

Inter-annotator Agreement vs. System Performance (F1 measure)

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1 Introduction

Abstract

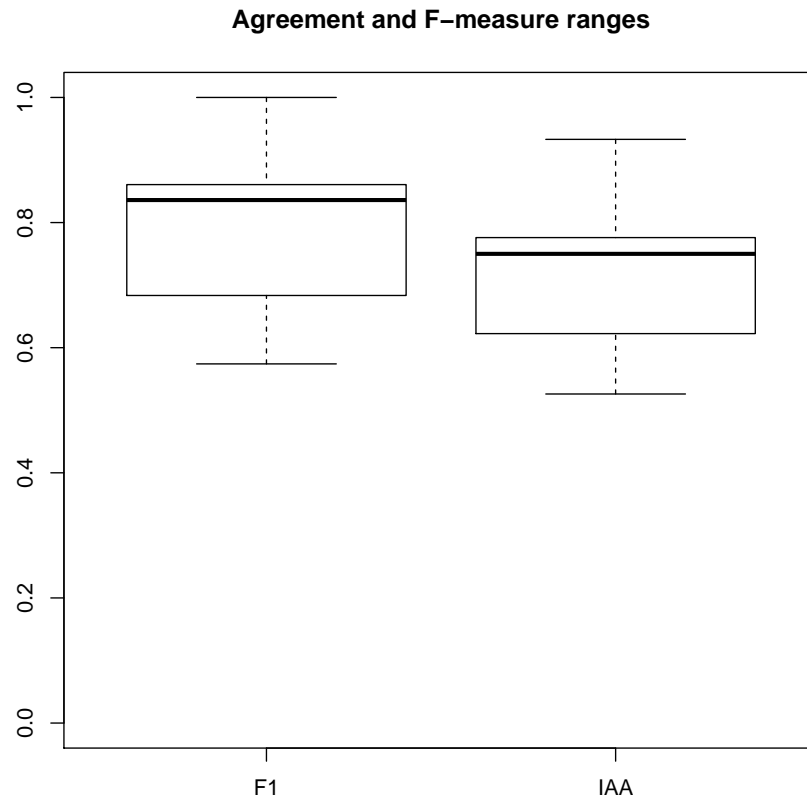
To classify texts in natural language processing, we compute the agreement between annotators: do annotators classify texts the same? It is often thought that the agreement between annotators is the upper limit on system performance: if humans cannot agree with each other about the classification more than some percentage of the time, then we do not expect a computer to do any better. We trace the logical positivist roots of the motivation for measuring inter-annotator agreement, trace the origins of the widely-held belief about the relationship between inter-annotator agreement and system performance, and present data on 6 articles that suggest that inter-annotator agreement is not in fact an upper bound, with evidence from the biomedical and general domains. Further, we found a significantly positive correlation between inter-annotator agreement and system performance.

2 IAA < System Performance (F1 measure mostly)

```
iaa_F1GthanIAA <- c(0.5535, 0.5535, 0.5535, 0.617, 0.526,
                    0.69, 0.933, 0.819, 0.779, 0.815,
                    0.798, 0.773, 0.628, 0.75, 0.75,
                    0.75, 0.75, 0.75, 0.75, 0.75)

# F-measure, except two that are precision
system_F1GthanIAA <- c(0.5741, 0.6504, 0.6649, 0.63, 0.664,
                      0.725, 0.978, 0.875, 0.824, 0.87,
                      0.857, 0.823, 0.702, 0.839, 0.839,
                      0.845, 0.8644, 1, 0.845, 0.833)
```

```
#basic distributional aspects
labels1 <- c(rep("IAA", 20), rep("F1", 20))
iaa.and.f1_F1GthanIAA <- c(iaa_F1GthanIAA, system_F1GthanIAA)
boxplot(iaa.and.f1_F1GthanIAA~labels1, ylim=c(0, 1.0), main="Agreement and F-measure ranges")
```



```
#summary statistics
summary(iaa_F1GthanIAA)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.5260  0.6252  0.7500  0.7144  0.7745  0.9330

summary(system_F1GthanIAA)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.5741  0.6927  0.8360  0.7951  0.8588  1.0000
```

```

#Shapiro-Wilk normality test
#null hypothesis = the data is normally distributed (p >0.05)
#or not if p<0.05
shapiro.test(iaa_F1GthanIAA) #not normally distributed

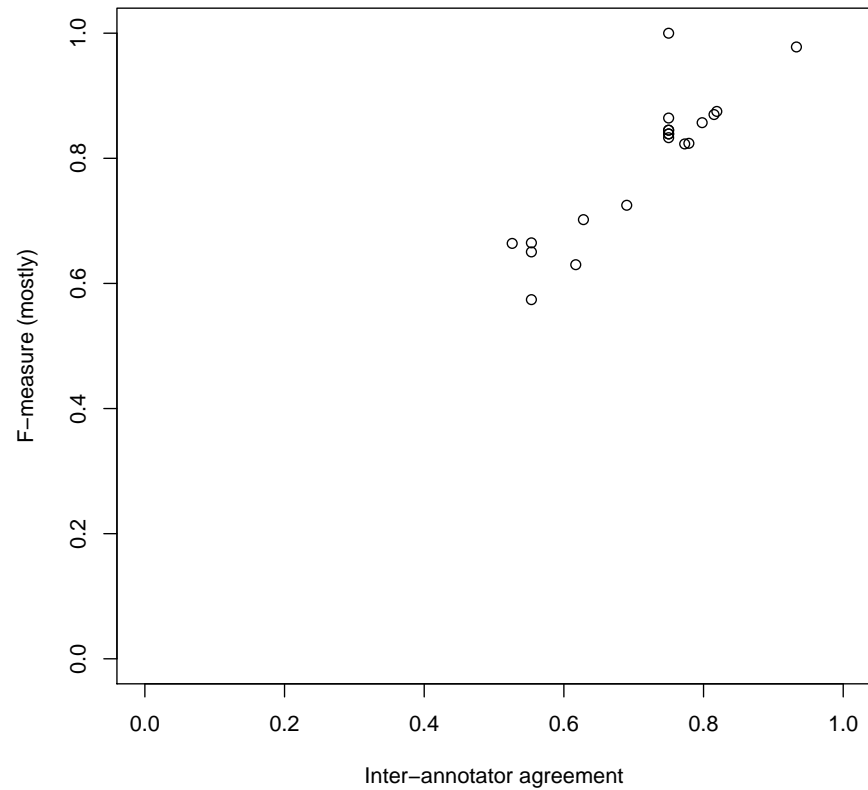
##
## Shapiro-Wilk normality test
##
## data: iaa_F1GthanIAA
## W = 0.90252, p-value = 0.046

shapiro.test(system_F1GthanIAA) #normally distributed

##
## Shapiro-Wilk normality test
##
## data: system_F1GthanIAA
## W = 0.92209, p-value = 0.1087

#plot of IAA vs F measure
plot(iaa_F1GthanIAA, system_F1GthanIAA,
      xlim=c(0,1.0), ylim=c(0,1.0),
      xlab="Inter-annotator agreement",
      ylab="F-measure (mostly)")

```



```
#Spearman's correlation
# positive = 0.8069756
cor(iaa_F1GthanIAA,system_F1GthanIAA, method ="spearman")

## [1] 0.8069756

# spearman's rank test
## positive correlation for iaa and system:
cor.test(iaa_F1GthanIAA,system_F1GthanIAA, alternative = 'greater',
         method="spearman", exact = TRUE,
         conf.level = 0.95, continuity = FALSE)

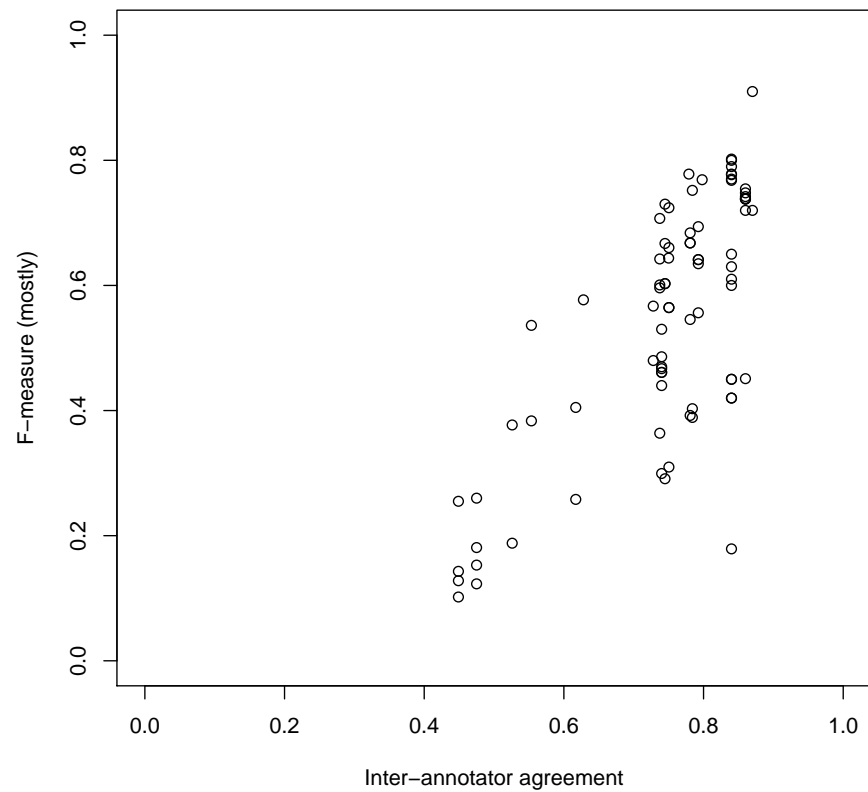
##
## Spearman's rank correlation rho
##
## data: iaa_F1GthanIAA and system_F1GthanIAA
```

```
## S = 256.72, p-value = 8.56e-06
## alternative hypothesis: true rho is greater than 0
## sample estimates:
##      rho
## 0.8069756
```

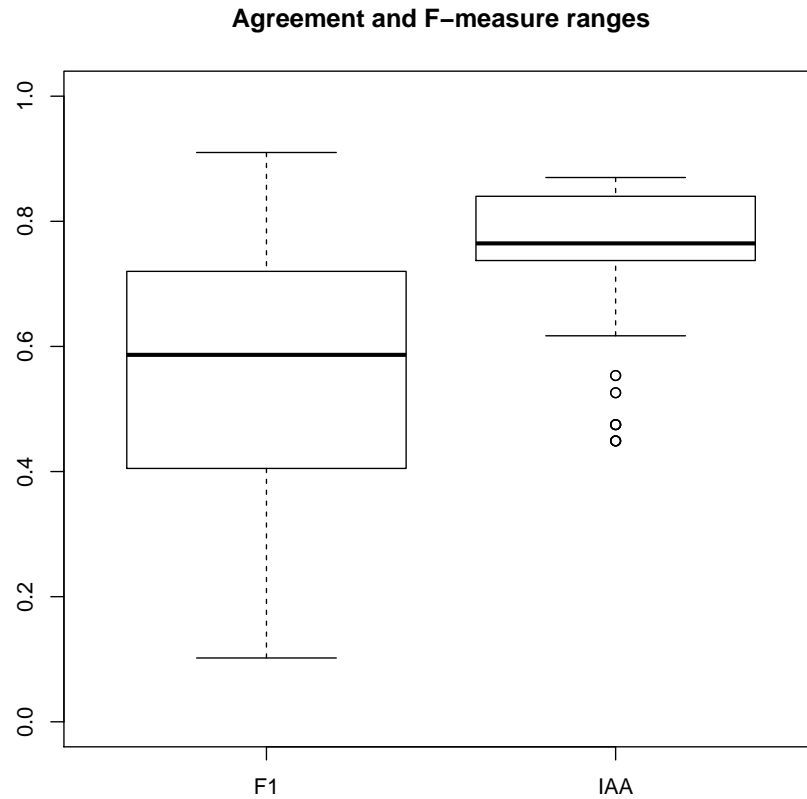
3 IAA > System Performance (F1 measure mostly)

```
IAAGThanFmeasure <- read.table(file = 'IAAGthanFmeasure.csv',
                                header = TRUE, sep=',', dec='.')

plot(IAAGThanFmeasure$IAA, IAAGThanFmeasure$System,
     xlim=c(0,1.0), ylim=c(0,1.0),
     xlab="Inter-annotator agreement",
     ylab="F-measure (mostly)")
```



```
#basic distributional aspects
labels2 <- c(rep("IAA", 82), rep("F1", 82))
iaa.and.f1_IAAGthanF1 <- c(IAAGthanFmeasure$IAA,
                           IAAGthanFmeasure$System)
boxplot(iaa.and.f1_IAAGthanF1~labels2, ylim=c(0, 1.0),
        main="Agreement and F-measure ranges")
```



```
#summary statistics
summary(IAAGThanFmeasure$IAA)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.4490  0.7373  0.7647  0.7422  0.8400  0.8700

summary(IAAGThanFmeasure$System)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.1020  0.4088  0.5865  0.5411  0.7168  0.9100

#Shapiro-Wilk normality test
#the data is normally distributed (p >0.05)
#or not if p<0.05
shapiro.test(IAAGThanFmeasure$IAA) #not normally distributed
##
```

```
## Shapiro-Wilk normality test
##
## data: IAAGThanFmeasure$IAA
## W = 0.79957, p-value = 3.384e-09

shapiro.test(IAAGThanFmeasure$System) # not normally distributed

##
## Shapiro-Wilk normality test
##
## data: IAAGThanFmeasure$System
## W = 0.94439, p-value = 0.001425

#Spearman's correlation
cor(IAAGThanFmeasure$IAA, IAAGThanFmeasure$System,
    method = "spearman")

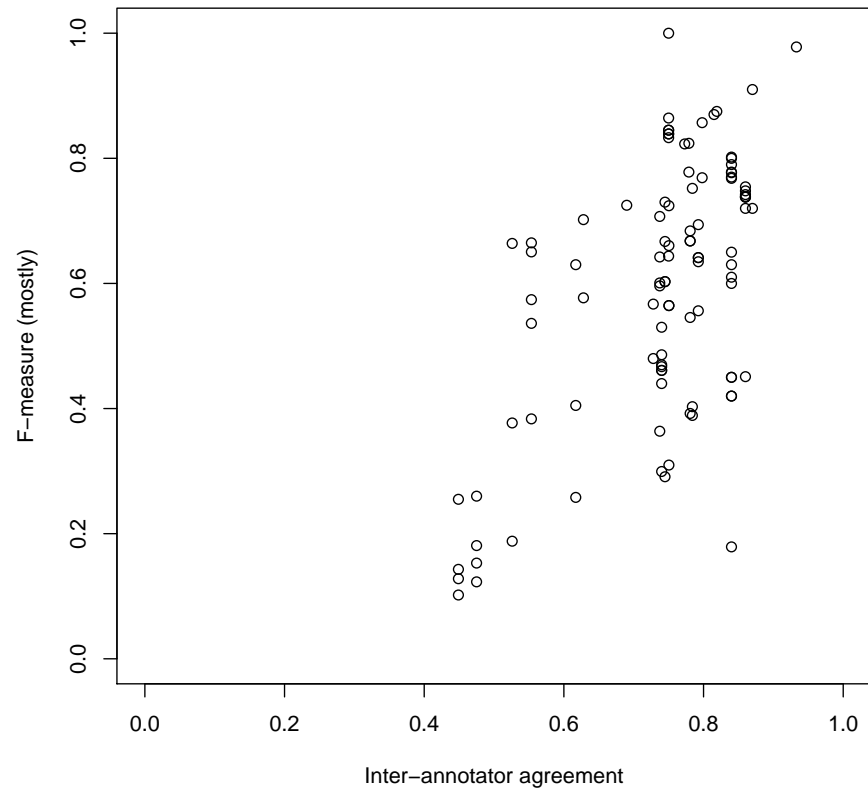
## [1] 0.6532331

# spearman's rank test
## positive correlation for iaa and system significant
cor.test(IAAGThanFmeasure$IAA, IAAGThanFmeasure$System,
    alternative = 'greater' , method="spearman", exact = TRUE,
    conf.level = 0.95, continuity = FALSE)

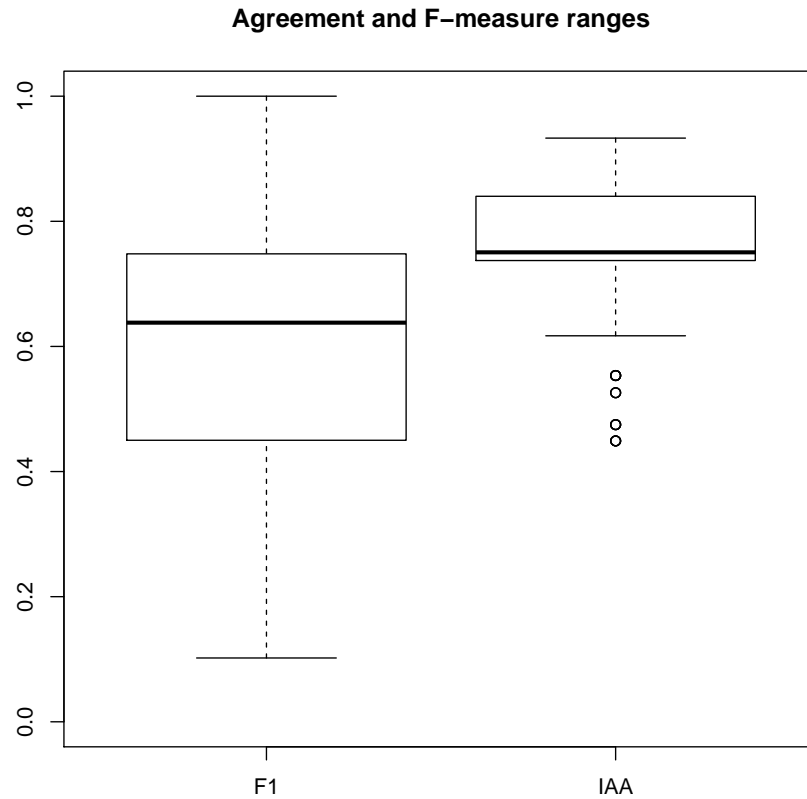
##
## Spearman's rank correlation rho
##
## data: IAAGThanFmeasure$IAA and IAAGThanFmeasure$System
## S = 31861, p-value = 1.449e-11
## alternative hypothesis: true rho is greater than 0
## sample estimates:
##      rho
## 0.6532331
```

4 All Data Combined

```
alldata <- read.table(file = 'All_IAA_Fmeasure.csv',
    header = TRUE, sep=',', dec='.')
plot(alldata$IAA, alldata$System,
    xlim=c(0,1.0), ylim=c(0,1.0),
    xlab="Inter-annotator agreement",
    ylab="F-measure (mostly)")
```

```
#basic distributional aspects
labels <- c(rep("IAA", 102), rep("F1", 102))
iaa.and.f1_alldata <- c(alldata$IAA, alldata$System)
boxplot(iaa.and.f1_alldata~labels, ylim=c(0, 1.0),
        main="Agreement and F-measure ranges")
```



```
#summary statistics
summary(alldata$IAA)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.4490 0.7373 0.7504 0.7368 0.8400 0.9330

#Shapiro-Wilk normality test
#the data is normally distributed (p >0.05)
#or not if p<0.05
shapiro.test(alldata$IAA) #not normally distributed

##
## Shapiro-Wilk normality test
##
## data:  alldata$IAA
## W = 0.84755, p-value = 7.518e-09
```

```

shapiro.test(alldata$System) #not normally distributed

##
## Shapiro-Wilk normality test
##
## data:  alldata$System
## W = 0.95872, p-value = 0.00289

#Spearman's correlation
cor(alldata$IAA, alldata$System, method="spearman")

## [1] 0.5126484

# spearman's rank test
## positive correlation for iaa and system significant
cor.test(alldata$IAA, alldata$System,
         alternative = 'greater' , method="spearman", exact = TRUE,
         conf.level = 0.95, continuity = FALSE)

##
## Spearman's rank correlation rho
##
## data:  alldata$IAA and alldata$System
## S = 86189, p-value = 1.81e-08
## alternative hypothesis: true rho is greater than 0
## sample estimates:
##      rho
## 0.5126484

```