Corispermum spp

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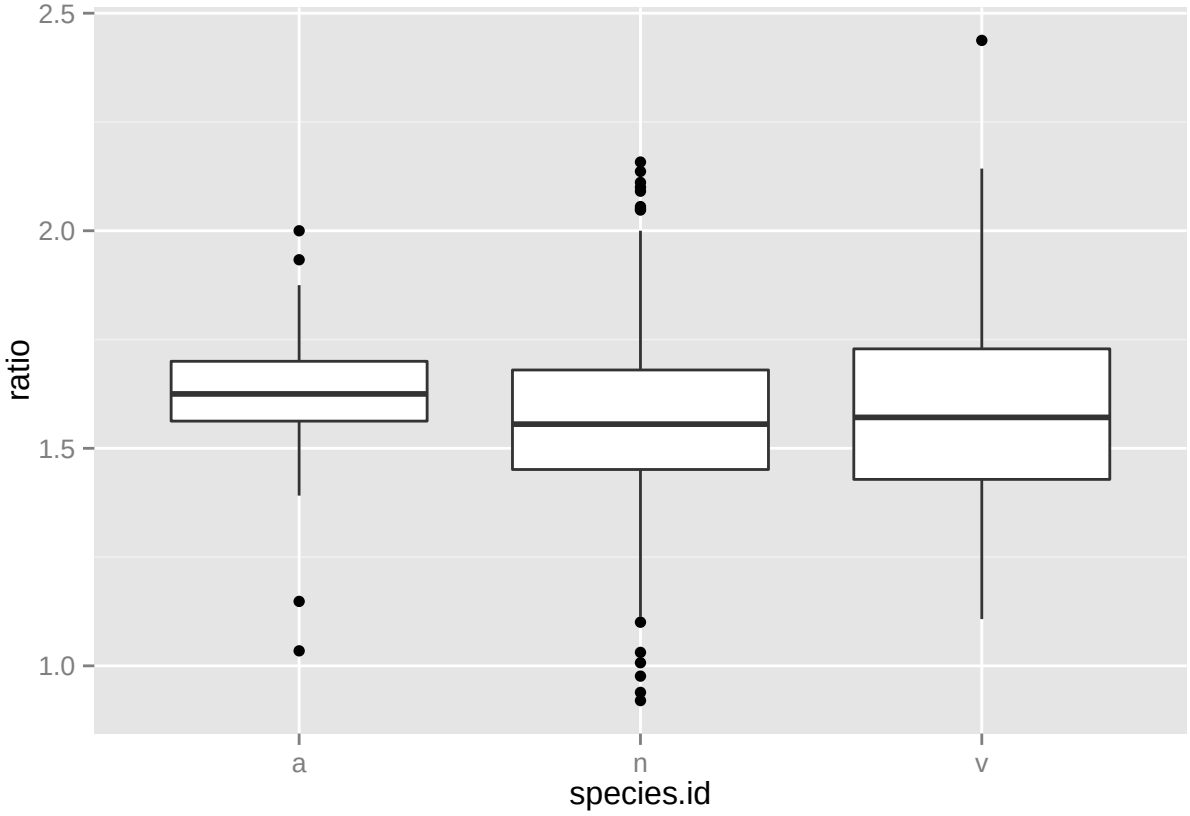
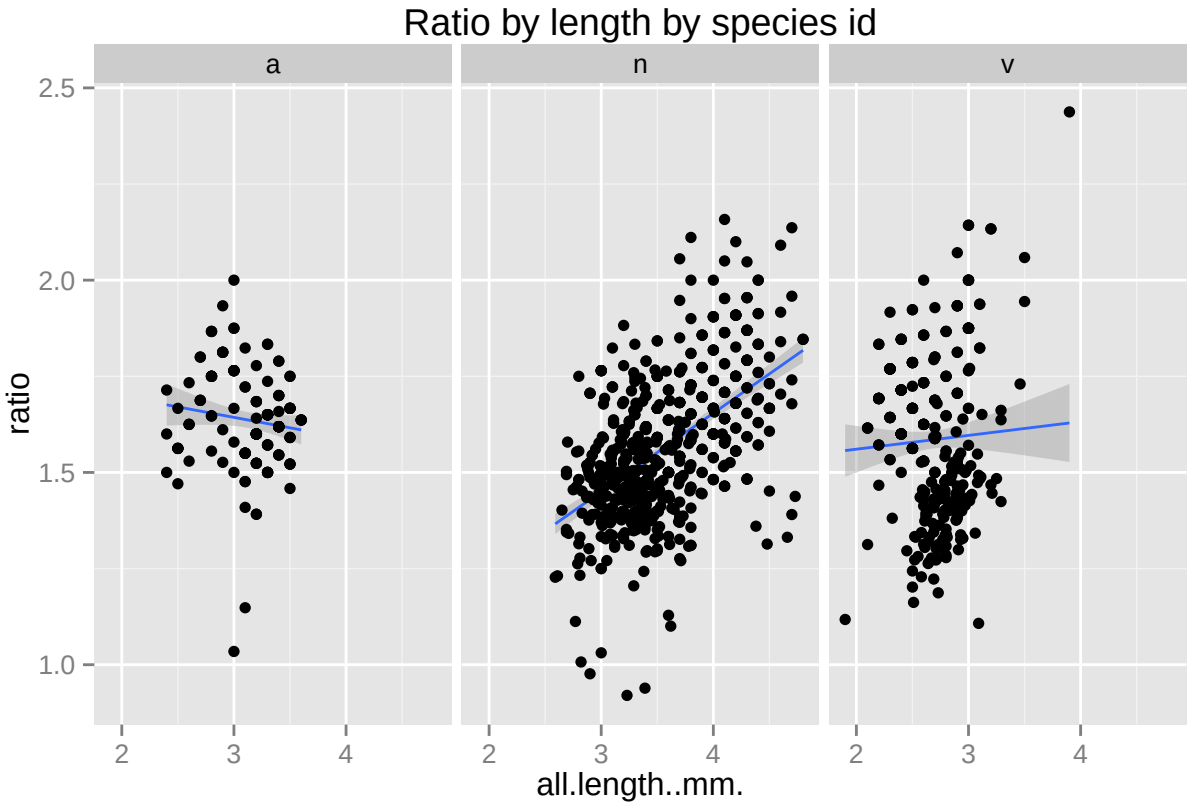
```
library(ggplot2)
```

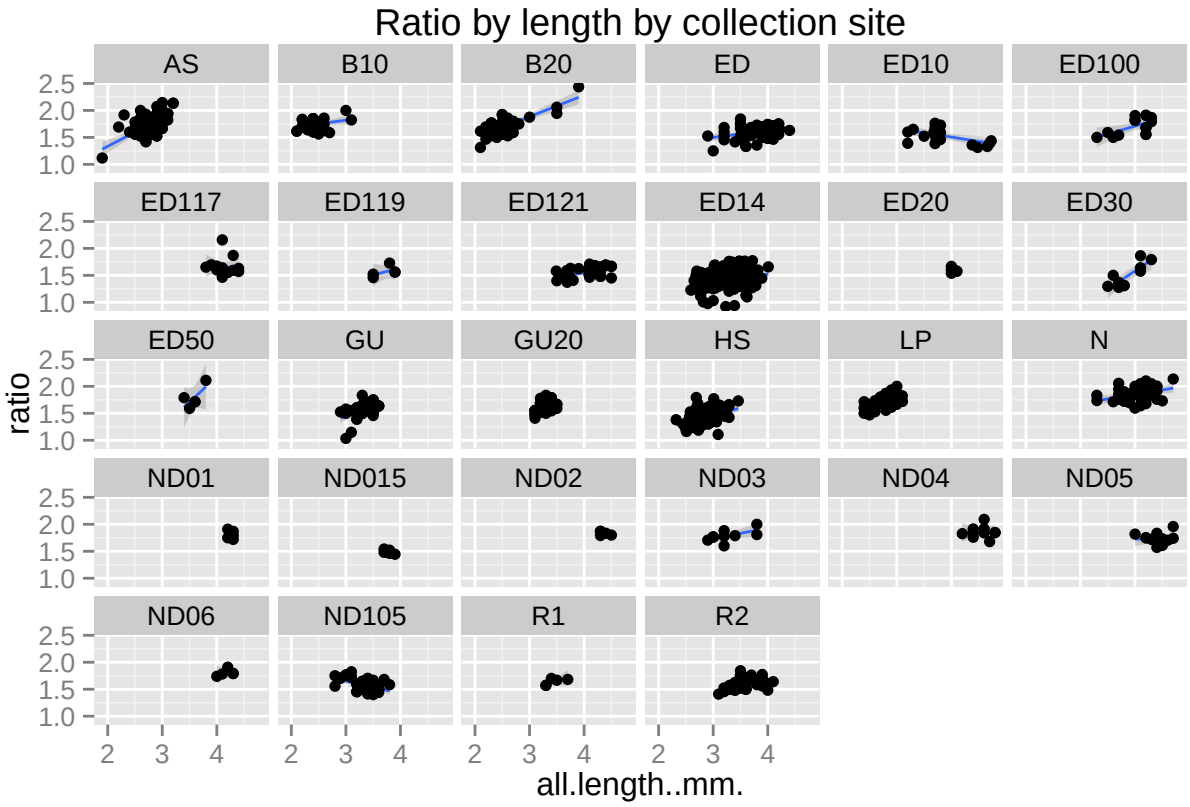
```
cori <- read.csv(path.expand("Q:/Research/All_Projects_by_Species/Corispermum_navicula/2015.data.update/
head(cori)
```

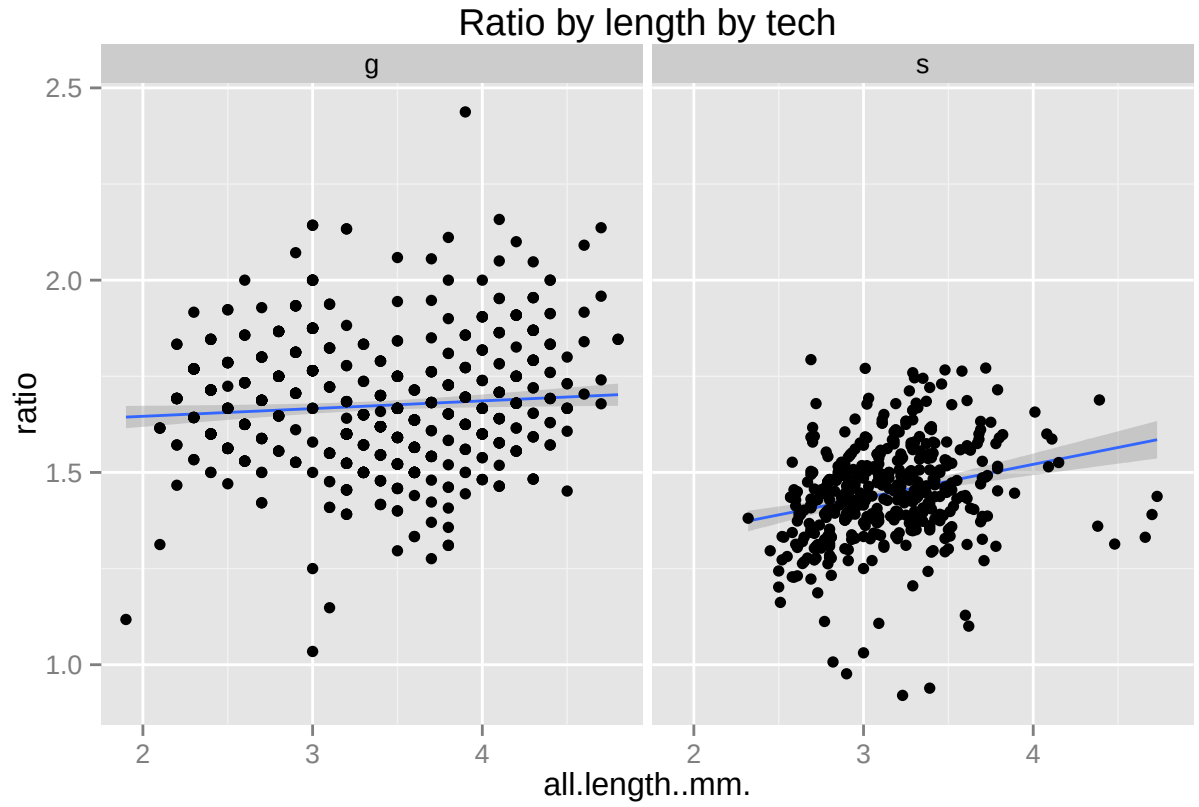
```
##   year tech species.id morph coll.site all.populations all.individual
## 1 2009    g          n     a        ED               E              1
## 2 2009    g          n     a        ED               E              1
## 3 2009    g          n     a        ED               E              1
## 4 2009    g          n     a        ED               E              1
## 5 2009    g          n     a        ED               E              1
## 6 2009    g          n     a        ED               E              2
##   all.fruit all.length..mm. all.width..mm. all.wing..mm.
## 1         1             4.1            2.4           0.3
## 2         2             3.6            2.4           0.3
## 3         3             3.8            2.3           0.2
## 4         4             4.0            2.4           0.3
## 5         5             3.9            2.4           0.2
## 6         1             3.7            2.2           0.3
```

Fruit length to width ratio


2.5
2.0
1.5
1.0
ratio
a
n
v
species.id

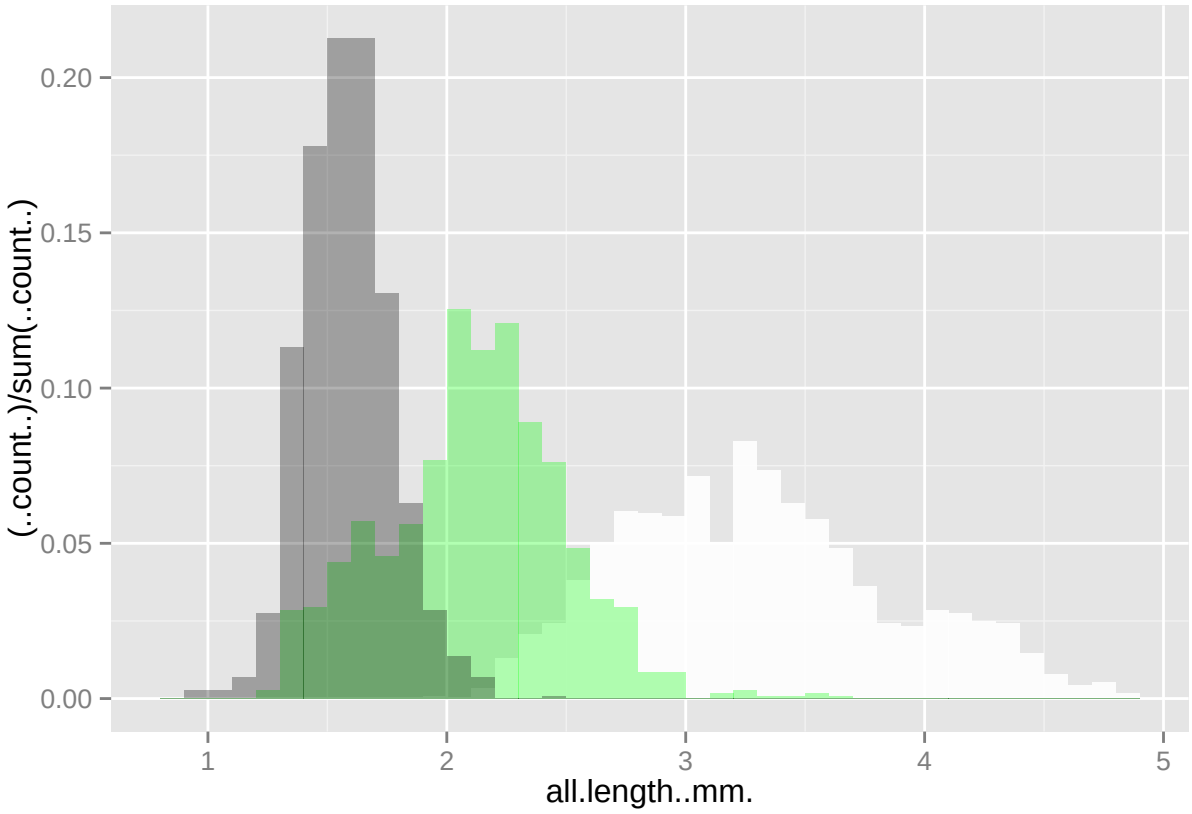

Ratio by length by species id
a
n
v
ratio
2.5
2.0
1.5
1.0
2
3
4
all.length..mm.


Ratio by length by collection site
AS
B10
B20
ED
ED10
ED100
ED117
ED119
ED121
ED14
ED20
ED30
ED50
GU
GU20
HS
LP
N
ND01
ND015
ND02
ND03
ND04
ND05
ND06
ND105
R1
R2
ratio
2.5
2.0
1.5
1.0
2
3
4
all.length..mm.



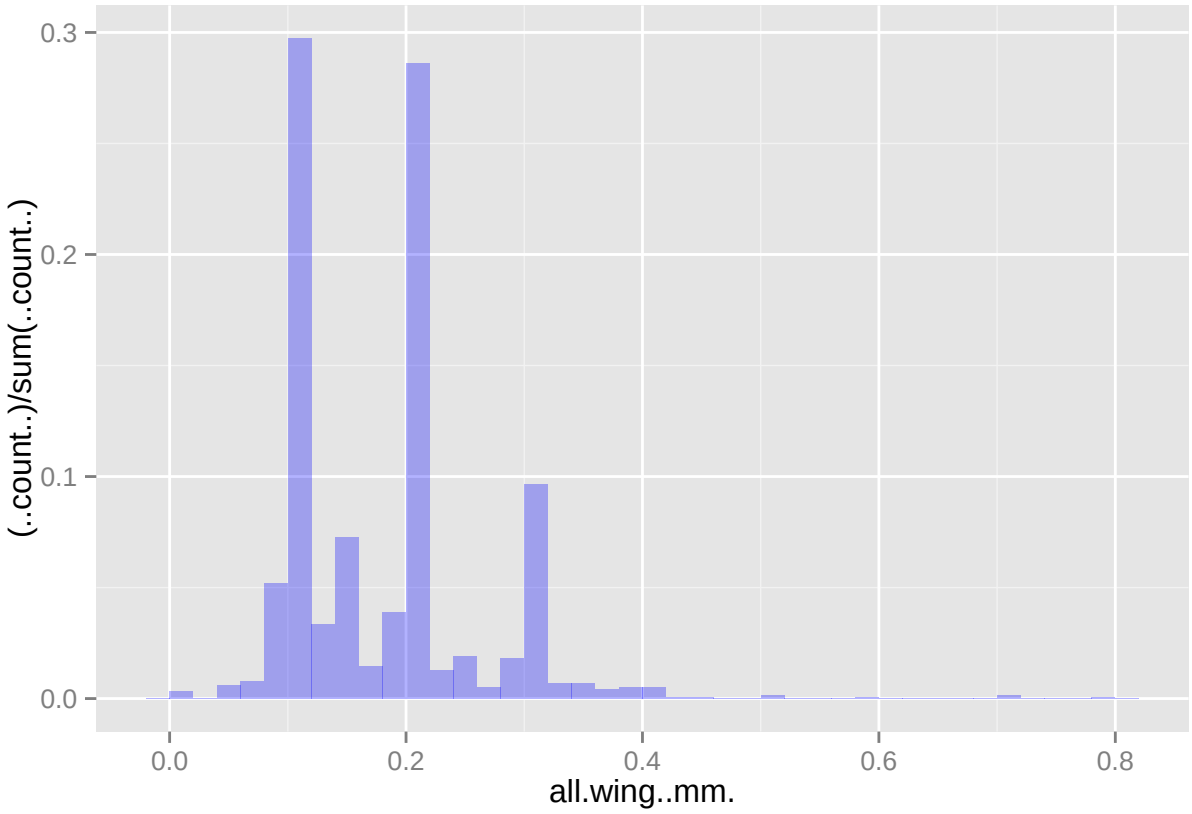
Distribution of data

```
ggplot(cori) +
  geom_histogram(aes(x = all.length..mm., y=(..count..)/sum(..count..)),
                       alpha=0.9, fill ="white",binwidth=.1,position="dodge") +
  geom_histogram(aes(x = all.width..mm., y=(..count..)/sum(..count..)),
                       alpha=0.3,, fill ="green",binwidth=.1,position="dodge") +
  geom_histogram(aes(x = ratio, y=(..count..)/sum(..count..)),
                       alpha=0.3,, fill ="black",binwidth=.1,position="dodge")
```

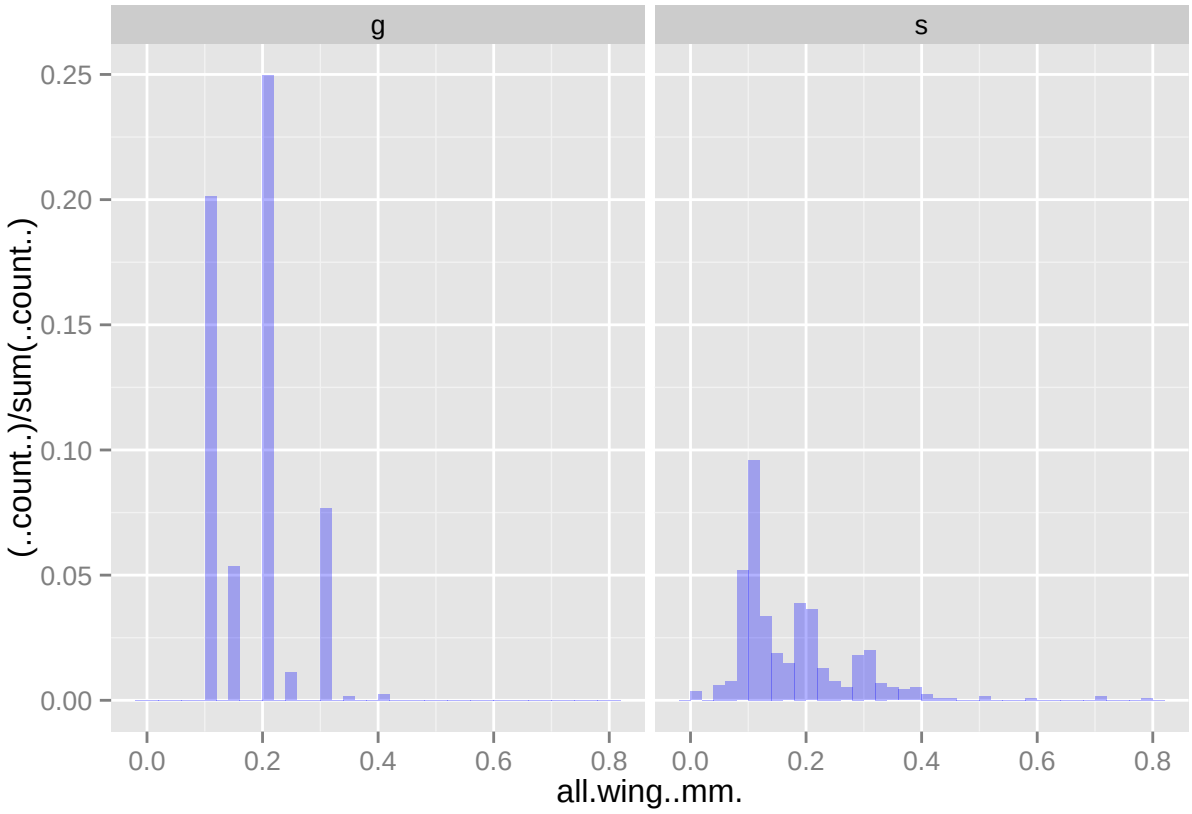


Wing is right skewed when taken all together. Not if by species. morph is missing many values

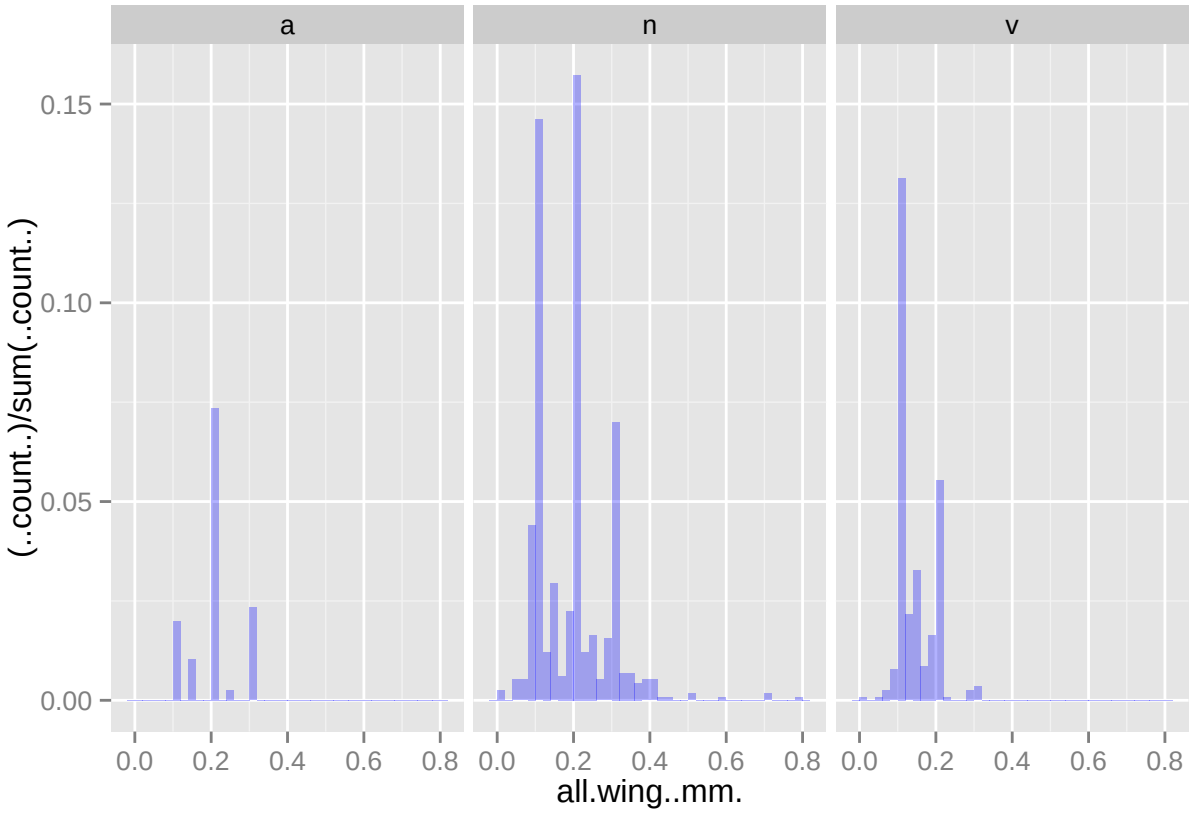
```
ggplot(cori) +
    geom_histogram(aes(x = all.wing..mm., y=(..count..)/sum(..count..)),
                        alpha=0.3,, fill ="blue",binwidth=.02,position="dodge")
```




```
ggplot(cori) +
    geom_histogram(aes(x = all.wing..mm., y=(..count..)/sum(..count..)),
                       alpha=0.3,, fill ="blue",binwidth=.02,position="dodge") +
    facet_wrap(~tech)
```




```
ggplot(cori) +
    geom_histogram(aes(x = all.wing..mm., y=(..count..)/sum(..count..)),
                       alpha=0.3,, fill ="blue",binwidth=.02,position="dodge") +
    facet_wrap(~species.id)
```


a
n
v
0.15
0.10
0.05
0.00
(..count..)/sum(..count..)
0.0
0.2
0.4
0.6
0.8
all.wing..mm.