

Foi utilizada a semente 369; $m = 950$; $\mu = 9.11$; $\sigma = 2.31$; $\mu_C = 15$; $\epsilon = 0.3$; $(1 - \alpha) = 0.99$.

```
library(ggplot2)
```

```
set.seed(369)
```

```
maNC=c() #Store non-contaminated amplitude averages
maC=c() #Store contaminated amplitude averages
nv=c() #Store n values
```

```
for(i in 1:50)
```

```
{
  ampNC=c() #Store non-contaminated amplitudes
  ampC=c() #Store contaminated amplitudes
  n=i*100
```

```
  nv<-append(nv, n)
```

```
  contaminationN=0.3*n #Number of contaminated observations
```

```
  for(j in 1:950)
```

```
  {
    amostraC<-rnorm(contaminationN, 15, 2.31) #Generate contaminated sample
```

```
    amostra<-rnorm(n-contaminationN, 9.11, 2.31) #Generate 70% of non-contaminated sample
```

```
    amostraC=append(amostraC, amostra) #Finish contaminated sample
```

```
    cfi = t.test(amostraC, conf.level=0.99)$"conf.int" #Get contaminated confidence level
```

```
    ampC<-append(ampC, cfi[2]-cfi[1]) #Get contaminated amplitude
```

```
    amostra=append(amostra, rnorm(contaminationN, 9.11, 2.31)) #Finish non-contaminated sample
```

```
    cfi = t.test(amostra, conf.level=0.99)$"conf.int" #Get non-contaminated confidence level
```

```
    ampNC<-append(ampNC, cfi[2]-cfi[1]) #Get non-contaminated amplitude
```

```
  }
```

```
  maNC<-append(maNC, mean(ampNC))
```

```
  maC<-append(maC, mean(ampC))
```

```
}
```

```
data<-data.frame(nv, maNC, maC)
```

```
#Plot
```

```
ggplot(data, aes())+
```

```
  geom_point(aes(nv, maNC, color="Nao contaminada"), size=1.5)+
```

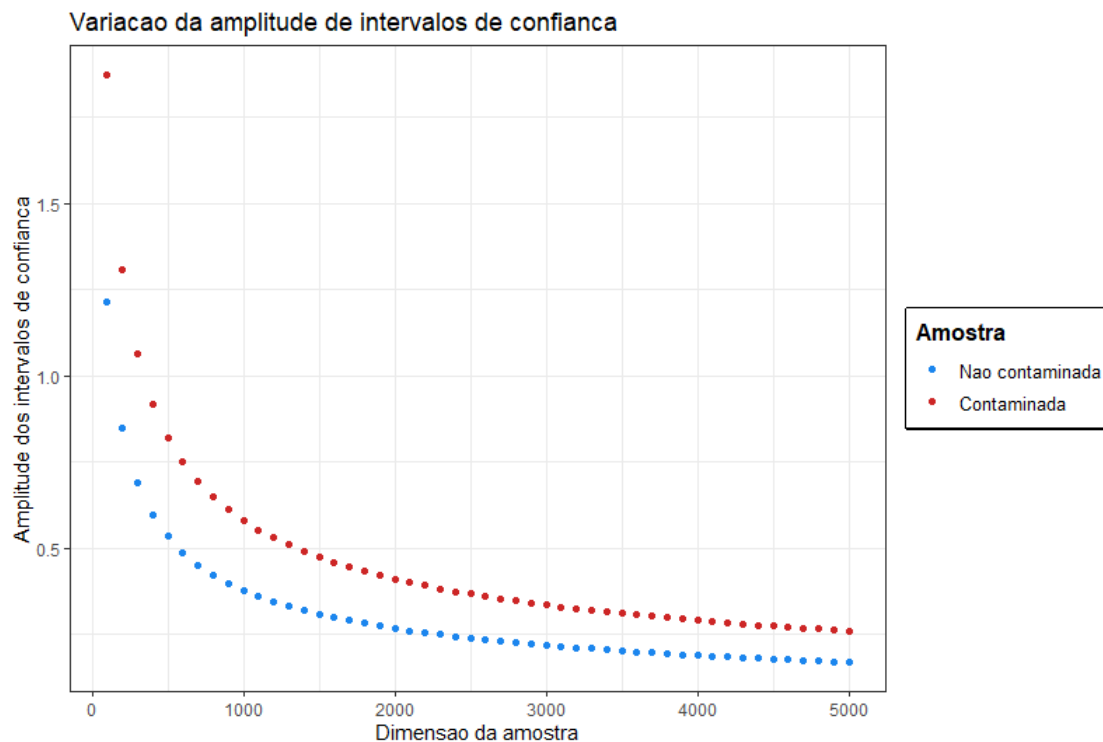
```
  geom_point(aes(nv, maC, color="Contaminada"), size=1.5)+
```

```
  scale_color_manual(name="Amostra", values=c("Nao contaminada"="dodgerblue2", "Contaminada"="firebrick3"))+
```

```
  labs(title = "Variacao da amplitude de intervalos de confianca", x = "Dimensao da amostra", y = "Amplitude dos intervalos de confianca")+
```

```
  theme_bw()+
```

```
  theme(legend.position="right", legend.title=element_text(face="bold", size=12), legend.text=element_text(size = 10), legend.box.background=element_rect(
    color="black", size=1.2))
```



Reiterando a conclusão da pergunta 9, o aumento da dimensão da amostra diminui a amplitude dos intervalos de confiança, sendo que esta diminui com $1/\sqrt{n}$.

A contaminação da amostra torna os dados menos fiáveis e, tal como esperado, esta contaminação torna a amplitude dos intervalos de confiança maior, uma vez que a contaminação torna os dados mais dispersos.