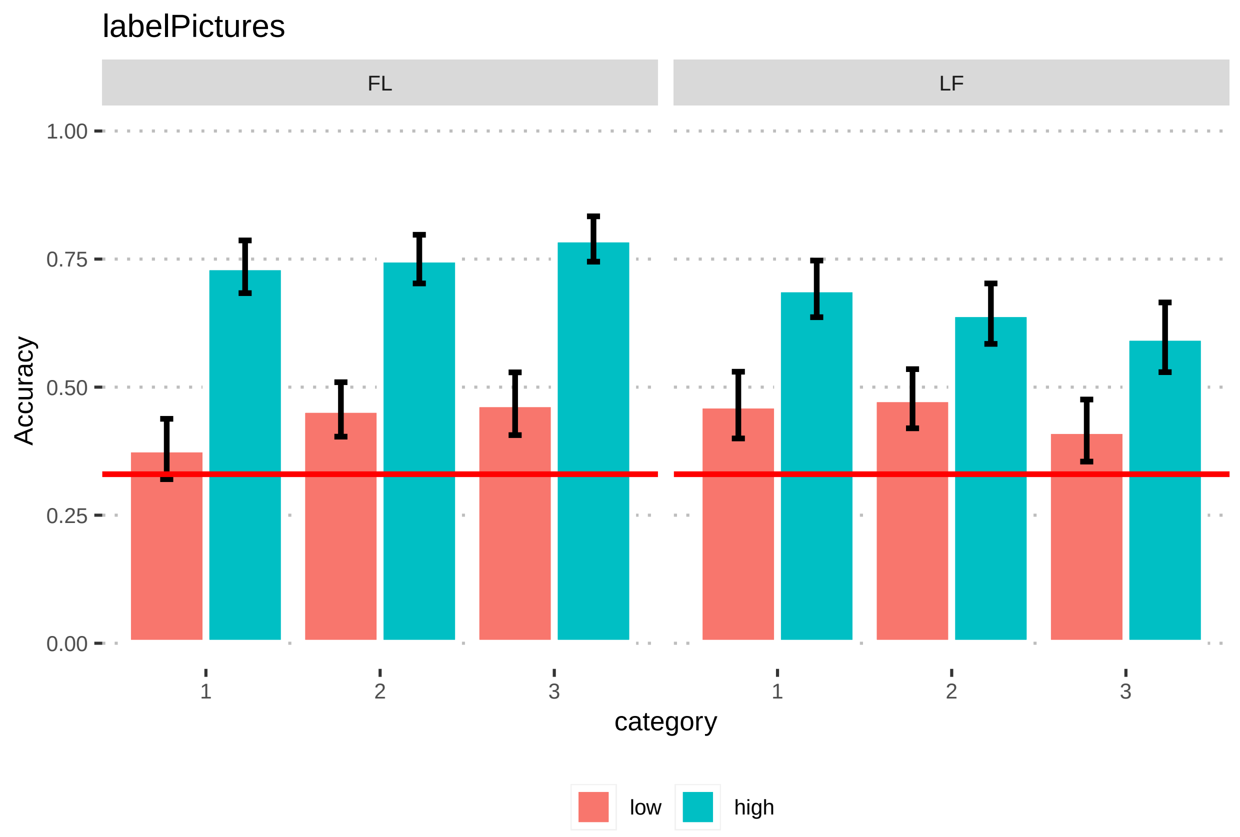
```
rm(n, nrows, subjs, totsubjs);
labelPicture$acc <- 0;
labelPicture[labelPicture$category==1 & labelPicture$label=='dep',]$acc <- 1;
labelPicture[labelPicture$category==2 & labelPicture$label=='bim',]$acc <- 1;
labelPicture[labelPicture$category==3 & labelPicture$label=='tob',]$acc <- 1;
```

Barplot accuracy by category+learning+frequency Calculate the proportion of correct in each condition

```
rm(subjmissed)
ss_prop<-aggregate(acc ~ frequency+category+subjID+learning,
                   data = labelPicture[labelPicture$rt > 100 &
                                         labelPicture$rt <= 2500 &
                                         !(labelPicture$subjID %in% badsubjs),], FUN = mean)
```

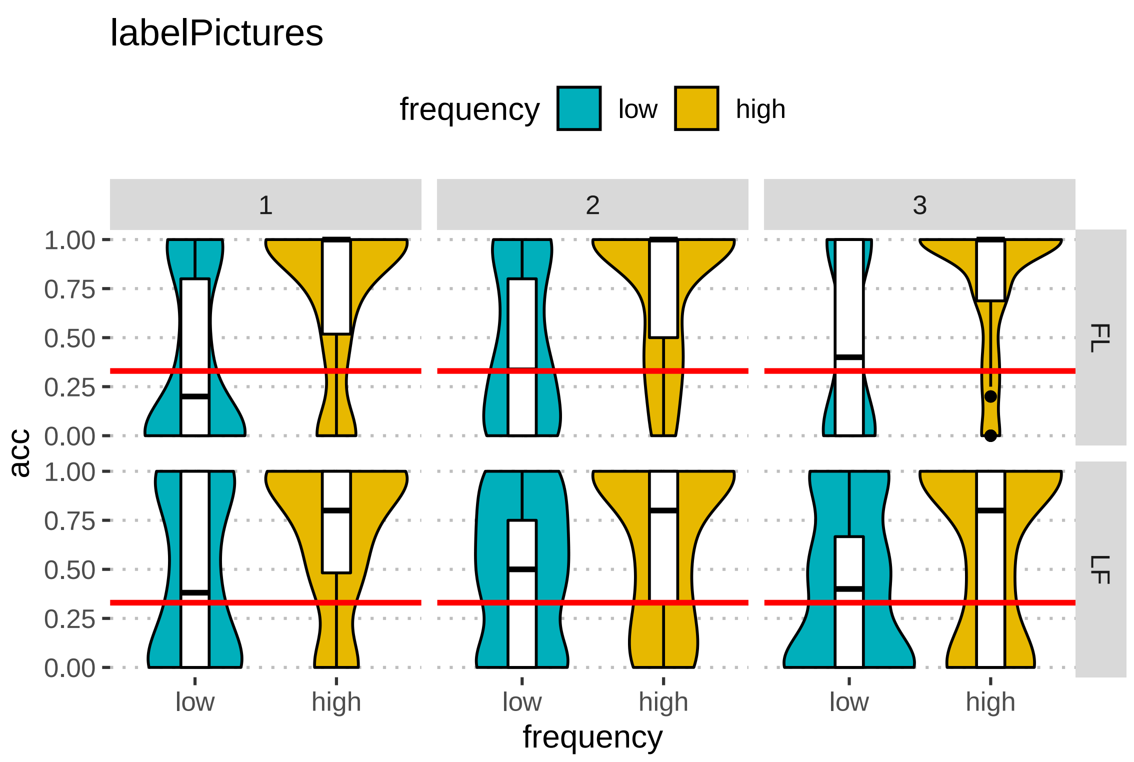
Plot aggregated over subjs. To see accuracy distributed over categories.

```
ms <- ss_prop %>%
  group_by(category, frequency, learning) %>%
  summarise(
    n=n(),
    mean=mean(acc),
    sd=sd(acc)
  ) %>%
  mutate( se=sd/sqrt(n))  %>%
  mutate( ci=se * qt((1-0.05)/2 + .5, n-1))

ms$frequency <- as.factor(ms$frequency)
plyr::revalue(ms$frequency, c("25"="low"))-> ms$frequency;
plyr::revalue(ms$frequency, c("75"="high"))-> ms$frequency;

ggplot(aes(x = category, y = mean, fill = frequency), data = ms) +
  facet_grid( . ~ learning) +
  geom_bar(stat = "identity", color='white', position=position_dodge(), size=1.2) +
  geom_errorbar(aes(ymin=mean-se, ymax=mean+se), width=.15, size=1,position=position_dodge(.9)) +
  ylab("Accuracy ") +
  xlab("category") +
  ggtitle('labelPictures') +
  coord_cartesian(ylim = c(0, 1))+
  ggpubr::theme_pubclean() +
  theme(legend.position="bottom", legend.title = element_blank()) +
  theme(text = element_text(size=10)) +
  geom_hline(yintercept = .33, col='red', lwd=1);
```



```
ms <- aggregate(acc ~ subjID+frequency+learning+category,
                data = labelPicture[labelPicture$rt > 100 &
                                      labelPicture$rt <=2500 &
                                        !(labelPicture$subjID %in% badsubjs),], mean)

ms$frequency <- as.factor(ms$frequency)
plyr::revalue(ms$frequency, c("25"="low"))-> ms$frequency;
plyr::revalue(ms$frequency, c("75"="high"))-> ms$frequency;

ggviolin(ms, x = "frequency", y = "acc", fill = "frequency",
         palette = c("#00AFBB", "#E7B800"),
         add = "boxplot",
         add.params = list(fill = "white"),
         trim=TRUE) +
         ggtitle('labelPictures') +
        facet_grid( learning ~ category) +
        theme_pubclean()+
  geom_hline(yintercept = .33, col='red', lwd=1);
```

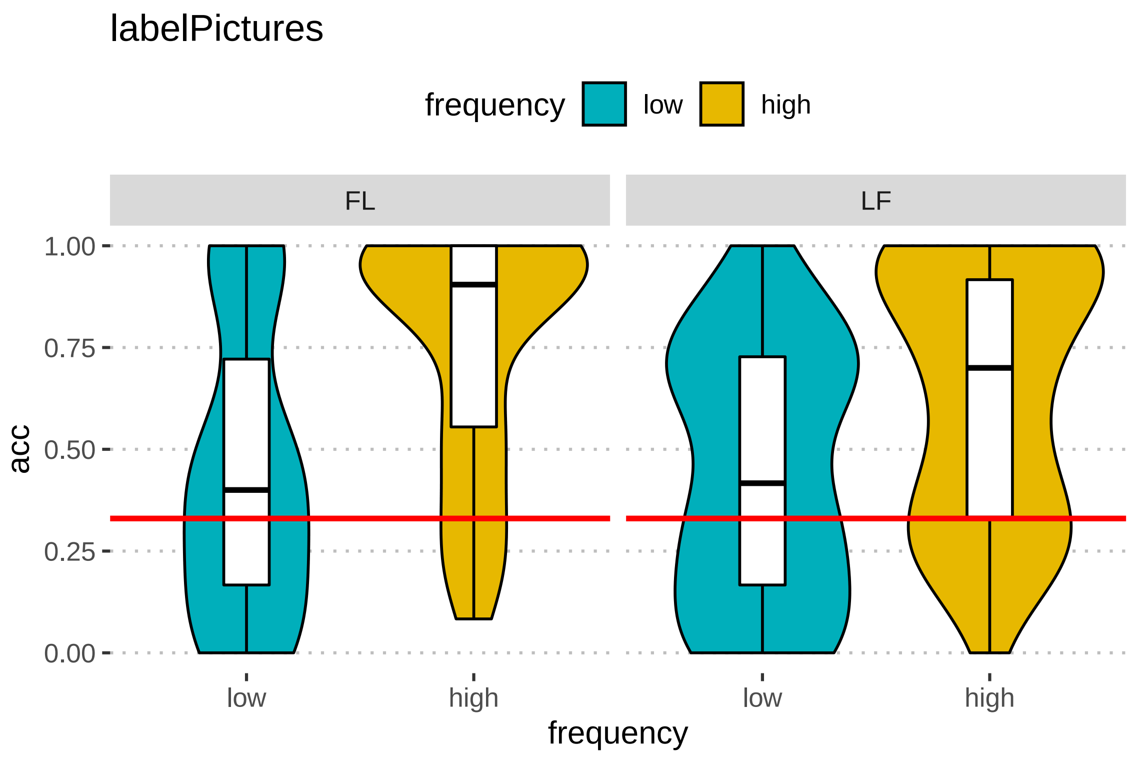
Violin plot accuracy by category+learning+frequency



```
#rm(ms, ss_prop)
```

```
ms <- aggregate(acc ~ subjID+frequency+learning,
                data = labelPicture[labelPicture$rt > 100 &
                                      labelPicture$rt <= 2500 &
                                        !(labelPicture$subjID %in% badsubjs),], mean)

ms$frequency <- as.factor(ms$frequency)
plyr::revalue(ms$frequency, c("25"="low"))-> ms$frequency;
plyr::revalue(ms$frequency, c("75"="high"))-> ms$frequency;

ggviolin(ms, x = "frequency", y = "acc", fill = "frequency",
         palette = c("#00AFBB", "#E7B800"),
         add = "boxplot",
         add.params = list(fill = "white"),
         trim=TRUE) +
         ggtitle('labelPictures') +
        facet_grid( . ~ learning) +
        theme_pubclean()+
  geom_hline(yintercept = .33, col='red', lwd=1);
```

Violinplot accuracy by learning+frequency

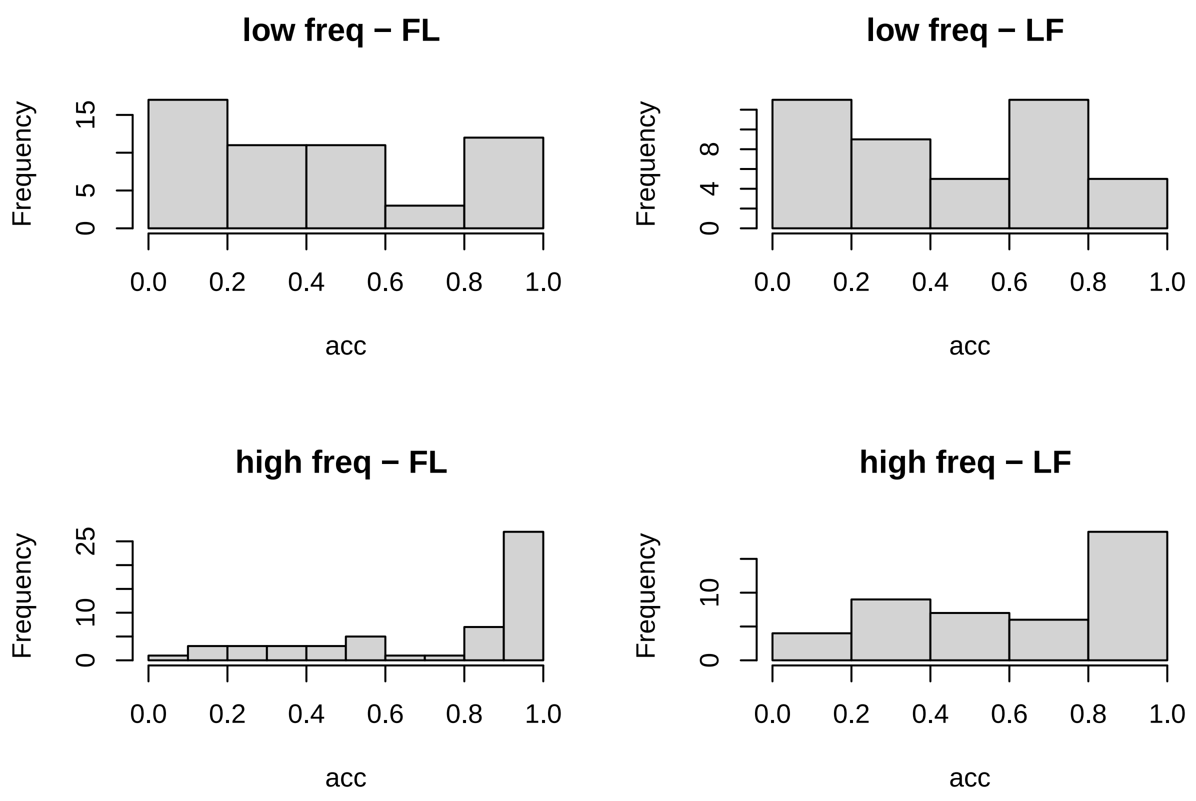


```
#rm(ms, ss_prop)
```

```
ms %>%
  group_by(learning, frequency) %>%
  summarise(mean(acc))
```

```
## # A tibble: 4 x 3
## # Groups:   learning [2]
##   learning frequency `mean(acc)`
##   <fct>    <fct>           <dbl>
## 1 FL       low             0.439
## 2 FL       high            0.750
## 3 LF       low             0.439
## 4 LF       high            0.644
```

```
par(mfrow=c(2,2))
hist(ms[ms$frequency=='low' & ms$learning=='FL',]$acc, xlab = 'acc', main = 'low freq - FL ')
hist(ms[ms$frequency=='low' & ms$learning=='LF',]$acc, xlab = 'acc', main = 'low freq - LF ')
hist(ms[ms$frequency=='high' & ms$learning=='FL',]$acc, xlab = 'acc', main = 'high freq - FL ')
hist(ms[ms$frequency=='high' & ms$learning=='LF',]$acc, xlab = 'acc', main = 'high freq - LF ')
```



```r
par(mfrow=c(1,1))
```

```r
#barPlot aggregated over categories:

ms <- aggregate(acc ~ subjID+frequency+learning,
                data=labelPicture[labelPicture$rt > 100 &
                                    labelPicture$rt <= 2500 &
                                  !(labelPicture$subjID %in% badsubjs)  ,], FUN= mean)

df<- ms %>%
  group_by(frequency, learning)%>%
  summarise(
    mean = mean(acc),
    sd = sd(acc),
    n = n()) %>%
  mutate( se=sd/sqrt(n))  %>%
  mutate( ci=se * qt((1-0.05)/2 + .5, n-1))

df$frequency <- as.factor(df$frequency)
plyr::revalue(df$frequency, c("25"="low"))-> df$frequency;
plyr::revalue(df$frequency, c("75"="high"))-> df$frequency;
```

```r
lp<-ggplot(aes(x = frequency, y = mean, fill = frequency), data = df) +
  facet_grid( . ~ learning) +
  geom_bar(stat = "identity", color='white', position=position_dodge(), size=1.2) +
  geom_errorbar(aes(ymin=mean-se, ymax=mean+se), width=.15, size=1,position=position_dodge(.9)) +
  ylab("Accuracy ") +
  xlab("frequency") +
  ggtitle('labelPictures') +
  coord_cartesian(ylim = c(0, 1))+
  ggpubr::theme_pubclean() +
  theme(legend.position="bottom", legend.title = element_blank()) +
  theme(text = element_text(size=10)) +
  geom_hline(yintercept = .33, col='red', lwd=1);
```

Barplot accuracy by frequency + learning

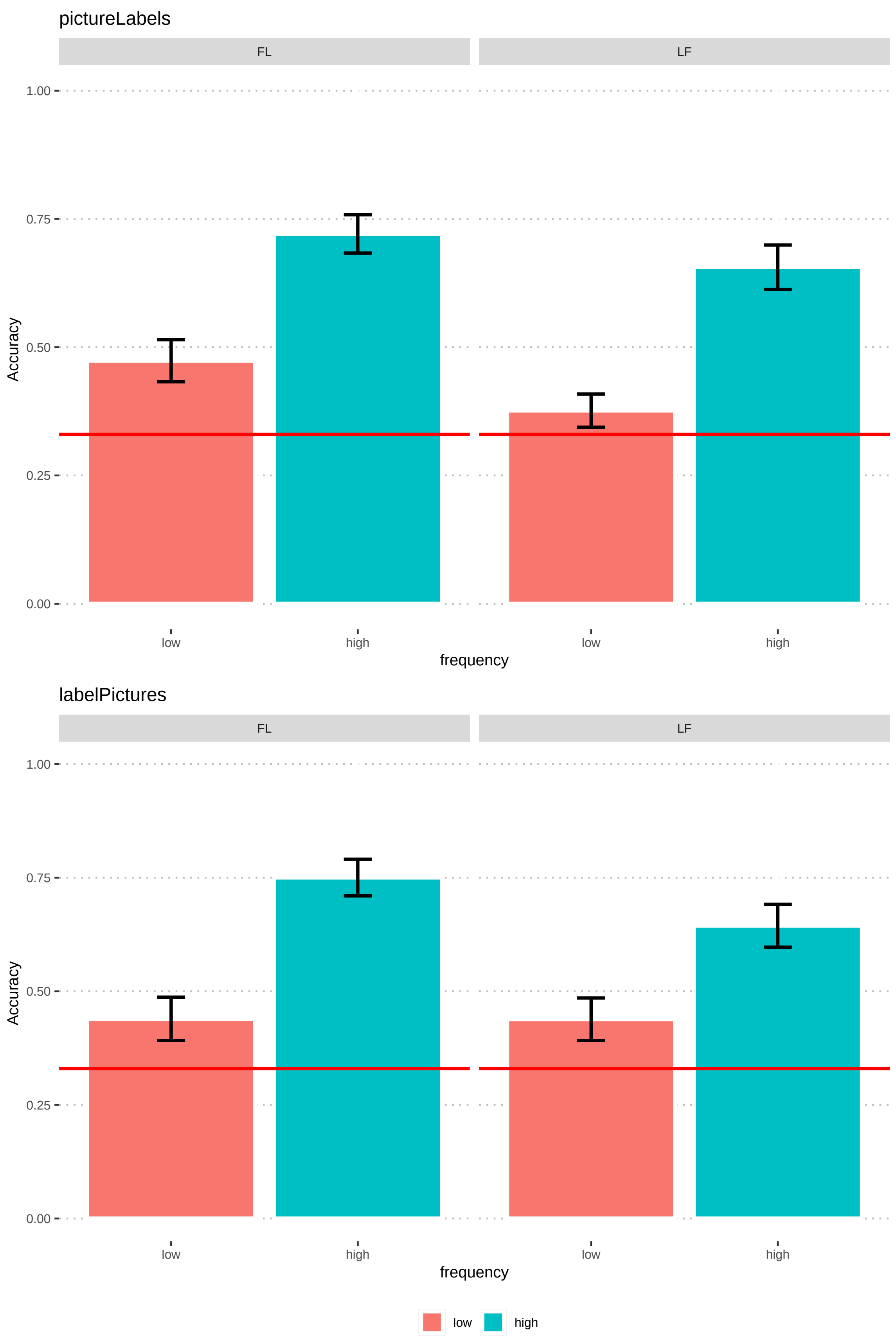
```r


rbind(lowFreqFL, highFreqFL, lowFreqLF, highFreqLF)-> labelPicture_respType
rm(lowFreqFL, highFreqFL, lowFreqLF, highFreqLF)
```

Response type: match, mismatch-type1, mismatch-type2

Comparison by frequency by learning by tasks

Quick summary of what we have so far:

```r
grid.arrange(pl,lp)
```


pictureLabels
FL
LF
Accuracy
1.00
0.75
0.50
0.25
0.00
low
high
low
high
frequency
labelPictures
FL
LF
Accuracy
1.00
0.75
0.50
0.25
0.00
low
high
low
high
frequency
low
high

What's going on in the low frequency condition? One way to see whether they simply learned another association is to check that wrong choices are distributed equally (50%) to the other two categories. If they are, then they didn't learn anything, but if they are not distributed equally, they have learned another association.

Label picture:

```
#select only inaccurate trials
temp <- labelPicture[labelPicture$acc==0,]

round(nrow(temp)/nrow(labelPicture)*100,2)
```

```
## [1] 46.07
```

How many of those are low frequency trials?

```
round(nrow(temp[temp$frequency==25,])/nrow(labelPicture)*100,2)
```

```
## [1] 29.5
```

How many of those are low frequency trials and how are they distributed across learnings?

```
round(nrow(temp[temp$frequency==25 & temp$learning=="FL",])/nrow(labelPicture)*100,2)
```

```
## [1] 15.79
```

```
round(nrow(temp[temp$frequency==25 & temp$learning=="LF",])/nrow(labelPicture)*100,2)
```

```
## [1] 13.71
```

FL people make more errors in the low freq condition

How many of those are high frequency trials and how are they distributed across learnings?

```
round(nrow(temp[temp$frequency==75 & temp$learning=="FL",])/nrow(labelPicture)*100,2)
```

```
## [1] 7.19
```

```
round(nrow(temp[temp$frequency==75 & temp$learning=="LF",])/nrow(labelPicture)*100,2)
```

```
## [1] 9.39
```

While they are pretty much the same in the high frequency

Label picture task:

correct choice is listed in "label", that is, label presented. Participant's choice is listed in "category", that is, the fribble's category.

```
temp %>%
  filter(frequency=="25") %>%
  group_by(learning, label, category) %>%
  count()
```

```
## # A tibble: 12 x 4
## # Groups:   learning, label, category [12]
##    learning label category     n
##    <fct>    <fct>    <int> <int>
##  1 FL       bim          1    36
##  2 FL       bim          3    92
##  3 FL       dep          2   107
##  4 FL       dep          3    43
##  5 FL       tob          1   107
##  6 FL       tob          2    39
##  7 LF       bim          1    22
##  8 LF       bim          3   100
##  9 LF       dep          2    74
## 10 LF       dep          3    44
## 11 LF       tob          1    78
## 12 LF       tob          2    50
```

Nope, they definitely learned another association. The association they have learned is based on the high saliency feature, rather than on the low saliency one. Let's see if that is the case also for the other task:

Picture label task:

```
#select only inaccurate trials
temp <- pictureLabel[pictureLabel$acc==0,]

round(nrow(temp)/nrow(pictureLabel)*100,2)
```

```
## [1] 46.26
```

How many of those are low frequency trials?

```
round(nrow(temp[temp$frequency==25,])/nrow(pictureLabel)*100,2)
```

```
## [1] 29.93
```

How many of those are low frequency trials and how are they distributed across learnings?

```
round(nrow(temp[temp$frequency==25 & temp$learning=="FL",])/nrow(pictureLabel)*100,2)
```

```
## [1] 15.44
```

```
round(nrow(temp[temp$frequency==25 & temp$learning=="LF",])/nrow(pictureLabel)*100,2)
```

```
## [1] 14.48
```

How many of those are high frequency trials and how are they distributed across learnings?

```r
round(nrow(temp[temp$frequency==75 & temp$learning=="FL",])/nrow(pictureLabel)*100,2)
```

```
## [1] 7.93
```

```r
round(nrow(temp[temp$frequency==75 & temp$learning=="LF",])/nrow(pictureLabel)*100,2)
```

```
## [1] 8.41
```

Picture label task:

correct choice is listed in "category", that is, the category of the fribble presented. Participant's choice is listed in "resp" column, that is, the label chosen.

```r
temp %>%
  filter(frequency=="25") %>%
  group_by(learning, category, resp) %>%
  count()
```

```
## # A tibble: 12 x 4
## # Groups:   learning, category, resp [12]
##    learning category resp      n
##    <fct>       <int> <fct> <int>
##  1 FL              1 bim      44
##  2 FL              1 tob     110
##  3 FL              2 dep      78
##  4 FL              2 tob      60
##  5 FL              3 bim      83
##  6 FL              3 dep      42
##  7 LF              1 bim      53
##  8 LF              1 tob      93
##  9 LF              2 dep      61
## 10 LF              2 tob      55
## 11 LF              3 bim      91
## 12 LF              3 dep      38
```

In both tasks participants were driven by the high salient feature in making errors, they simply learned only one association between the label and the high salient feature, and made decisions based on this.

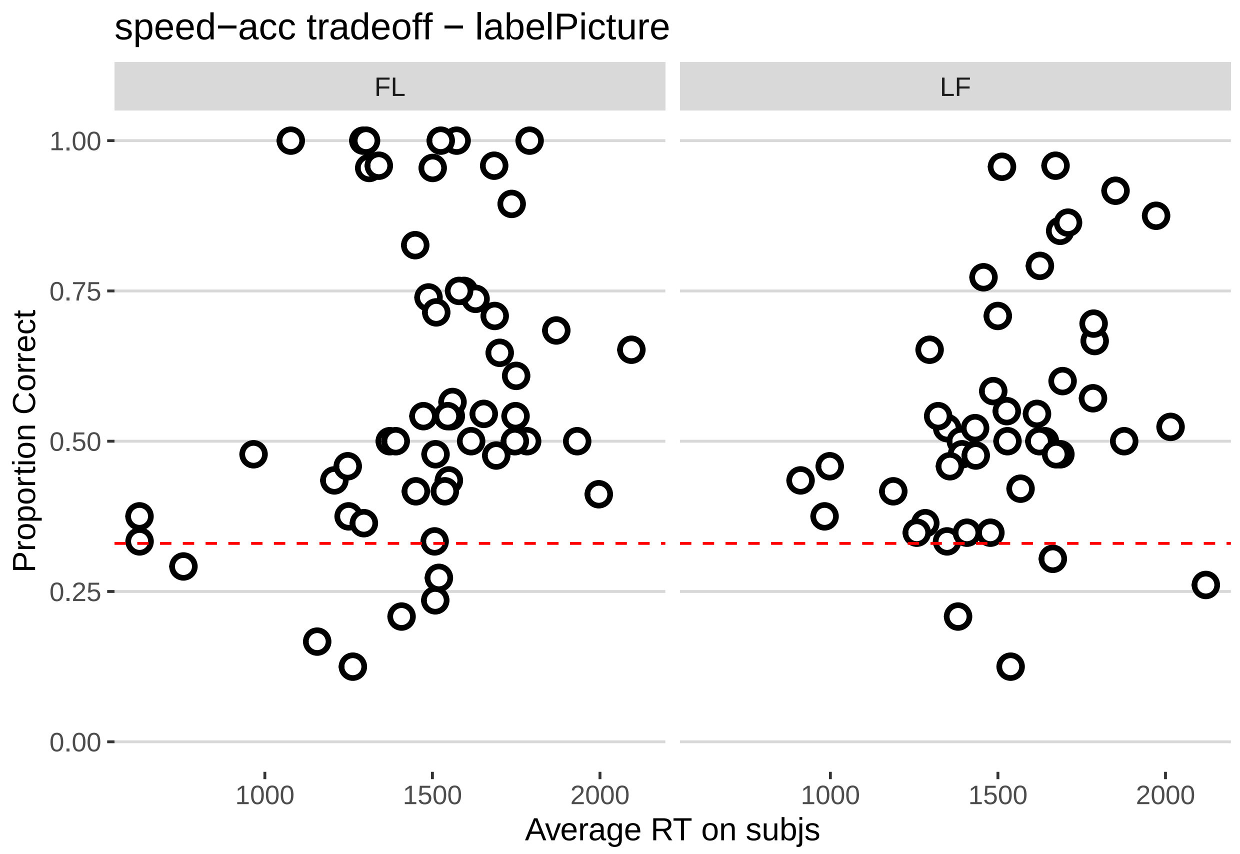
Speed-accuracy trade-off by tasks

Inspection of the speed-accuracy trade-off:

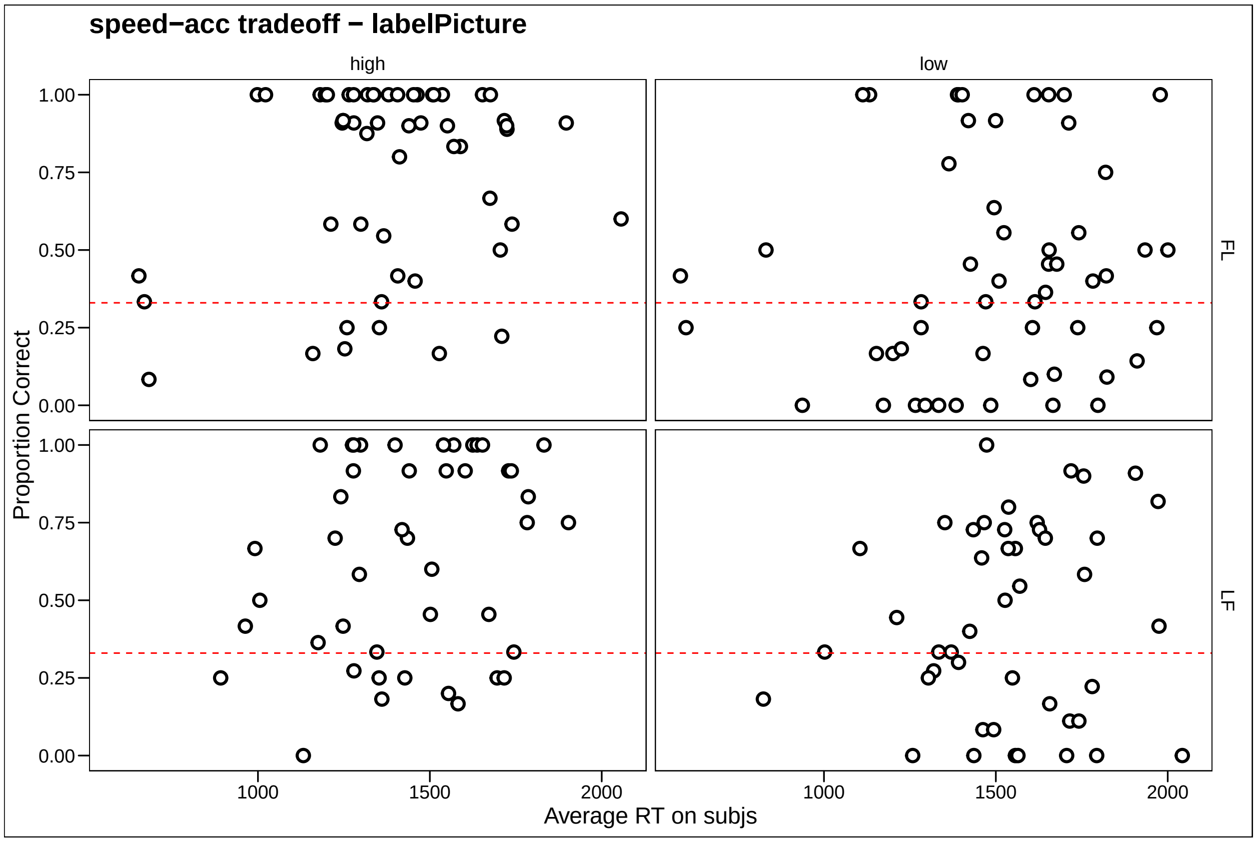
Label Picture

```r
aggregate(acc ~ subjID+learning, labelPicture[labelPicture$rt > 100 &
                                        !(labelPicture$subjID %in% badsubjs) ,], mean)-> speedacc

aggregate(rt ~ subjID+learning, labelPicture[labelPicture$rt > 100 &
                                        !(labelPicture$subjID %in% badsubjs),], mean)-> speedacc2
merge(speedacc, speedacc2, by =  c("subjID", "learning"))-> speedacc
```

```
ggplot(aes(x=rt, y=acc),
           data = speedacc) +
  facet_grid( . ~ learning) +
  geom_point( shape = 21, fill = "white", size = 3, stroke = 1.5) +
  #geom_smooth(method = "lm", formula = y ~ poly(x,2), se = TRUE, color = "#0892d0", fill = "lightgray"
  geom_hline(yintercept = 0.33, lty = "dashed", color = 'red') +
  coord_cartesian(ylim = c(0, 1))+
  ggthemes::theme_hc()+
  xlab("Average RT on subjs") +
  ylab("Proportion Correct") +
  ggtitle("speed-acc tradeoff - labelPicture")
```



```
aggregate(acc ~ subjID+learning+frequency, labelPicture[labelPicture$rt > 100 &
                                                         labelPicture$rt <= 2500 &
                                               !(labelPicture$subjID %in% badsubjs) ,], mean)-> speedacc

aggregate(rt ~ subjID+learning+frequency, labelPicture[labelPicture$rt > 100 &
                                                        labelPicture$rt <= 2500 &
                                               !(labelPicture$subjID %in% badsubjs),], mean)-> speedacc2
merge(speedacc, speedacc2, by =  c("subjID", "learning", "frequency"))-> speedacc
rm(speedacc2)
dplyr::recode(speedacc$frequency, "25"="low", "75"="high")-> speedacc$frequency;

ggplot(aes(x=rt, y=acc),
           data = speedacc) +
  facet_grid( learning ~ frequency) +
  geom_point( shape = 21, fill = "white", size = 3, stroke = 1.5) +
  #geom_smooth(method = "lm", formula = y ~ poly(x,2), se = TRUE, color = "#0892d0", fill = "lightgray"
  geom_hline(yintercept = 0.33, lty = "dashed", color = 'red') +
  coord_cartesian(ylim = c(0, 1))+
  ggthemes::theme_base()+
  xlab("Average RT on subjs") +
  ylab("Proportion Correct") +
  ggtitle("speed-acc tradeoff - labelPicture")
```

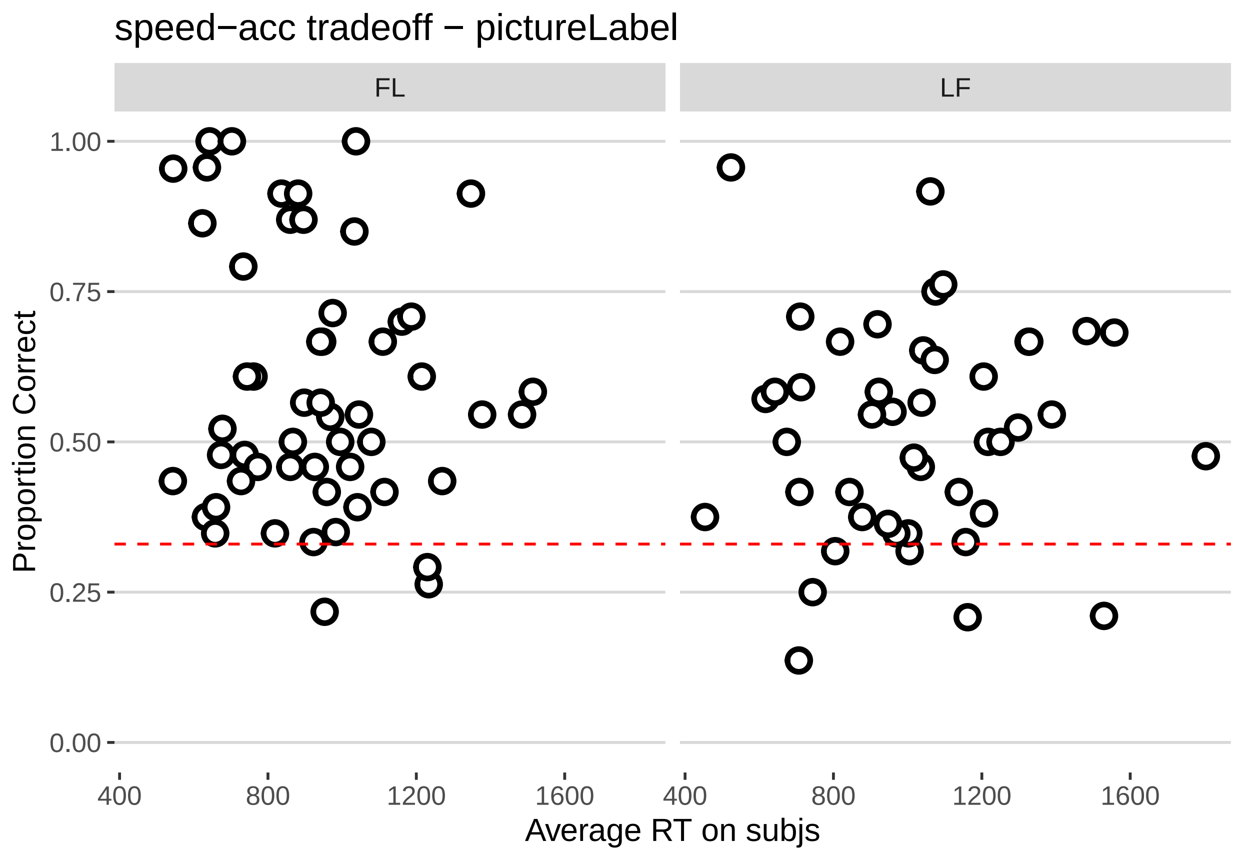


```
speedacc %>%
  group_by(frequency, learning) %>%
  summarise(mean(rt), median(rt))
```

```
## # A tibble: 4 x 4
## # Groups:   frequency [2]
##   frequency learning `mean(rt)` `median(rt)`
##   <chr>     <fct>         <dbl>        <dbl>
## 1 high      FL            1390.        1373.
## 2 high      LF            1441.        1435.
## 3 low       FL            1489.        1504.
## 4 low       LF            1539.        1537.
```

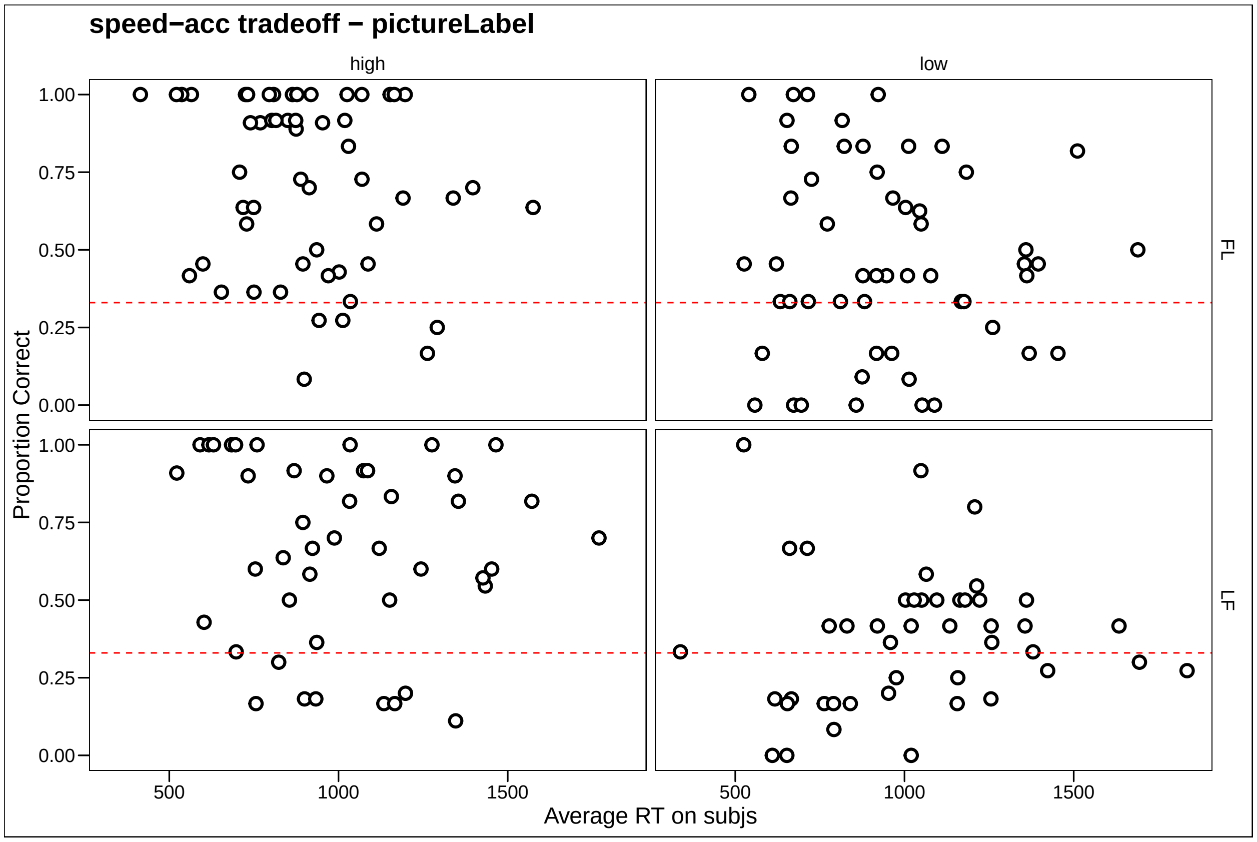
PictureLabel

```r
aggregate(acc ~ subjID+learning, pictureLabel[pictureLabel$rt > 100  &
                                        !(pictureLabel$subjID %in% badsubjs),], mean)-> speedacc

aggregate(rt ~ subjID+learning, pictureLabel[pictureLabel$rt > 100  &
                                        !(pictureLabel$subjID %in% badsubjs),], mean)-> speedacc2
merge(speedacc, speedacc2, by =  c("subjID", "learning"))-> speedacc

ggplot(aes(x=rt, y=acc),
           data = speedacc) +
  facet_grid( . ~ learning) +
  geom_point( shape = 21, fill = "white", size = 3, stroke = 1.5) +
  #geom_smooth(method = "lm", formula = y ~ poly(x,2), se = TRUE, color = "#0892d0", fill = "lightgray"
  geom_hline(yintercept = 0.33, lty = "dashed", color = 'red') +
  coord_cartesian(ylim = c(0, 1))+
  ggthemes::theme_hc()+
  xlab("Average RT on subjs") +
  ylab("Proportion Correct") +
  ggtitle("speed-acc tradeoff - pictureLabel")
```



```r
aggregate(acc ~ subjID+learning+frequency, pictureLabel[pictureLabel$rt > 100  &
                                        !(pictureLabel$subjID %in% badsubjs),], mean)-> speedacc
aggregate(rt ~ subjID+learning+frequency, pictureLabel[pictureLabel$rt > 100  &
                                        !(pictureLabel$subjID %in% badsubjs),], mean)-> speedacc2
merge(speedacc, speedacc2, by =  c("subjID", "learning", "frequency"))-> speedacc
rm(speedacc2)
```

```
dplyr::recode(speedacc$frequency, "25"="low", "75"="high")-> speedacc$frequency;

ggplot(aes(x=rt, y=acc),
           data = speedacc) +
  facet_grid( learning ~ frequency) +
  geom_point( shape = 21, fill = "white", size = 3, stroke = 1.5) +
  #geom_smooth(method = "lm", formula = y ~ poly(x,2), se = TRUE, color = "#0892d0", fill = "lightgray"
  geom_hline(yintercept = 0.33, lty = "dashed", color = 'red') +
  coord_cartesian(ylim = c(0, 1))+
  ggthemes::theme_base()+
  xlab("Average RT on subjs") +
  ylab("Proportion Correct") +
  ggtitle("speed-acc tradeoff - pictureLabel")
```



```
speedacc %>%
  group_by(frequency, learning) %>%
  summarise(mean(rt), median(rt))
```

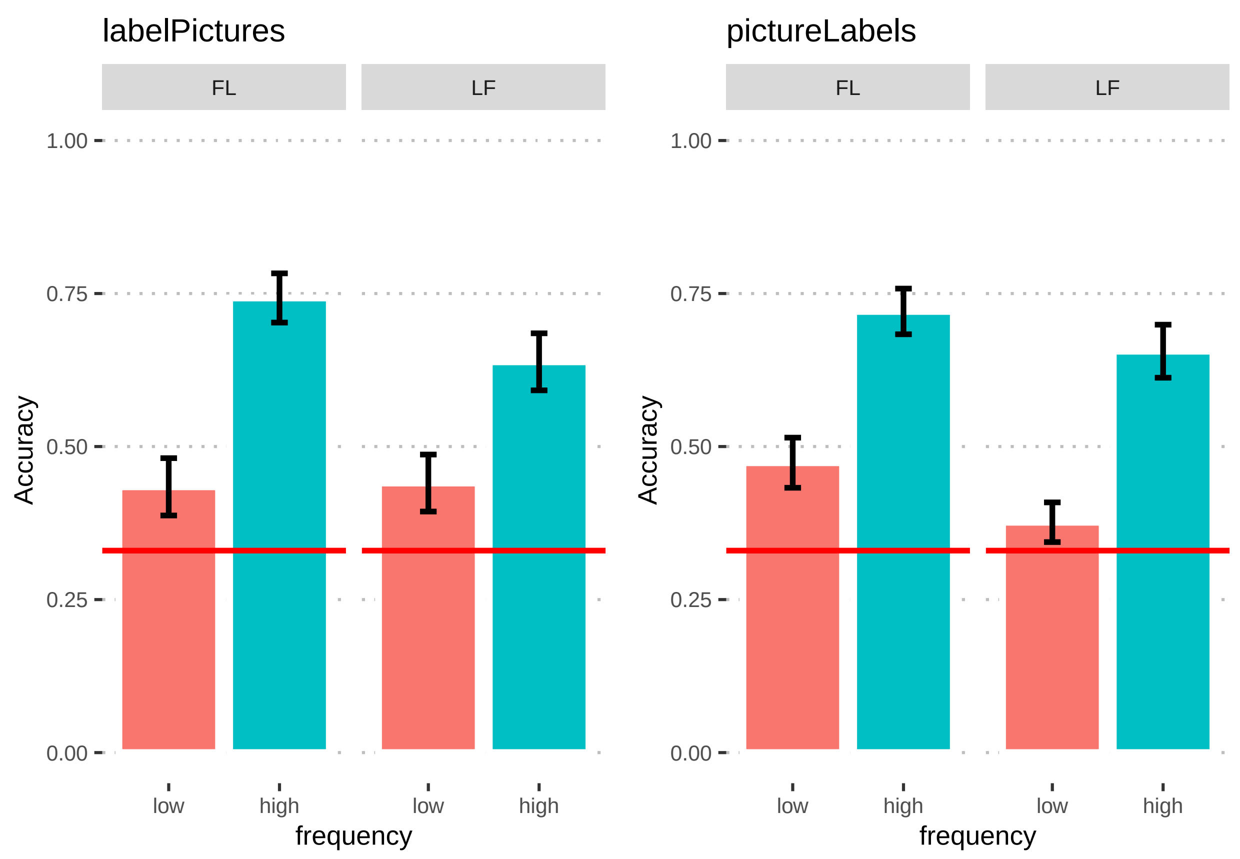
```
## # A tibble: 4 x 4
## # Groups:   frequency [2]
##   frequency learning `mean(rt)` `median(rt)`
##   <chr>     <fct>         <dbl>        <dbl>
## 1 high      FL             911.         892.
## 2 high      LF            1016.         966.
## 3 low       FL              948.         918.
## 4 low       LF             1028.        1029.
```

Final Comparisons

Barplot labelPicture

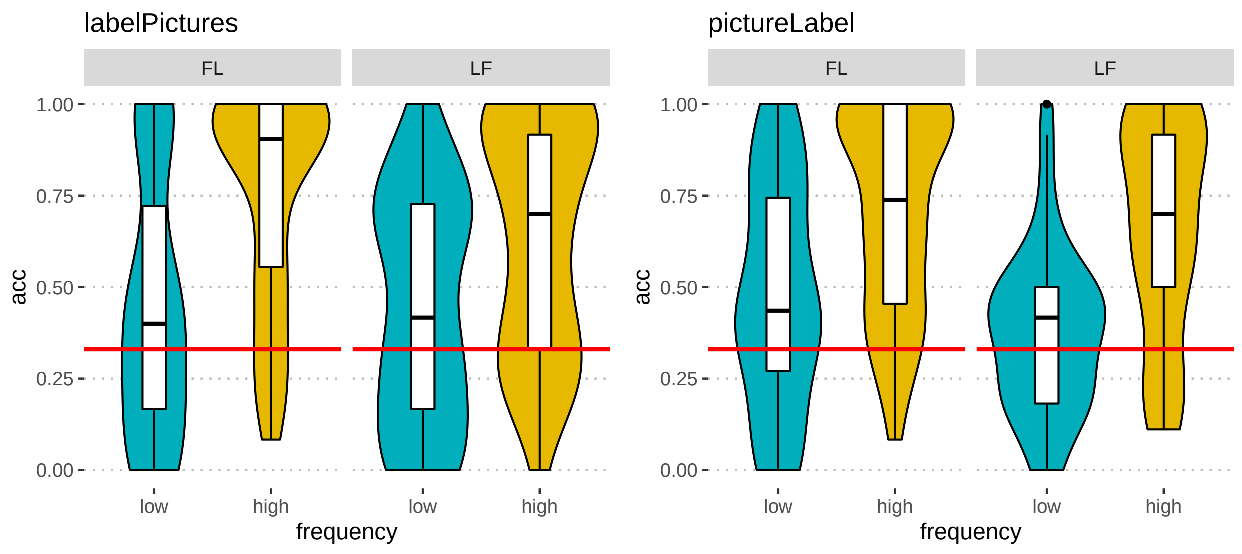
```
ms <- aggregate(acc ~ subjID+frequency+learning,
                data=labelPicture[labelPicture$rt > 100  &
                                                 !(labelPicture$subjID %in% badsubjs),], FUN= mean)

df<- ms %>%
  group_by(frequency, learning)%>%
  summarise(
    mean = mean(acc),
    sd = sd(acc),
    n = n()) %>%
  mutate( se=sd/sqrt(n))  %>%
  mutate( ci=se * qt((1-0.05)/2 + .5, n-1))

df$frequency <- as.factor(df$frequency)
plyr::revalue(df$frequency, c("25"="low"))-> df$frequency;
plyr::revalue(df$frequency, c("75"="high"))-> df$frequency;


lp<-ggplot(aes(x = frequency, y = mean, fill = frequency), data = df) +
  facet_grid( . ~ learning) +
  geom_bar(stat = "identity", color='white', position=position_dodge(), size=1.2) +
  geom_errorbar(aes(ymin=mean-se, ymax=mean+se), width=.15, size=1,position=position_dodge(.9)) +
  ylab("Accuracy ") +
  xlab("frequency") +
  ggtitle("labelPictures") +
  coord_cartesian(ylim = c(0, 1))+
  ggpubr::theme_pubclean() +
  theme(legend.position = "none")  +
  theme(text = element_text(size=10)) +
  geom_hline(yintercept = .33, col='red', lwd=1);
```

```
grid.arrange(lp, pl, ncol=2)
```



```
ms <- aggregate(acc ~ subjID+frequency+learning,
                data=labelPicture[labelPicture$rt > 100  &
                                    labelPicture$rt <=2500 &
                                      !(labelPicture$subjID %in% badsubjs),], FUN= mean)

ms$frequency <- as.factor(ms$frequency)
plyr::revalue(ms$frequency, c("25"="low"))-> ms$frequency;
plyr::revalue(ms$frequency, c("75"="high"))-> ms$frequency;

lp_violin<- ggviolin(ms, x = "frequency", y = "acc", fill = "frequency",
         palette = c("#00AFBB", "#E7B800"),
         add = "boxplot",
         add.params = list(fill = "white"),
         trim=TRUE) +
         ggtitle('labelPictures') +
        facet_grid( . ~ learning) +
        theme_pubclean()+
  theme(legend.position = "none") +
  geom_hline(yintercept = .33, col='red', lwd=1);


ms <- aggregate(acc ~ subjID+frequency+learning,
                data=pictureLabel[pictureLabel$rt > 100  &
                                      !(pictureLabel$subjID %in% badsubjs),], FUN= mean)

ms$frequency <- as.factor(ms$frequency)
```

```
plyr::revalue(ms$frequency, c("25"="low"))-> ms$frequency;
plyr::revalue(ms$frequency, c("75"="high"))-> ms$frequency;

pl_violin<- ggviolin(ms, x = "frequency", y = "acc", fill = "frequency",
         palette = c("#00AFBB", "#E7B800"),
         add = "boxplot",
         add.params = list(fill = "white"),
         trim=TRUE) +
         ggtitle('pictureLabel') +
        facet_grid( . ~ learning) +
        theme_pubclean()+
  theme(legend.position = "none") +
  geom_hline(yintercept = .33, col='red', lwd=1);

grid.arrange(lp_violin, pl_violin, ncol=2)
```

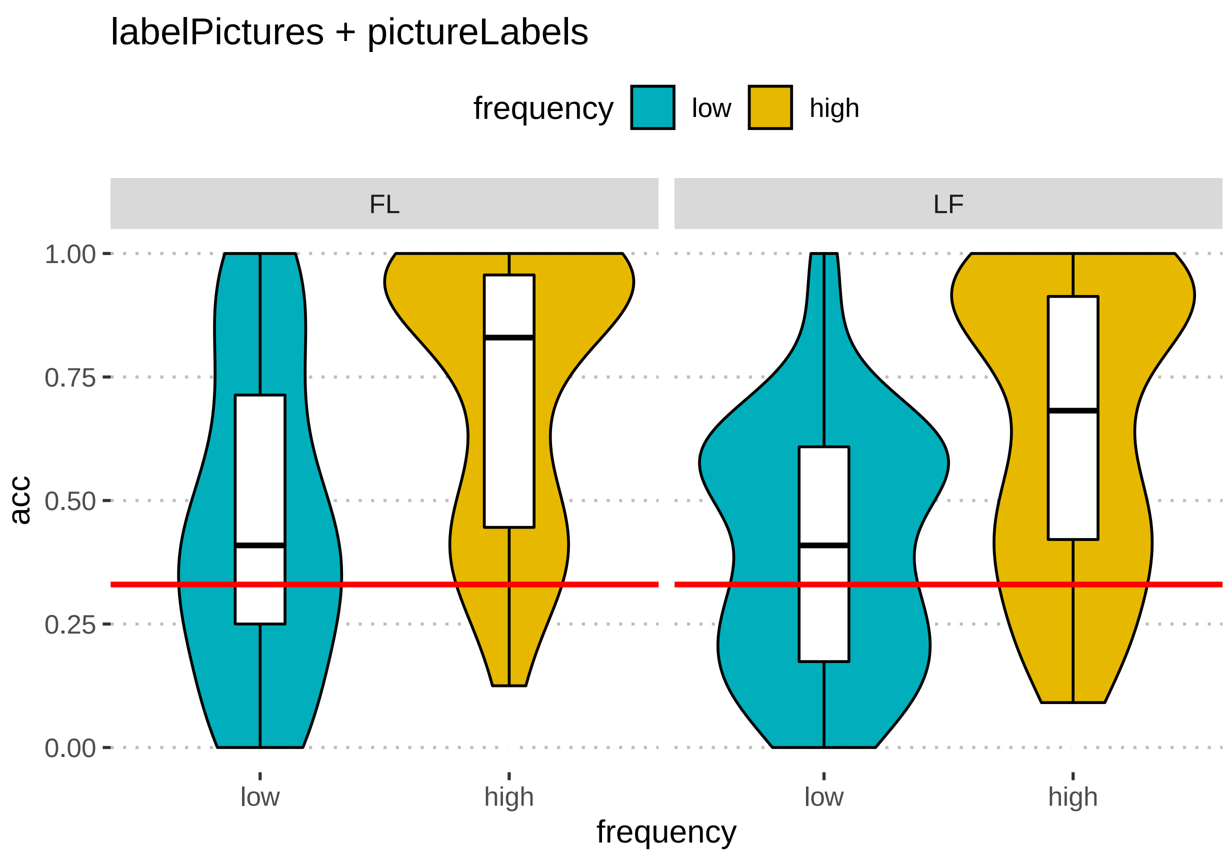


```
#rm(ms, ss_prop)
```

Barplots + violinPlots with data from both tasks:

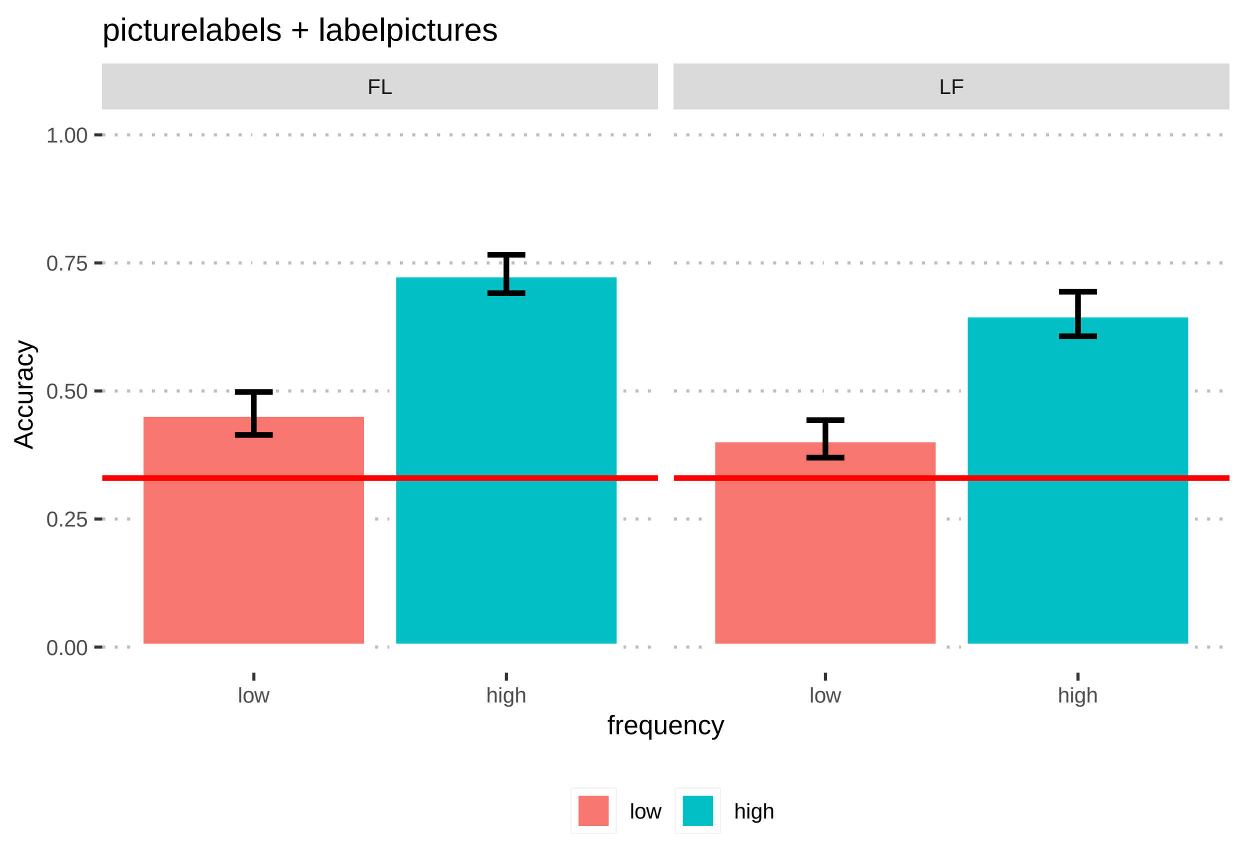
```
rm(ms, df, ss_prop)
genTask <- rbind(labelPicture, pictureLabel)
```

```
ms <- aggregate(acc ~ subjID+frequency+learning, data = genTask[genTask$rt>100 &
                                         !(genTask$subjID %in% badsubjs),], mean)

ms$frequency <- as.factor(ms$frequency)
plyr::revalue(ms$frequency, c("25"="low"))-> ms$frequency;
plyr::revalue(ms$frequency, c("75"="high"))-> ms$frequency;

ggviolin(ms, x = "frequency", y = "acc", fill = "frequency",
         palette = c("#00AFBB", "#E7B800"),
         add = "boxplot",
         add.params = list(fill = "white"),
         trim=TRUE) +
       ggtitle('labelPictures + pictureLabels') +
       facet_grid( . ~ learning) +
       theme_pubclean()+
  geom_hline(yintercept = .33, col='red', lwd=1);
```



```
ms <- aggregate(acc ~ subjID+frequency+learning, data=genTask[genTask$rt>100 &
                                          !(genTask$subjID %in% badsubjs),], FUN= mean)

df<- ms %>%
  group_by(frequency, learning)%>%
  summarise(
    mean = mean(acc),
    sd = sd(acc),
    n = n()) %>%
  mutate( se=sd/sqrt(n))  %>%
  mutate( ci=se * qt((1-0.05)/2 + .5, n-1))

df$frequency <- as.factor(df$frequency)
plyr::revalue(df$frequency, c("25"="low"))-> df$frequency;
plyr::revalue(df$frequency, c("75"="high"))-> df$frequency;
```

```r
ggplot(aes(x = frequency, y = mean, fill = frequency), data = df) +
  facet_grid( . ~ learning) +
  geom_bar(stat = "identity", color='white', position=position_dodge(), size=1.2) +
  geom_errorbar(aes(ymin=mean-se, ymax=mean+se), width=.15, size=1,position=position_dodge(.9)) +
  ylab("Accuracy ") +
  xlab("frequency") +
  ggtitle("labelPicture") +
  ggtitle('picturelabels + labelpictures') +
  coord_cartesian(ylim = c(0, 1))+
  ggpubr::theme_pubclean() +
  theme(legend.position="bottom", legend.title = element_blank()) +
  theme(text = element_text(size=10)) +
  geom_hline(yintercept = .33, col='red', lwd=1);
```



Task 3: Contingency judgement

```r
length(unique(contingencyJudgement$subjID))
```

```
## [1] 120
```

```r
fl<- length(unique(contingencyJudgement[contingencyJudgement$learning=='FL' ,]$subjID))

lf<- length(unique(contingencyJudgement[contingencyJudgement$learning=='LF' ,]$subjID))

fl
```

```
## [1] 63
```

```r
lf
```

```
## [1] 57
```

We have 63 for feature-label learning, and 57 for label-feature learning.

```r
rm(fl,lf)
conjudge <- contingencyJudgement[!(is.na(contingencyJudgement$resp)),]
n<- length(unique(conjudge$subjID))
nrows <- (nrow(contingencyJudgement)) - (nrow(conjudge))

sort(unique(conjudge$subjID))-> subjs;
sort(unique(contingencyJudgement$subjID)) ->totsubjs;

subjmissed<- setdiff(totsubjs, subjs);

badsubjs <- c(badsubjs, subjmissed)
badsubjs <- unique(badsubjs)

(nrow(contingencyJudgement[contingencyJudgement$learning=='LF',])) - (nrow(conjudge[conjudge$learning==
```

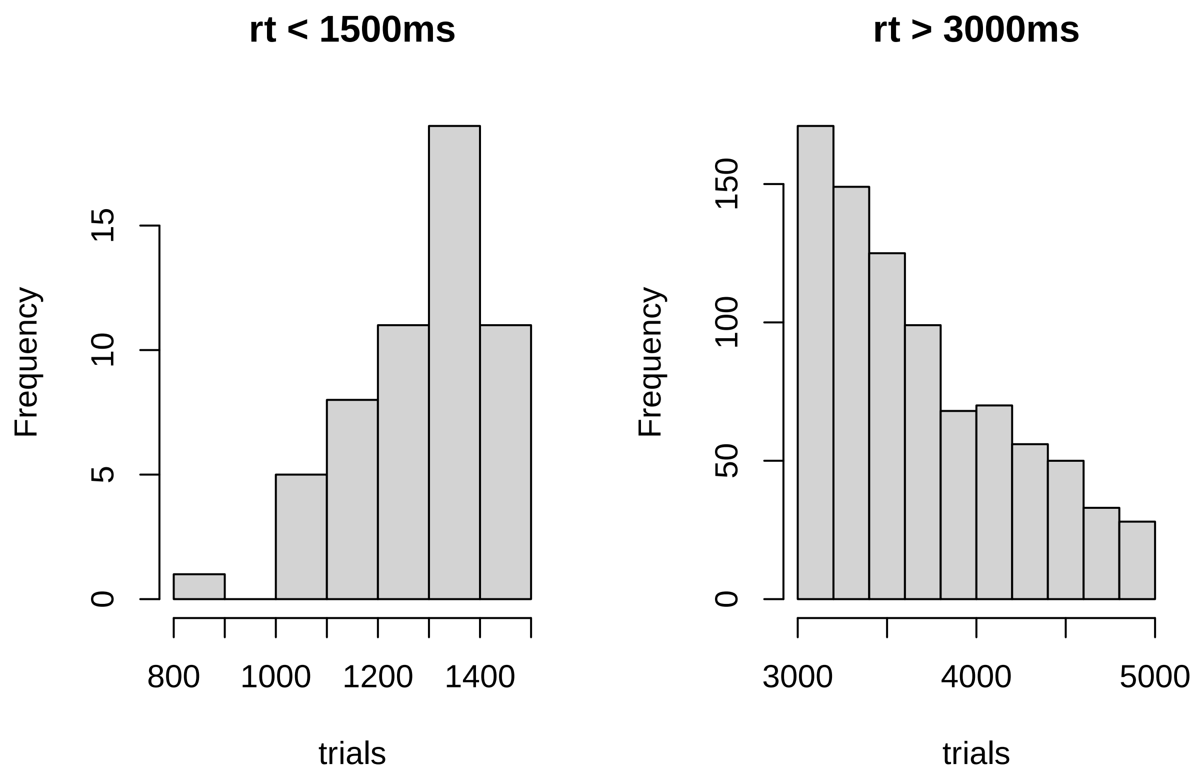
```
## [1] 301
```

We have 111 participants in this task, so -9, and we have missed 559 over the total 2880, that is 19.41%. The subject(s) that missed completely the task is/are: 1414932, 1420171, 1420199, 1422475, 1431960, 1431997, 1459020, 1459057, 1459078.

Distribution of the missing data across condition:

- LF learning, 22.003%
  - LF learning, Low freq: 23.392%
  - LF learning, High freq: 20.614%
- FL learning, 17.063%
  - FL learning, Low freq: 19.18%
  - FL learning, High freq: 14.947%

```r
par(mfrow=c(1,2))
hist(conjudge[conjudge$rt<1500 & !(conjudge$subjID %in% badsubjs),]$rt, main = 'rt < 1500ms', xlab = 't
hist(conjudge[conjudge$rt>3000 & !(conjudge$subjID %in% badsubjs),]$rt, main = 'rt > 3000ms', xlab = 't
```

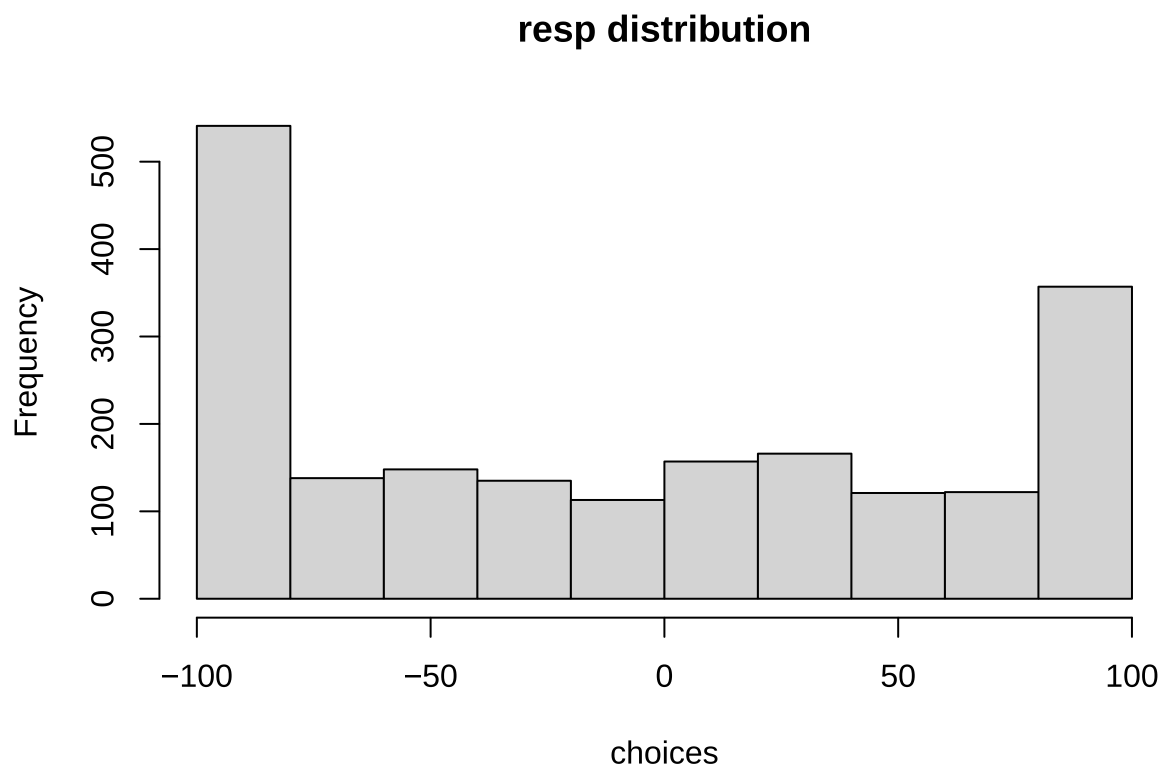


```
par(mfrow=c(1,1))
```

Resp is coded as factor, need to correct this:

```
as.numeric(levels(conjudge$resp))[conjudge$resp]-> conjudge$resp
```

```
hist(conjudge[!(conjudge$subjID %in% badsubjs),]$resp, main = 'resp distribution', xlab = 'choices')
```



Ok, here we don't have right or wrong answers, but we are more interested in take a look how the participants rated the fribble label association:

```
aggregate(resp ~ category, data = conjudge[!(conjudge$subjID %in% badsubjs),], FUN = mean)
```

```
##   category       resp
## 1        1 -12.119084
## 2        2  -6.564636
## 3        3 -10.635821
```

Okay, in this task one fribble was presented along with a label. The association between the fribble presented and the label could have been correct, or wrong. In this case then accuracy column does **not** refer to the participants' accuracy, but rather to the fribble-label pair presented. This should be therefore necessarily equal to the chance level, i.e, around 33%, of course this number is dependent by the number of datapoints left without no-responses because we filtered out those.

```
conjudge$acc <- 0;
conjudge[conjudge$category==1 & conjudge$label=='dep',]$acc <- 1;
conjudge[conjudge$category==2 & conjudge$label=='bim',]$acc <- 1;
conjudge[conjudge$category==3 & conjudge$label=='tob',]$acc <- 1;
```

```
mean(conjudge[!(conjudge$subjID %in% badsubjs),]$acc)
```

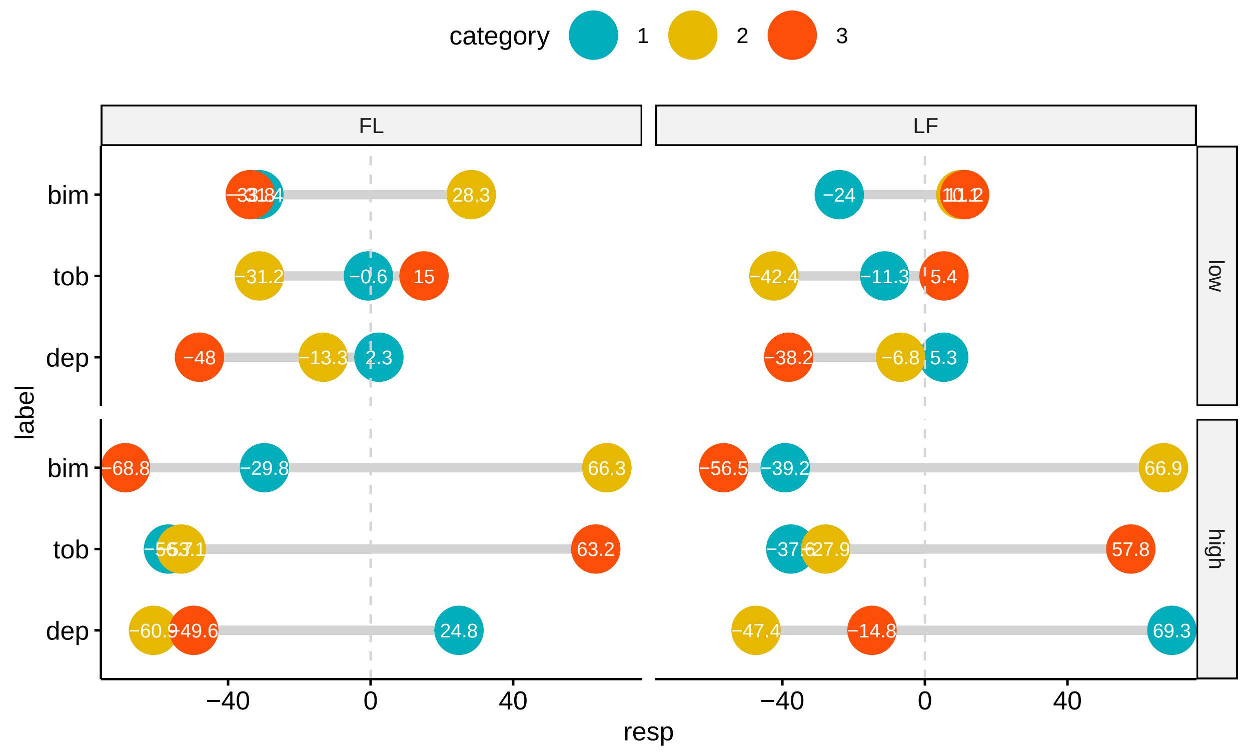
```
## [1] 0.3523524
```

Quite there, everything good.

plot mean responses

```
respDistr<- aggregate(resp ~ learning + frequency + category + label, data = conjudge[!(conjudge$subjID
```

```
plyr::revalue(as.factor(respDistr$frequency), c("25"="low"))-> respDistr$frequency;
plyr::revalue(as.factor(respDistr$frequency), c("75"="high"))-> respDistr$frequency;
respDistr$category <- as.factor(respDistr$category)

lollipop<-ggdotchart(respDistr, x = "label", y = "resp",
           color = "category",                                # Color by groups
           palette = c("#00AFBB", "#E7B800", "#FC4E07"), # Custom color palette
           add = "segments",                             # Add segments from y = 0 to dots
           rotate = T,
           add.params = list(color = "lightgray", size = 2), # Change segment color and size
           group = "category",                                # Order by groups
           dot.size = 10,                                 # Large dot size
           label = round(respDistr$resp,1),                        # Add mpg values as dot labels
           font.label = list(color = "white", size = 9,
                             vjust = 0.5),               # Adjust label parameters
           ggtheme = theme_pubr()                        # ggplot2 theme
           )+ facet_grid( frequency ~ learning) +
  geom_hline(yintercept = 0, linetype = 2, color = "lightgray")

lollipop
```



Plot to compare with RW weights:

```r
plyr::revalue(as.factor(conjudge$frequency), c("25"="low"))-> conjudge$frequency;
plyr::revalue(as.factor(conjudge$frequency), c("75"="high"))-> conjudge$frequency;
```

For each learning condition, look at their average score for each of the 6 combinations of frequency and type:

High frequency:

```r
highFreqFL<-data.frame(
           learning = rep("FL",9),
           frequency = rep("high",9),
           type = c(rep("match",3),
                    rep("mismatch-type1",3),
                    rep("mismatch-type2",3)),
           label = c("dep_cat1", "bim_cat2", "tob_cat3"),
           fribble = c(1.1,2.1,3.1,
                       3.1,1.1,2.1,
                       2.1,3.1,1.1),
           fribbleCategory = c("cat1", "cat2", "cat3", #match
                                "cat3", "cat1", "cat2", #mis-type1
                                "cat2", "cat3", "cat1")) #mis-type2

highFreqLF<-data.frame(
           learning = rep("LF",9),
           frequency = rep("high",9),
           type = c(rep("match",3),
                    rep("mismatch-type1",3),
                    rep("mismatch-type2",3)),
           label = c("dep_cat1", "bim_cat2", "tob_cat3"),
           fribble = c(1.1,2.1,3.1,
                       3.1,1.1,2.1,
                       2.1,3.1,1.1),
           fribbleCategory = c("cat1", "cat2", "cat3", #match
                                "cat3", "cat1", "cat2", #mis-type1
                                "cat2", "cat3", "cat1")) #mis-type2

rbind(highFreqFL, highFreqLF)-> highFreq
rm(highFreqFL, highFreqLF)
```

Low frequency:

```r
lowFreqFL<-data.frame(
           learning = rep("FL",9),
           frequency = rep("low",9),
           type = c(rep("match",3),
                    rep("mismatch-type1",3),
                    rep("mismatch-type2",3)),
           label = c("dep_cat1", "bim_cat2", "tob_cat3"),
           fribble = c(1.2,2.2,3.2,
                       2.2,3.2,1.2,
                       3.2,1.2,2.2),
           fribbleCategory = c("cat1", "cat2", "cat3", #match
                                       "cat2", "cat3", "cat1", #mis-type1
                                       "cat3", "cat1", "cat2")) #mis-type2
```

```
lowFreqLF<-data.frame(
           learning = rep("LF",9),
           frequency = rep("low",9),
           type = c(rep("match",3),
                    rep("mismatch-type1",3),
                    rep("mismatch-type2",3)),
           label = c("dep_cat1", "bim_cat2", "tob_cat3"),
           fribble = c(1.2,2.2,3.2,
                       2.2,3.2,1.2,
                       3.2,1.2,2.2),
           fribbleCategory = c("cat1", "cat2", "cat3", #match
                               "cat2", "cat3", "cat1", #mis-type1
                               "cat3", "cat1", "cat2")) #mis-type2
lowFreq<- rbind(lowFreqFL, lowFreqLF)
rm(lowFreqFL, lowFreqLF)
```

```
rbind(highFreq, lowFreq)-> humansWeights
humansWeights$learning <- as.factor(humansWeights$learning); humansWeights$frequency <- as.factor(humans
rm(highFreq, lowFreq)
summary(humansWeights)
```

```
##  learning frequency             type         label       fribble
##  FL:18    high:18   match         :12   bim_cat2:12   Min.   :1.10
##  LF:18    low :18   mismatch-type1:12   dep_cat1:12   1st Qu.:1.20
##                     mismatch-type2:12   tob_cat3:12   Median :2.15
##                                                       Mean   :2.15
##                                                       3rd Qu.:3.10
##                                                       Max.   :3.20
##  fribbleCategory      resp
##  cat1:12         Min.   :-68.79
##  cat2:12         1st Qu.:-39.98
##  cat3:12         Median :-19.43
##                  Mean   :-11.04
##                  3rd Qu.: 10.34
##                  Max.   : 69.30
```

```
dataWeight <- aggregate(resp ~ learning + frequency + type, data = humansWeights,FUN = mean)
```

Plot of human responses considered as summed weights of the label-feature association.

```
lollipopWeight<-ggdotchart(dataWeight, x = "type", y = "resp",
           #color = "learning",                                    # Color by groups
           palette = c("#00AFBB", "#E7B800", "#FC4E07"), # Custom color palette
           add = "segments",                             # Add segments from y = 0 to dots
           rotate = T,
           add.params = list(color = "lightgray", size = 2), # Change segment color and size
           #group = "learning",                                     # Order by groups
           dot.size = 10,                                 # Large dot size
           label = round(dataWeight$resp,1),                        # Add mpg values as dot labels
           font.label = list(color = "white", size = 9,
                             vjust = 0.5),               # Adjust label parameters
```

```
          ggtheme = theme_pubr(),                         # ggplot2 theme
          title = "human performance",
          ylab = "average response",
          xlab = " "
          )+ facet_grid( learning ~ frequency) +
  geom_hline(yintercept = 0, linetype = 2, color = "lightgray")

lollipopWeight
```

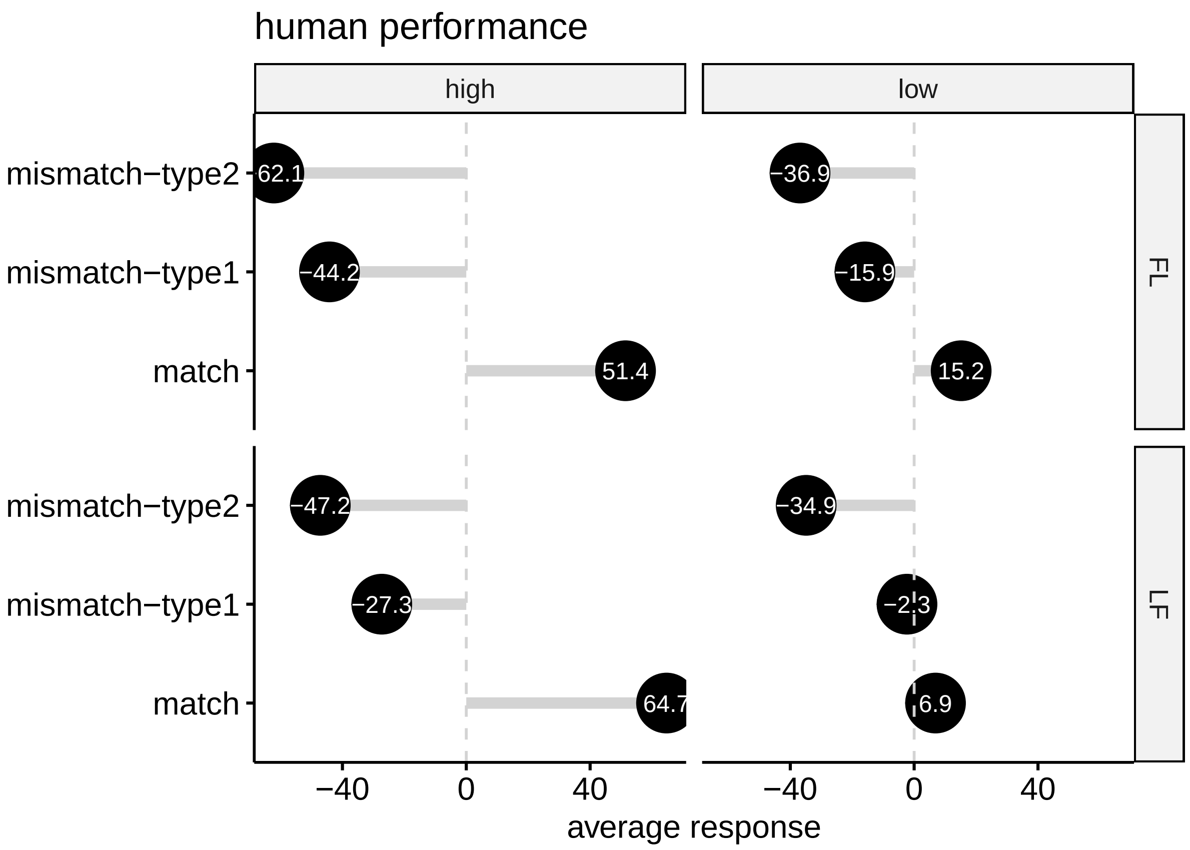


Figure 1: Summed weights of the label-feature association by frequency by learning

```
dataWeight$respZ.score <- as.vector(scale(dataWeight$resp))
head(dataWeight)
```

```
##   learning frequency          type       resp respZ.score
## 1       FL      high         match  51.436170   1.5772919
## 2       LF      high         match  64.678091   1.9115761
## 3       FL       low         match  15.190638   0.6622956
## 4       LF       low         match   6.902998   0.4530793
## 5       FL      high mismatch-type1 -44.191206  -0.8367626
## 6       LF      high mismatch-type1 -27.296453  -0.4102649
```

```
lollipopWeightZ<-ggdotchart(dataWeight, x = "type", y = "respZ.score",
           #color = "learning",                                  # Color by groups
           palette = c("#00AFBB", "#E7B800", "#FC4E07"), # Custom color palette
           add = "segments",                             # Add segments from y = 0 to dots
           rotate = T,
           add.params = list(color = "lightgray", size = 2), # Change segment color and size
           #group = "learning",                                  # Order by groups
           dot.size = 10,                                 # Large dot size
           label = round(dataWeight$respZ.score,1),                        # Add mpg values as dot labe
           font.label = list(color = "white", size = 9,
                             vjust = 0.5),               # Adjust label parameters
           ggtheme = theme_pubr(),                        # ggplot2 theme
           title = "human performance",
           ylab = "average response",
           xlab = " "
           )+ facet_grid( learning ~ frequency) +
  geom_hline(yintercept = 0, linetype = 2, color = "lightgray")

lollipopWeightZ
```

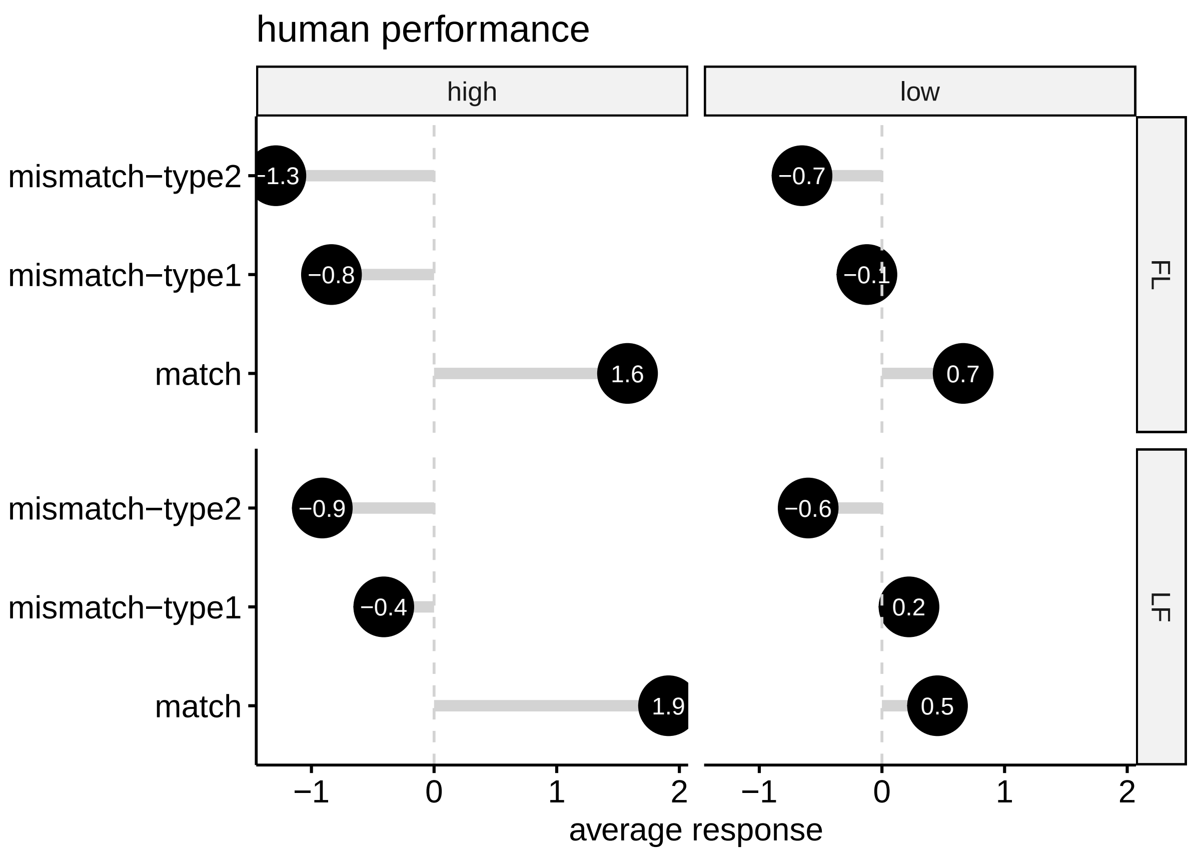


Figure 2: Z-score of the Summed weights of the label-feature association by frequency by learning

What about having the same info by subject instead of the grand average?

```
listSubj <-unique(conjudge[conjudge$learning=="FL" & !(conjudge$subjID %in% badsubjs),]$subjID)
```

For loop across participants for FL learning:

```
rbind(lowFreqFL, highFreqFL)->humansWeights_FL
```

For loop across participants for LF learning:

```
listSubj <-unique(conjudge[conjudge$learning=="LF" & !(conjudge$subjID %in% badsubjs),]$subjID)
```

```
rbind(lowFreqLF, highFreqLF)->humansWeights_LF
rm(lowFreqLF, highFreqLF, lowFreqFL, highFreqFL)
```

```
humansTypeWeigths<-rbind(humansWeights_FL, humansWeights_LF)
rm(humansWeights_FL, humansWeights_LF)
```

RW comparison

How do we compare these measures with the RW?

```
## [1] "FL learning"
## [1] 0.3335453
## [1] 0.2218817
## [1] 0
## [1] 0.4996484
## [1] 0.3879108
## [1] 0
## [1] -0.1660331
## [1] -0.1660419
## [1] 0

## [1] "FL learning"
## [1] 0.3336234
## [1] 0.2219494
## [1] 0
## [1] 0.4996488
## [1] 0.3879235
## [1] 0
## [1] -0.1660696
## [1] -0.1660033
## [1] 0

## [1] "LF learning"
## [1] 0.751511
## [1] 0.2382185
## [1] 0
## [1] 0.7477625
## [1] 0.2315229
## [1] 0
## [1] 0
## [1] 0
## [1] 0
## [1] "LF learning"
## [1] 0.7560272
## [1] 0.2674515
## [1] 0
## [1] 0.7393796
## [1] 0.1950576
## [1] 0
## [1] 0
## [1] 0
## [1] 0
```

In the FLO paper there were 15 high freq exemplars, and 5 low frequency exemplar per category (proportion: 1/3). This is approximated here in this input where for every category/label, there are 3 high freq exemplars and 1 low freq exemplar. Frequency of presentation kept constant: 250.

```
myexp
```

```
##             Cues Outcomes Frequency
## 1    blue_d1_i1      dep       250
## 2    blue_d1_i2      dep       250
## 3    blue_d1_i3      dep       250
## 4     red_d2_j1      dep       250
## 5  purple_d3_k1      bim       250
## 6  purple_d3_k2      bim       250
## 7  purple_d3_k3      bim       250
## 8    blue_d4_l1      bim       250
## 9     red_d5_x1      tob       250
## 10    red_d5_x2      tob       250
## 11    red_d5_x3      tob       250
## 12 purple_d6_y1      tob       250
```

For the label "dep" - category 1:

Let's store the equilibrium weigths from the RW

```
# label dep
equilibriumsFL<-data.frame(
  learning="FL",
  label=c(rep("dep",9),rep("bim",9),rep("tob",9)),
  singleCues=c("blue","red","purple","d1","d2","d3","d4","d5","d6"),
  Equilibriums=c(.33,.22,0,.5,.39,0,-.17,-.17,0,
                 .22,0,.33,-.17,0,.5,.39,0,-.17,
                 0,.33,.22,0,-.17,-.17,0,.5,.39)
)

equilibriumsLF<-data.frame(
  learning="LF",
  label=c(rep("dep",9),rep("bim",9),rep("tob",9)),
  singleCues=c("blue","red","purple","d1","d2","d3","d4","d5","d6"),
  Equilibriums=c(.75,.25,0,.75,.25,0,0,0,0,
                 .25,0,.75,0,0,.75,.25,0,0,
                 0,.75,.25,0,0,0,0,.75,.25)
)
```

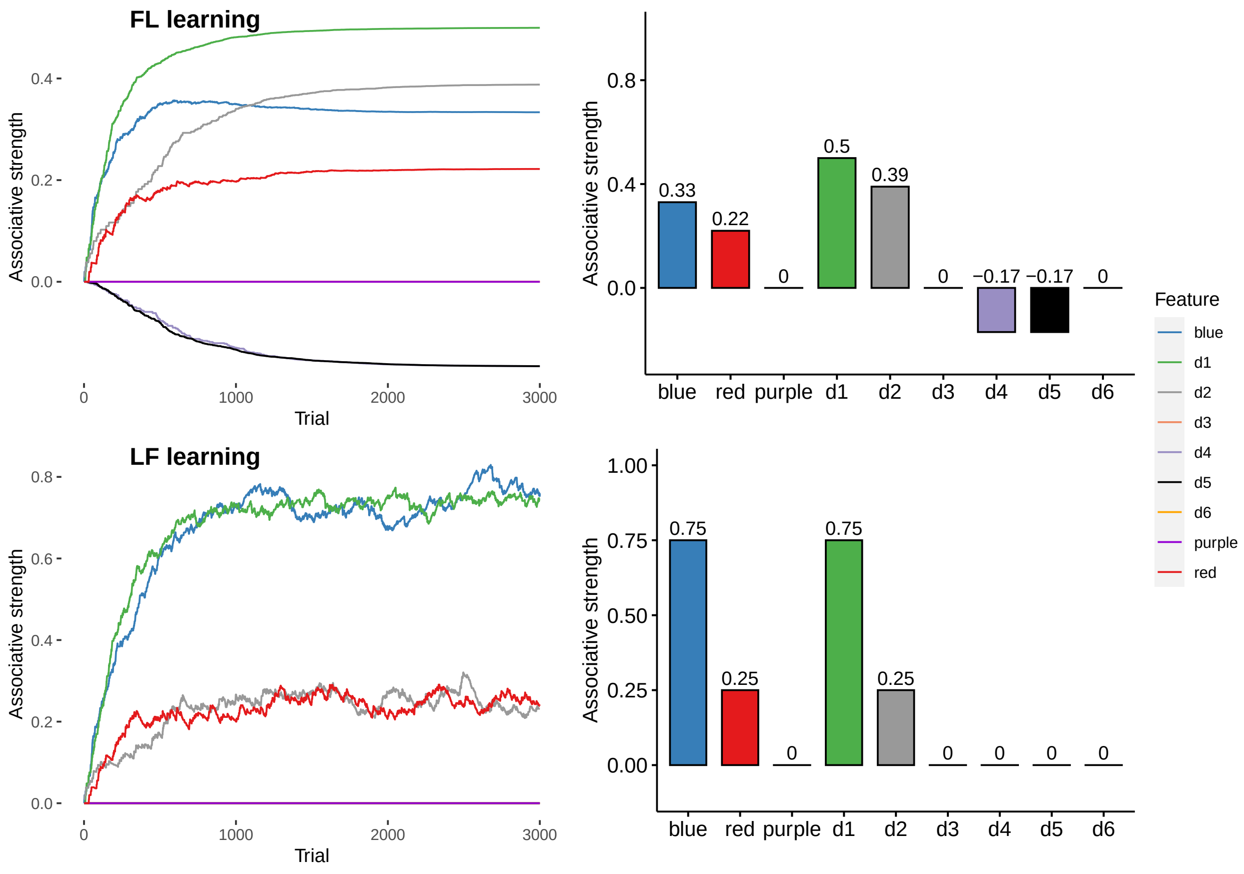


Figure 3: Predictions from the FLO paper for the label DEP-Cat 1

Now let's build a dataframe that looks like humans weights

```r
highFreqFL_modelWeights <-data.frame(
  learning = rep("FL",9),
  frequency = rep("high",9),
  type = c(rep("match",3),
           rep("mismatch-type1",3),
           rep("mismatch-type2",3)),
  label = c("dep_cat1", "bim_cat2", "tob_cat3"),
  fribble = c(1.1,2.1,3.1,
              3.1,1.1,2.1,
              2.1,3.1,1.1),
  fribbleCategory = c("cat1", "cat2", "cat3", #match
                      "cat3", "cat1", "cat2", #mis-type1
                      "cat2", "cat3", "cat1")) #mis-type2

highFreqLF_modelWeights<-data.frame(
           learning = rep("LF",9),
           frequency = rep("high",9),
           type = c(rep("match",3),
                    rep("mismatch-type1",3),
                    rep("mismatch-type2",3)),
           label = c("dep_cat1", "bim_cat2", "tob_cat3"),
           fribble = c(1.1,2.1,3.1,
                       3.1,1.1,2.1,
                       2.1,3.1,1.1),
           fribbleCategory = c("cat1", "cat2", "cat3", #match
                        "cat3", "cat1", "cat2", #mis-type1
                        "cat2", "cat3", "cat1")) #mis-type2
```

```r
lowFreqFL_modelWeights<-data.frame(
           learning = rep("FL",9),
           frequency = rep("low",9),
           type = c(rep("match",3),
                    rep("mismatch-type1",3),
                    rep("mismatch-type2",3)),
           label = c("dep_cat1", "bim_cat2", "tob_cat3"),
           fribble = c(1.2,2.2,3.2,
                       2.2,3.2,1.2,
                       3.2,1.2,2.2),
           fribbleCategory = c("cat1", "cat2", "cat3", #match
                               "cat2", "cat3", "cat1", #mis-type1
                               "cat3", "cat1", "cat2")) #mis-type2

lowFreqLF_modelWeights<-data.frame(
           learning = rep("LF",9),
           frequency = rep("low",9),
           type = c(rep("match",3),
                    rep("mismatch-type1",3),
                    rep("mismatch-type2",3)),
           label = c("dep_cat1", "bim_cat2", "tob_cat3"),
           fribble = c(1.2,2.2,3.2,
                       2.2,3.2,1.2,
                       3.2,1.2,2.2),
           fribbleCategory = c("cat1", "cat2", "cat3", #match
                               "cat2", "cat3", "cat1", #mis-type1
                               "cat3", "cat1", "cat2")) #mis-type2
```

```
##   learning frequency          type    label fribble fribbleCategory
## 1       FL      high         match dep_cat1     1.1            cat1
## 2       FL      high         match bim_cat2     2.1            cat2
## 3       FL      high         match tob_cat3     3.1            cat3
## 4       FL      high mismatch-type1 dep_cat1     3.1            cat3
## 5       FL      high mismatch-type1 bim_cat2     1.1            cat1
## 6       FL      high mismatch-type1 tob_cat3     2.1            cat2
##   equilibriumWeigths
## 1               0.83
## 2               0.83
## 3               0.83
## 4               0.05
## 5               0.05
## 6               0.05
```

```
modelWeight <- aggregate(equilibriumWeigths ~ learning + frequency + type, data = modelWeights,FUN = mea
head(modelWeight)
```

```
##   learning frequency           type equilibriumWeigths
## 1       FL      high          match               0.83
## 2       LF      high          match               1.50
## 3       FL       low          match               0.61
## 4       LF       low          match               0.50
## 5       FL      high mismatch-type1               0.05
## 6       LF      high mismatch-type1               0.25
```

okay, in order to compare human with model performance, the equilibrium weigths *I think* should be normalised over a 0 that is the average of the weights.

```
modelWeight$equilibriumWeigthsZ.score <- as.vector(scale(modelWeight$equilibriumWeigths))
```

Plot of human and model responses considered as summed weights of the label-feature association.

```
lollipop_modelWeight<-ggdotchart(modelWeight, x = "type", y = "equilibriumWeigths",
           #color = "learning",                              # Color by groups
           palette = c("#00AFBB", "#E7B800", "#FC4E07"), # Custom color palette
           add = "segments",                             # Add segments from y = 0 to dots
           rotate = T,
           add.params = list(color = "lightgray", size = 2), # Change segment color and size
           #group = "learning",                              # Order by groups
           dot.size = 10,                                 # Large dot size
           label = round(modelWeight$equilibriumWeigths,1),                        # Add mpg values as
           font.label = list(color = "white", size = 9,
                             vjust = 0.5),               # Adjust label parameters
           ggtheme = theme_pubr(),                        # ggplot2 theme
           title = "model predictions",
           ylab = "association strength",
           xlab = " "
           )+ facet_grid( learning ~ frequency) +
  geom_hline(yintercept = 0, linetype = 2, color = "lightgray")
lollipop_modelWeight
```

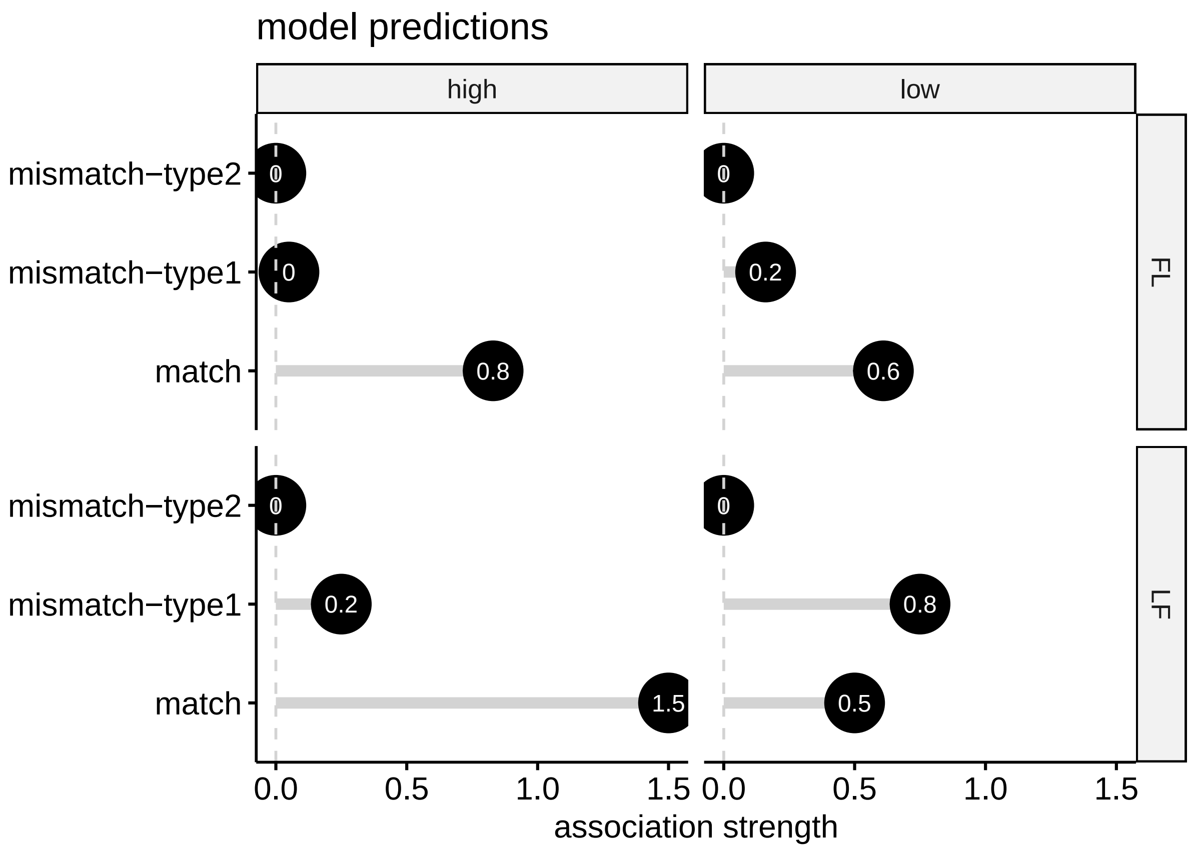


Figure 4: Summed weights of the label-feature association by frequency by learning

```
lollipop_modelWeightZ<-ggdotchart(modelWeight, x = "type", y = "equilibriumWeigthsZ.score",
           #color = "learning",                                 # Color by groups
           palette = c("#00AFBB", "#E7B800", "#FC4E07"), # Custom color palette
           add = "segments",                             # Add segments from y = 0 to dots
           rotate = T,
           add.params = list(color = "lightgray", size = 2), # Change segment color and size
           #group = "learning",                                 # Order by groups
           dot.size = 10,                                 # Large dot size
           label = round(modelWeight$equilibriumWeigthsZ.score,1),                        # Add mpg val
           font.label = list(color = "white", size = 9,
                             vjust = 0.5),               # Adjust label parameters
           ggtheme = theme_pubr(),                        # ggplot2 theme
           title = "model predictions",
           ylab = "association strength Z-scored",
           xlab = " "
           )+ facet_grid( learning ~ frequency) +
  geom_hline(yintercept = 0, linetype = 2, color = "lightgray")
```

```
lollipop_modelWeightZ
```

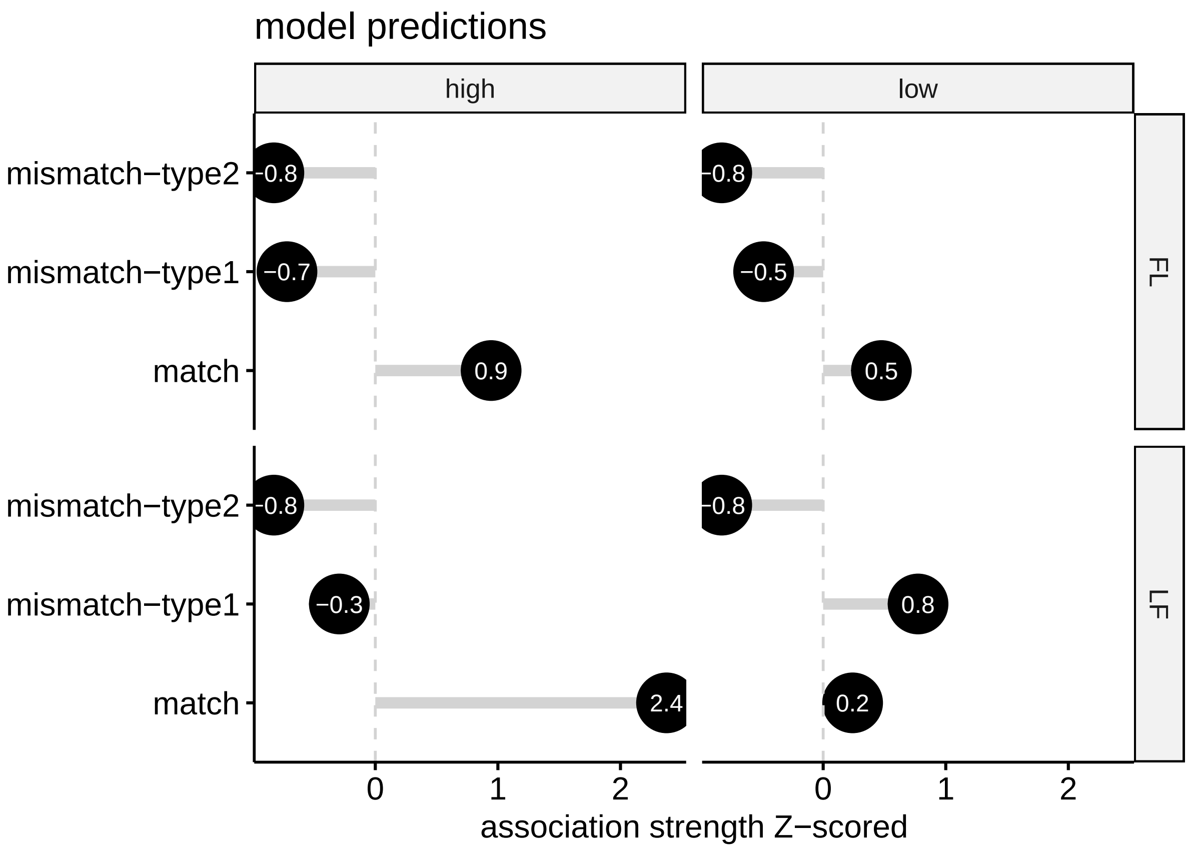
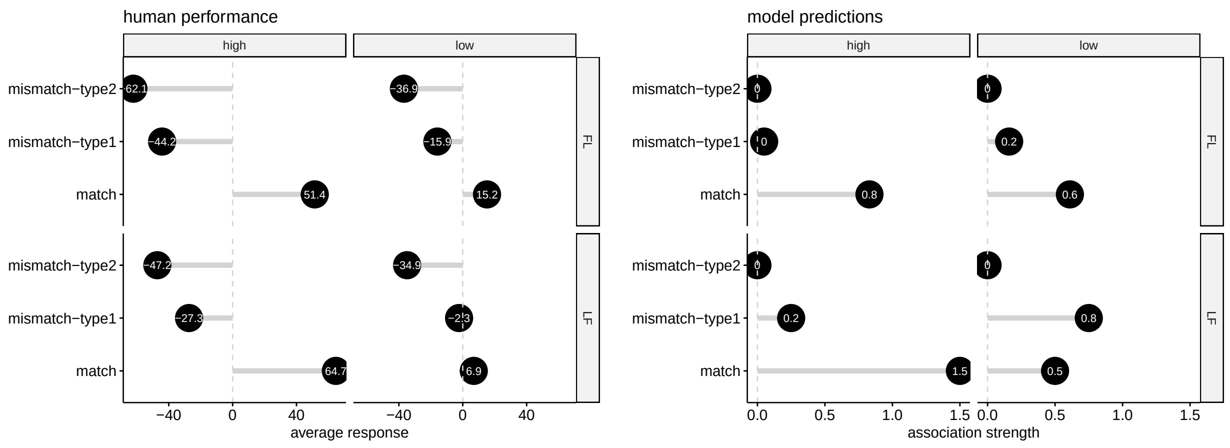


Figure 5: Summed weights of the label-feature association by frequency by learning

Human and model performance

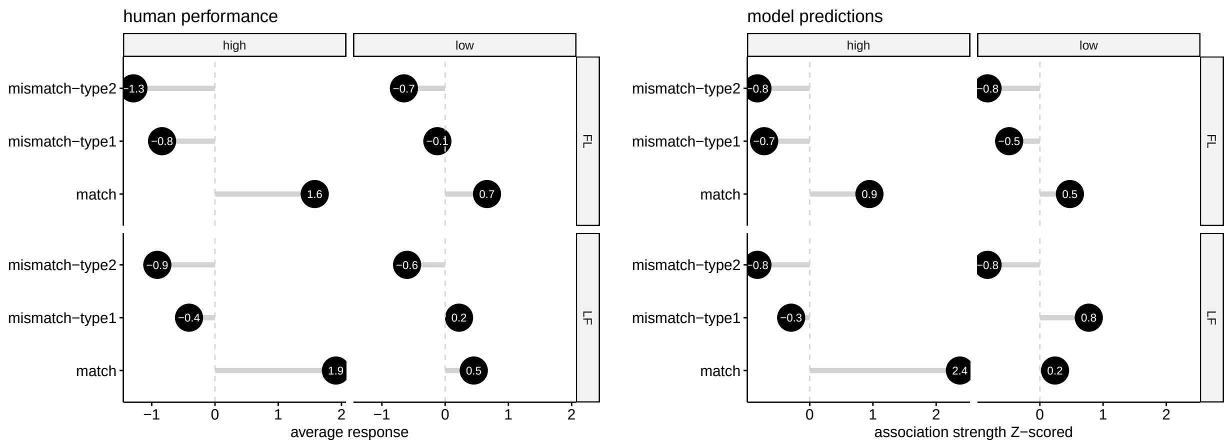
Raw data for humans and the model:

```
ggarrange(lollipopWeight, lollipop_modelWeight)
```



Transformation in Z-scores for both humans and model performance:

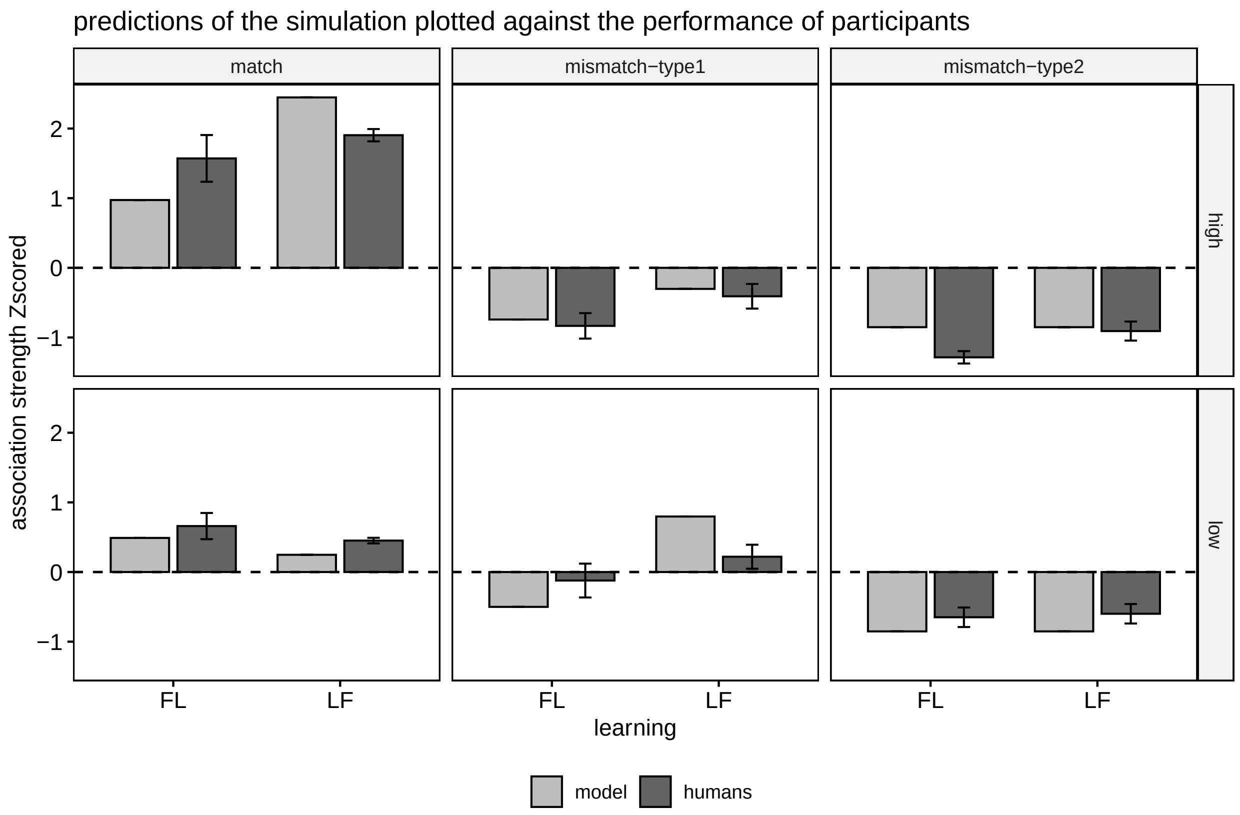
```
ggarrange(lollipopWeightZ, lollipop_modelWeightZ)
```



```
humansWeights$equilibriumWeigthsZ.score <- as.vector(scale(humansWeights$resp))
humansWeights$what <- as.factor(c("humans"))

modelWeights$equilibriumWeigthsZ.score <- as.vector(scale(modelWeights$equilibriumWeigths))
modelWeights$what <- as.factor(c("model"))

associationStrengths <- rbind(
  modelWeights[,c("learning","frequency","type","label","fribble",
                  "fribbleCategory","equilibriumWeigthsZ.score","what")],
  humansWeights[,c("learning","frequency","type","label","fribble",
                  "fribbleCategory","equilibriumWeigthsZ.score","what")])

summary(associationStrengths)
```

```
##  learning frequency              type        label             fribble
##  FL:36    high:36   match          :24   Length:72          1.1:12
##  LF:36    low :36   mismatch-type1:24   Class :character   1.2:12
##                     mismatch-type2:24   Mode  :character   2.1:12
##                                                            2.2:12
##                                                            3.1:12
##                                                            3.2:12
##  fribbleCategory equilibriumWeigthsZ.score     what
##  cat1:24         Min.   :-1.4519          model :36
##  cat2:24         1st Qu.:-0.8522          humans:36
##  cat3:24         Median :-0.3143
##                  Mean   : 0.0000
##                  3rd Qu.: 0.5378
##                  Max.   : 2.4466
```

Barplot



Analysis on response type

Contingency Judgement task:

```
relevel(humansTypeWeigths$type, ref = "mismatch-type1")->humansTypeWeigths$type
lm1<-lmer(resp ~  type * frequency * learning  +(frequency|subjID), data = humansTypeWeigths[!(humansTy
car::Anova(lm1)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
```

```
##
## Response: resp
##                           Chisq Df Pr(>Chisq)
## type                    79.0590  1  < 2.2e-16 ***
## frequency                1.2171  1     0.2699
## learning                 1.5121  1     0.2188
## type:frequency          42.2081  1  8.206e-11 ***
## type:learning            1.3205  1     0.2505
## frequency:learning       0.8495  1     0.3567
## type:frequency:learning  1.6299  1     0.2017
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(lm1)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: resp ~ type * frequency * learning + (frequency | subjID)
##    Data: humansTypeWeigths[!(humansTypeWeigths$type == "mismatch-type2"),
##     ]
##
## REML criterion at convergence: 4043.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3792 -0.5743  0.0291  0.6066  2.5232
##
## Random effects:
##  Groups   Name          Variance Std.Dev. Corr
##  subjID   (Intercept)   1578     39.72
##           frequencyhigh 2993     54.71    -0.84
##  Residual               2483     49.83
## Number of obs: 374, groups:  subjID, 95
##
## Fixed effects:
##                                   Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)                        -10.518     10.477 128.883  -1.004 0.317291
## typematch                           24.864     12.698 282.983   1.958 0.051211
## frequencyhigh                      -32.784     13.929 187.886  -2.354 0.019623
## learningLF                          17.270     15.821 138.077   1.092 0.276900
## typematch:frequencyhigh             68.250     17.388 322.152   3.925 0.000106
## typematch:learningLF               -32.320     18.816 281.966  -1.718 0.086955
## frequencyhigh:learningLF            -1.793     20.811 191.975  -0.086 0.931436
## typematch:frequencyhigh:learningLF  32.843     25.725 316.672   1.277 0.202648
##
## (Intercept)
## typematch                         .
## frequencyhigh                     *
## learningLF
## typematch:frequencyhigh           ***
## typematch:learningLF              .
## frequencyhigh:learningLF
## typematch:frequencyhigh:learningLF
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) typmtc frqncy lrnnLF typmt: typ:LF frq:LF
## typematch   -0.623
## frequncyhgh -0.773  0.467
## learningLF  -0.662  0.413  0.512
## typmtch:frq  0.449 -0.744 -0.612 -0.298
## typmtch:lLF  0.421 -0.675 -0.315 -0.649  0.502
## frqncyhg:LF  0.517 -0.312 -0.669 -0.781  0.410  0.492
## typmtch::LF -0.304  0.503  0.414  0.469 -0.676 -0.746 -0.629
```

```
lm1.emm <- emmeans(lm1 , ~ type |frequency| learning )
contrast(lm1.emm, "consec",  simple = "each", combine = T, adjust = "bonferroni")
```

```
##  frequency learning type           contrast                estimate   SE  df
##  low       FL       .              match - mismatch-type1    24.86 12.8 281
##  high      FL       .              match - mismatch-type1    93.11 11.8 258
##  low       LF       .              match - mismatch-type1    -7.46 14.0 279
##  high      LF       .              match - mismatch-type1    93.64 12.8 229
##  .         FL       mismatch-type1 high - low               -32.78 14.0 190
##  .         FL       match          high - low                35.47 14.2 120
##  .         LF       mismatch-type1 high - low               -34.58 15.5 198
##  .         LF       match          high - low                66.52 15.0 104
##  low       .        mismatch-type1 LF - FL                   17.27 15.9 134
##  low       .        match          LF - FL                  -15.05 14.9 112
##  high      .        mismatch-type1 LF - FL                   15.48 13.1 126
##  high      .        match          LF - FL                   16.00 13.2 125
##  t.ratio p.value
##    1.937  0.6457
##    7.910  <.0001
##   -0.531  1.0000
##    7.343  <.0001
##   -2.341  0.2431
##    2.493  0.1686
##   -2.224  0.3273
##    4.437  0.0003
##    1.085  1.0000
##   -1.012  1.0000
##    1.182  1.0000
##    1.214  1.0000
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: bonferroni method for 12 tests
```

Picture label task

```
df<-aggregate(acc ~ frequency + learning + subjID, data = pictureLabel_respType, mean)
```

```
lm2<-lmer(acc ~  frequency * learning + (1|subjID), data = df)
car::Anova(lm2)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: acc
##                      Chisq Df Pr(>Chisq)
## frequency          48.6566  1  3.049e-12 ***
## learning            3.2245  1    0.07254 .
## frequency:learning  0.0066  1    0.93545
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(lm2)$coefficients
```

```
##                             Estimate Std. Error        df     t value
## (Intercept)              0.429242424 0.03356626 196.80375 12.78791395
## frequencyhigh            0.237121212 0.04558184  98.99994  5.20209829
## learningLF              -0.062834557 0.04973759 196.80375 -1.26332139
## frequencyhigh:learningLF -0.005470073 0.06754195  98.99994 -0.08098779
##                             Pr(>|t|)
## (Intercept)             1.190887e-27
## frequencyhigh           1.065764e-06
## learningLF              2.079682e-01
## frequencyhigh:learningLF 9.356152e-01
```

```
rm(df)
```

Label picture task

```
df<-aggregate(acc ~  frequency + learning + subjID, data = labelPicture_respType, mean)
```

```
lm3<-lmer(acc ~   frequency * learning + (1|subjID), data = df)
car::Anova(lm3)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: acc
##                      Chisq Df Pr(>Chisq)
## frequency          31.1902  1  2.339e-08 ***
## learning            1.8628  1     0.1723
## frequency:learning  0.9516  1     0.3293
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(lm3)$coefficients
```

```
##                            Estimate Std. Error        df    t value
## (Intercept)              0.42248677 0.03940969 193.57353 10.7203769
## frequencyhigh            0.26020723 0.05441000  96.99999  4.7823422
## learningLF              -0.01835979 0.05845402 193.57353 -0.3140894
## frequencyhigh:learningLF -0.07872575 0.08070307  96.99999 -0.9754988
##                              Pr(>|t|)
## (Intercept)               2.388783e-21
## frequencyhigh             6.180321e-06
## learningLF                7.537914e-01
## frequencyhigh:learningLF 3.317394e-01
```

```
rm(df)
```

Clean the global environment:

```
rm( problematicPeople, frequency, dumbPeople,  task, temp,  p, ms, n, nrows, subjs, totsubjs ,genTask, 
```

```
## Warning in rm(problematicPeople, frequency, dumbPeople, task, temp, p, ms, :
## object 'df' not found
```

Bayes factor calculation with GLMMs

Estimates of the betas from the FLO paper

```
#means
highfreq_mean<- mean(88, 98)
lowfreq_mean <- mean(38, 78)

n <- c(32)

#sd
highfreq_sd <- c(5*sqrt(n))  #Paper has standard errors represented (I guess),
                     #I'm going to transform it back to standard deviations
lowfreq_sd <- c(5*sqrt(n)) #also, they look the same to me from the picture
                           #but low frequency should lead more variability.
```

Main effect of frequency:

```
frequency_beta<- logodds(highfreq_mean) - logodds(lowfreq_mean)
```

Main effect of learning:

```
#mean
LF_mean <- mean(38, 88)
FL_mean <- mean(78, 98)

n <- c(16)

#sd
LF_sd <- c(5*sqrt(n)) #how can be possible that learnings have the same se?
FL_sd <- c(5*sqrt(n))
```

```
learning_beta <- logodds(FL_mean) - logodds(LF_mean)
#positive > higher in the FL
```

Interaction between freq and learning:

Frequency effect (high-low) is greater in the LF than in FL:

```
#(logodds(highfreq_FL)-logodds(lowfreq_FL))- (logodds(highfreq_LF)-logodds(lowfreq_LF))
freqBylearning_beta <- (logodds(98)-logodds(78))- (logodds(88)-logodds(38))*-1
```

GLMMs with all tests separately

Picture label

```
pictureLabel$frequency <- as.factor(pictureLabel$frequency)
plyr::revalue(pictureLabel$frequency, c("25"="low"))-> pictureLabel$frequency;
plyr::revalue(pictureLabel$frequency, c("75"="high"))-> pictureLabel$frequency;

pictureLabel$learning = relevel(pictureLabel$learning, ref = "LF")
pictureLabel$frequency = relevel(pictureLabel$frequency, ref = "low")
pictureLabel <- lizCenter(pictureLabel, list("learning" , "frequency", "task"))
```

```
summarySEwithin(data = pictureLabel[pictureLabel$rt > 100 & !(pictureLabel$subjID %in% badsubjs),], mea
```

```
## Loading required package: plyr

## ------------------------------------------------------------------------------

## You have loaded plyr after dplyr - this is likely to cause problems.
## If you need functions from both plyr and dplyr, please load plyr first, then dplyr:
## library(plyr); library(dplyr)

## ------------------------------------------------------------------------------

##
## Attaching package: 'plyr'

## The following object is masked from 'package:ggpubr':
##
##     mutate

## The following objects are masked from 'package:dplyr':
##
##     arrange, count, desc, failwith, id, mutate, rename, summarise,
##     summarize

## The following object is masked from 'package:purrr':
##
##     compact
##   learning frequency   N       acc  acc_norm        sd         se         ci
## 1       FL      high 582 0.7079038 0.6729505 0.5831509 0.02417238 0.04747590
## 2       FL       low 611 0.4877250 0.4550235 0.6269022 0.02536175 0.04980694
## 3       LF      high 465 0.6688172 0.7084257 0.5947813 0.02758232 0.05420174
## 4       LF       low 494 0.3785425 0.4228856 0.6642473 0.02988590 0.05871944
```

```
piclab_model <- glmer(acc ~  frequency*learning + (frequency|subjID),
         data = pictureLabel[pictureLabel$rt > 100 & !(pictureLabel$subjID %in% badsubjs),],
         family="binomial",
         control=glmerControl(optimizer = "bobyqa"))

adjusted.piclab_model = adjust_intercept_model(piclab_model, chance = log(0.33/(1-0.33)))
round(adjusted.piclab_model,5)
```

```
##                            Estimate Std. Error  z value Pr(>|z|)
## (Intercept)                 0.09817    0.21988  0.44649  0.65524
## frequencyhigh               1.64364    0.35383  4.64523  0.00000
## learningFL                  0.55500    0.29760  1.86492  0.06219
## frequencyhigh:learningFL -0.18451    0.47891 -0.38527  0.70004
```

```
piclab_model.emm <- emmeans(piclab_model , ~ frequency* learning )
contrast(piclab_model.emm, "consec",  simple = "each", combine = F, adjust = "bonferroni")
```

```
## $`simple contrasts for frequency`
## learning = LF:
##  contrast   estimate    SE  df z.ratio p.value
##  high - low     1.64 0.354 Inf 4.645   <.0001
##
## learning = FL:
##  contrast   estimate    SE  df z.ratio p.value
##  high - low     1.46 0.328 Inf 4.448   <.0001
##
## Results are given on the log odds ratio (not the response) scale.
##
## $`simple contrasts for learning`
## frequency = low:
##  contrast estimate    SE  df z.ratio p.value
##  FL - LF     0.555 0.298 Inf 1.865   0.0622
##
## frequency = high:
##  contrast estimate    SE  df z.ratio p.value
##  FL - LF     0.370 0.387 Inf 0.957   0.3386
##
## Results are given on the log odds ratio (not the response) scale.
```

Label picture

```
labelPicture$frequency <- as.factor(labelPicture$frequency)
plyr::revalue(labelPicture$frequency, c("25"="low"))-> labelPicture$frequency;
plyr::revalue(labelPicture$frequency, c("75"="high"))-> labelPicture$frequency;

labelPicture$learning = relevel(labelPicture$learning, ref = "LF")
```

```
labelPicture$frequency = relevel(labelPicture$frequency, ref = "low")
labelPicture <- lizCenter(labelPicture, list("learning" , "frequency", "task"))
```

```
summarySEwithin(data = labelPicture[labelPicture$rt > 100 & labelPicture$rt <=2500 & !(labelPicture$sub
```

```
##   learning frequency   N       acc  acc_norm        sd         se         ci
## 1       FL      high 586 0.7440273 0.7151810 0.5322962 0.02198895 0.04318691
## 2       FL       low 554 0.4458484 0.4244508 0.5849702 0.02485300 0.04881783
## 3       LF      high 484 0.6508264 0.6784148 0.6177757 0.02808071 0.05517544
## 4       LF       low 460 0.4304348 0.4639248 0.6508264 0.03034494 0.05963222
```

```
labpic_model <- glmer(acc ~  frequency.ct*learning.ct + (frequency.ct|subjID),
         data = labelPicture[labelPicture$rt > 100 & labelPicture$rt <=2500 & !(labelPicture$subjID %in
         family="binomial",
         control=glmerControl(optimizer = "bobyqa"))

adjusted.labpic_model = adjust_intercept_model(labpic_model, chance = log(0.33/(1-0.33)))
round(adjusted.labpic_model,5)
```

```
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)                1.32254    0.17272 7.65720  0.00000
## frequency.ct               1.94468    0.35298 5.50936  0.00000
## learning.ct                0.51646    0.33501 1.54163  0.12316
## frequency.ct:learning.ct   0.59238    0.68714 0.86208  0.38864
```

```
labpic_model.emm <- emmeans(labpic_model, ~ frequency.ct* learning.ct )
contrast(labpic_model.emm, "consec",  simple = "each", combine = F, adjust = "bonferroni")
```

```
## $`simple contrasts for frequency.ct`
## learning.ct = -0.525:
##  contrast                              estimate    SE  df z.ratio p.value
##  0.491247672253259 - -0.508752327746741     1.63 0.505 Inf 3.233   0.0012
##
## learning.ct =  0.475:
##  contrast                              estimate    SE  df z.ratio p.value
##  0.491247672253259 - -0.508752327746741     2.23 0.480 Inf 4.637   <.0001
##
## Results are given on the log odds ratio (not the response) scale.
##
## $`simple contrasts for learning.ct`
## frequency.ct = -0.509:
##  contrast                              estimate    SE  df z.ratio p.value
##  0.475232774674115 - -0.524767225325885    0.215 0.468 Inf 0.460   0.6455
##
## frequency.ct =  0.491:
##  contrast                              estimate    SE  df z.ratio p.value
##  0.475232774674115 - -0.524767225325885    0.807 0.491 Inf 1.643   0.1003
##
## Results are given on the log odds ratio (not the response) scale.
```

Contingency judgement

```r
plyr::revalue(as.factor(conjudge$frequency), c("25"="low"))-> conjudge$frequency;
```

```
## The following `from` values were not present in `x`: 25
```

```r
plyr::revalue(as.factor(conjudge$frequency), c("75"="high"))-> conjudge$frequency;
```

```
## The following `from` values were not present in `x`: 75
```

```r
conjudge$learning = relevel(conjudge$learning, ref = "FL")
conjudge$frequency = relevel(conjudge$frequency, ref = "low")
conjudge <- lizCenter(conjudge, list("learning" , "frequency"))
```

```r
conjudge_model <- lmer(resp ~  learning * frequency +(frequency|subjID),
         data = conjudge[!(conjudge$subjID %in% badsubjs) & conjudge$acc==0,])
```

```r
car::Anova(conjudge_model)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: resp
##                      Chisq Df Pr(>Chisq)
## learning            1.3493  1  0.2454058
## frequency          11.7018  1  0.0006244 ***
## learning:frequency  0.7078  1  0.4001847
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
conjudge_model.emm <- emmeans(conjudge_model , ~ learning* frequency )
contrast(conjudge_model.emm, "consec",  simple = "each", combine = F, adjust = "bonferroni")
```

```
## $`simple contrasts for learning`
## frequency = low:
##  contrast estimate   SE   df t.ratio p.value
##  LF - FL      5.48 11.0 70.9 0.500   0.6187
##
## frequency = high:
##  contrast estimate   SE   df t.ratio p.value
##  LF - FL     16.13 11.2 71.8 1.434   0.1559
##
## Degrees-of-freedom method: kenward-roger
##
## $`simple contrasts for frequency`
## learning = FL:
##  contrast   estimate   SE df t.ratio p.value
##  high - low    -26.3 8.44 70 -3.111  0.0027
##
## learning = LF:
##  contrast   estimate   SE df t.ratio p.value
##  high - low    -15.6 9.45 72 -1.652  0.1030
##
## Degrees-of-freedom method: kenward-roger
```

Combine both generalization tasks in one dataset

I'm going to combine both generalization tasks in one single dataset called genTask

```
genTask <- rbind(labelPicture[labelPicture$rt > 100 & !(labelPicture$subjID %in% badsubjs),],
                 pictureLabel[pictureLabel$rt > 100 & !(pictureLabel$subjID %in% badsubjs),])

genTask$frequency <- as.factor(genTask$frequency)
plyr::revalue(genTask$frequency, c("25"="low"))-> genTask$frequency;
```

```
## The following `from` values were not present in `x`: 25
```

```
plyr::revalue(genTask$frequency, c("75"="high"))-> genTask$frequency;
```

```
## The following `from` values were not present in `x`: 75
```

Relevel the variables:

```
genTask$learning = relevel(genTask$learning, ref = "LF")
genTask$frequency = relevel(genTask$frequency, ref = "low")
genTask <- lizCenter(genTask, list("learning" , "frequency", "task"))
```

The model

```
genTask_model <- glmer(acc ~  frequency.ct*learning.ct + task.ct + (frequency.ct|subjID) ,
         data = genTask,
         family="binomial",
         control=glmerControl(optimizer = "bobyqa"))

adjusted.genTask_model = adjust_intercept_model(genTask_model, chance = log(0.33/(1-0.33)))
car::Anova(genTask_model)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: acc
##                              Chisq Df Pr(>Chisq)
## frequency.ct               41.2908  1  1.312e-10 ***
## learning.ct                 2.9250  1    0.08721 .
## task.ct                     0.2106  1    0.64630
## frequency.ct:learning.ct    0.2949  1    0.58710
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(genTask_model)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: acc ~ frequency.ct * learning.ct + task.ct + (frequency.ct |
##     subjID)
##    Data: genTask
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   4509.2   4560.2  -2246.6   4493.2     4298
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.1071 -0.6219  0.1839  0.5990  3.5444
##
## Random effects:
##  Groups Name         Variance Std.Dev. Corr
##  subjID (Intercept)  1.527    1.236
##         frequency.ct 5.577    2.362    0.12
## Number of obs: 4306, groups:  subjID, 95
##
## Fixed effects:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)                0.51409    0.13587   3.784 0.000155 ***
## frequency.ct               1.68180    0.26120   6.439 1.21e-10 ***
## learning.ct                0.47846    0.27079   1.767 0.077240 .
## task.ct                   -0.03490    0.07604  -0.459 0.646295
## frequency.ct:learning.ct  0.28263    0.52044   0.543 0.587097
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) frqnc. lrnng. tsk.ct
## frequncy.ct  0.143
## learning.ct  0.027  0.014
## task.ct     -0.001  0.005 -0.003
## frqncy.ct:.  0.014  0.028  0.132  0.000
```

Further inspection:

```
genTask_model.emm <- emmeans(genTask_model , ~ frequency.ct * learning.ct )
contrast(genTask_model.emm, "consec",  simple = "each", combine = F, adjust = "bonferroni")
```

```
## $`simple contrasts for frequency.ct`
## learning.ct = -0.55:
##  contrast                               estimate    SE  df z.ratio p.value
##  0.502322340919647 - -0.497677659080353     1.53 0.382 Inf 3.994   0.0001
##
## learning.ct =  0.45:
##  contrast                               estimate    SE  df z.ratio p.value
##  0.502322340919647 - -0.497677659080353     1.81 0.356 Inf 5.087   <.0001
##
## Results are averaged over the levels of: task.ct
## Results are given on the log odds ratio (not the response) scale.
##
## $`simple contrasts for learning.ct`
## frequency.ct = -0.498:
```

```
##  contrast                             estimate    SE  df z.ratio p.value
##  0.44960520204366 - -0.55039479795634    0.338 0.349 Inf 0.967   0.3333
##
## frequency.ct =  0.502:
##  contrast                             estimate    SE  df z.ratio p.value
##  0.44960520204366 - -0.55039479795634    0.620 0.400 Inf 1.549   0.1213
##
## Results are averaged over the levels of: task.ct
## Results are given on the log odds ratio (not the response) scale.
```

Okay, with both tasks together the take home message is the following:

- Main effect of frequency, with high frequency having higher accuracy than low frequency in both learnings.
- Main effect of learning, with FL learning having higher accuracy in the high frequency condition.
- No difference between learnings in the low frequency condition.
- No difference between tasks

```
genTask %>%
  group_by(frequency, learning) %>%
  summarise(mean = mean(acc))
```

```
##        mean
## 1 0.5652578
```

```
summarySEwithin(data = genTask, measurevar = "acc", betweenvars = "learning", withinvars = "frequency",
```

```
##   learning frequency    N       acc  acc_norm        sd         se         ci
## 1       FL      high 1182 0.7225042 0.6930796 0.5647076 0.01642536 0.03222614
## 2       FL       low 1188 0.4638047 0.4380815 0.6156339 0.01786135 0.03504334
## 3       LF      high  961 0.6566077 0.6885886 0.6131101 0.01977774 0.03881260
## 4       LF       low  975 0.4082051 0.4436979 0.6707224 0.02148031 0.04215301
```

I'm going to create a table with the estimates:

```
genTask_bf = data.frame(
    condition = c(
                   "frequency by learning",
                   "learning",
                   "frequency",
                   "task"
                   ),

    meandiff = c(
      round(summary(genTask_model)$coefficients["frequency.ct:learning.ct", "Estimate"],3),
       round(summary(genTask_model)$coefficients["learning.ct", "Estimate"],3),
       round(summary(genTask_model)$coefficients["frequency.ct", "Estimate"],3),
       round(summary(genTask_model)$coefficients["task.ct", "Estimate"],3)
       ),
    se = c(
      round(summary(genTask_model)$coefficients["frequency.ct:learning.ct", "Std. Error"],3),
       round(summary(genTask_model)$coefficients["learning.ct", "Std. Error"],3),
       round(summary(genTask_model)$coefficients["frequency.ct", "Std. Error"],3),
       round(summary(genTask_model)$coefficients["task.ct", "Std. Error"],3)
       )
)

genTask_bf
```

```
##               condition meandiff    se
## 1 frequency by learning    0.283 0.520
## 2              learning    0.478 0.271
## 3             frequency    1.682 0.261
## 4                  task   -0.035 0.076
```

BF for Frequency:

```
Bf(sd = genTask_bf[genTask_bf$condition=='frequency',]$se,
   obtained = genTask_bf[genTask_bf$condition=='frequency',]$meandiff,
   uniform = 0,
   sdtheory = highfreq_sd,
   meanoftheory = frequency_beta,
   tail = 1)
```

```
## $LikelihoodTheory
## [1] 0.028197
##
## $Likelihoodnull
## [1] 1.465403e-09
##
## $BayesFactor
## [1] 19241809
```

BF for learning:

```
Bf(sd = genTask_bf[genTask_bf$condition=='learning',]$se,
   obtained = genTask_bf[genTask_bf$condition=='learning',]$meandiff,
   uniform = 0,
   sdtheory = LF_sd,
   meanoftheory = learning_beta,
   tail = 1)
```

```
## $LikelihoodTheory
## [1] 0.03823377
##
## $Likelihoodnull
## [1] 0.3107198
```

```
##
## $BayesFactor
## [1] 0.123049
```

BF for the interaction frequency by learning

```
Bf(sd = genTask_bf[genTask_bf$condition=='frequency by learning',]$se,
   obtained = genTask_bf[genTask_bf$condition=='frequency by learning',]$meandiff,
   uniform = 0,
   sdtheory = LF_sd, #don't know how to compute sd of the interaction
   meanoftheory = freqBylearning_beta,
   tail = 1)
```

```
## $LikelihoodTheory
## [1] 0.02852534
##
## $Likelihoodnull
## [1] 0.6615924
##
## $BayesFactor
## [1] 0.04311618
```

```
rm(speedacc, n, lowfreq_mean, highfreq_mean, lowfreq_sd, highfreq_sd, LF_mean, FL_mean, LF_sd, FL_sd)
```

Summary of the results

We have collected 120 participants. Among these, 63 FL learning and 57 LF learning.

We had four tasks:

- Picture label task
- Label picture task
- Contingency judgement task
- Random dot task (attention check)

Participants that scored <=.5 accuracy and had >3 timeouts in the attention check (random dot task) were removed from the analysis. Participants that skipped completely one of the tasks were removed. Participants that had very few datapoints, i.e., less than 1/2 also removed. In total for picture label task we had 52 for FL learning, and 43 for LF learning.

Raw means/sd for the effects.

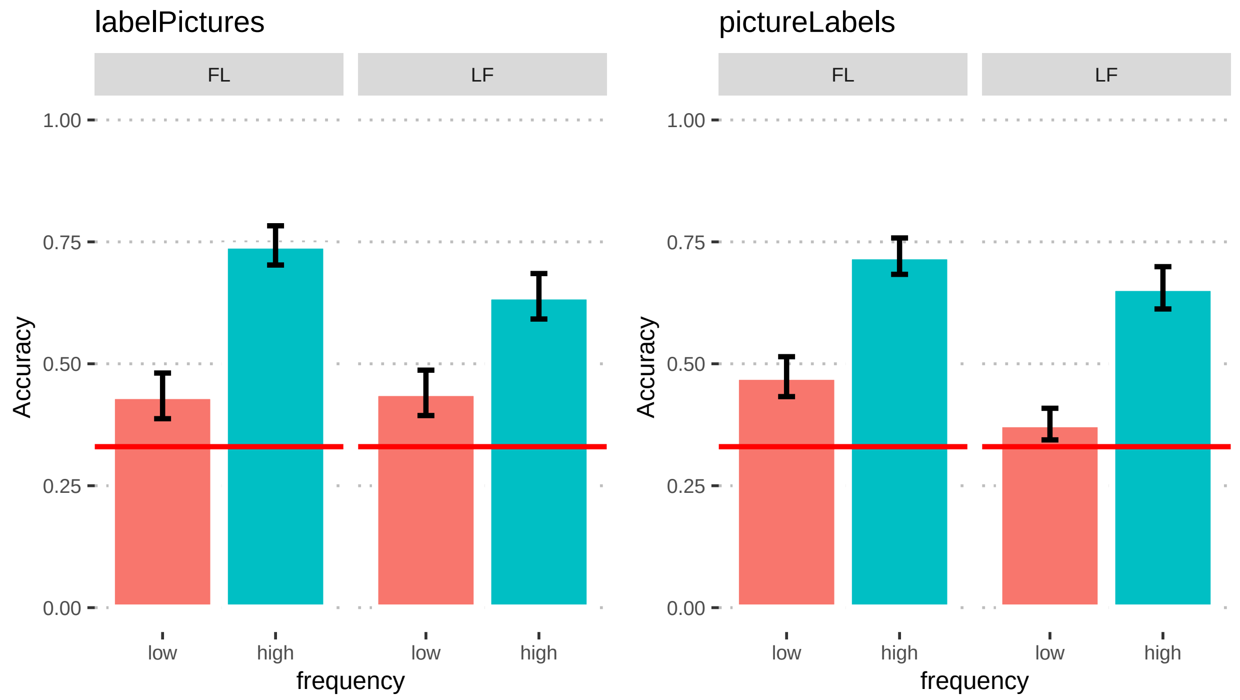
Label Picture:

```
##   learning frequency   N       acc  acc_norm        sd         se         ci
## 1       FL      high 586 0.7440273 0.7151810 0.5322962 0.02198895 0.04318691
## 2       FL       low 554 0.4458484 0.4244508 0.5849702 0.02485300 0.04881783
## 3       LF      high 484 0.6508264 0.6784148 0.6177757 0.02808071 0.05517544
## 4       LF       low 460 0.4304348 0.4639248 0.6508264 0.03034494 0.05963222
```

Picture Label:

```
##   learning frequency   N       acc  acc_norm        sd         se         ci
## 1       FL      high 582 0.7079038 0.6729505 0.5831509 0.02417238 0.04747590
## 2       FL       low 611 0.4877250 0.4550235 0.6269022 0.02536175 0.04980694
## 3       LF      high 465 0.6688172 0.7084257 0.5947813 0.02758232 0.05420174
## 4       LF       low 494 0.3785425 0.4228856 0.6642473 0.02988590 0.05871944
```

Data Visualization:



GLMMs models:

Picture label

```
##                           Estimate Std. Error  z value Pr(>|z|)
## (Intercept)                0.09817    0.21988  0.44649  0.65524
## frequencyhigh              1.64364    0.35383  4.64523  0.00000
## learningFL                 0.55500    0.29760  1.86492  0.06219
## frequencyhigh:learningFL -0.18451    0.47891 -0.38527  0.70004
```

Label picture

```
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)                1.32254    0.17272 7.65720  0.00000
## frequency.ct               1.94468    0.35298 5.50936  0.00000
## learning.ct                0.51646    0.33501 1.54163  0.12316
## frequency.ct:learning.ct   0.59238    0.68714 0.86208  0.38864
```

What we have learned from these data:

- Main effect of frequency, with high frequency having higher accuracy than low frequency in both learnings.
- Marginal effect of learning in the pictureLabel task, with FL learning having higher accuracy in the low frequency condition.
- No difference between learnings in the high frequency condition, although there is a trend for FL being higher than LF in the pictureLabel task
- What's important here is that the two tasks seems to behave completely differently.

This means that the effect of frequency (high vs low) was super robust, and this is the only thing that we have replicated 100%. The difference between learnings unfortunately wasn't there, although we see a trend in this direction in one task, but not the other. Why is this the case?

How do we explain these results: We don't know for sure, however, throughout this experiment we have realised several important details that are not identical to the FLO paper and therefore could have affected the results:

- Learning: stimuli were pseudo-randomised with exemplars belonging to high and low frequency category of one category never displayed consequentially.
- The whole FLO experiment was visual, not audio, therefore this might cause less ambiguity, i.e., higher accuracy, and perfect balance in the test tasks for the trial duration. Also, this would remove the confound due to the addition of the sentence, in fact, we speculated that the two learnings varies in the contiguity between stimulus and label. I.e., FL: [fribble]+"This was a .... X" Versus LF: "This is a ....X"+[fribble] introduces two different types of lags between the presentation of the label and the stimulus. We speculated that this might cause differences, we don't know how.
- Michael suggested that participants in his original experiment did only one of the two tasks, and not both. Exposition to both tasks might cause greater noise, especially in the labelPicture task where participants see 72 different fribbles. This might cause super confusion in the participants. Indeed, I found that from the folder Mike has shared with me (later on during this experiment) the number of stimuli didn't match with the number of test trials reported in the paper.

What we're going to do next: We're goint to re-do the replication! This time for real: by checking for the right amount of test trials, same fribbles used by Michael and same modality.

```r
rm(adjusted.genTask_model, adjusted.labpic_model, adjusted.piclab_model, pl, pl_violin, lp, lp_violin, 
```