

## Short\_Demo

```
library(rnaGinesis)
library(ggplot2)
library(reshape)
mu <- rnaGinesis::mu
A <- rnaGinesis::A
```

### a reasonably normal settings, modeling 4 tissues

```
simresult.a <- simulate_and_test(A_tumor = A[1:100,1:100],
                                mu_tumor = mu[1:100],
                                num.sim   = 20,
                                Samplesize = 100,
                                scaleFactor = rep(30, 3),
                                d.params   = c("Tumor"   = .3,
                                                "Stromal"  = .5,
                                                "Immune"   = .1,
                                                "Normal"   = .1),
                                noise_setting = 1.5,
                                seed       = 1234 )
```

### high noise

```
simresult.b <- simulate_and_test(A_tumor = A[1:100,1:100],
                                mu_tumor = mu[1:100],
                                num.sim   = 20,
                                Samplesize = 100,
                                scaleFactor = rep(30, 3),
                                d.params   = c("Tumor"   = .3,
                                                "Stromal"  = .5,
                                                "Immune"   = .1,
                                                "Normal"   = .1),
                                noise_setting = 10,
                                seed       = 1234 )
```

```
x.a <- melt(simresult.a[[1]])
x.b <- melt(simresult.b[[1]])
x.a$condition <- "normal noise"
x.b$condition <- "high noise"

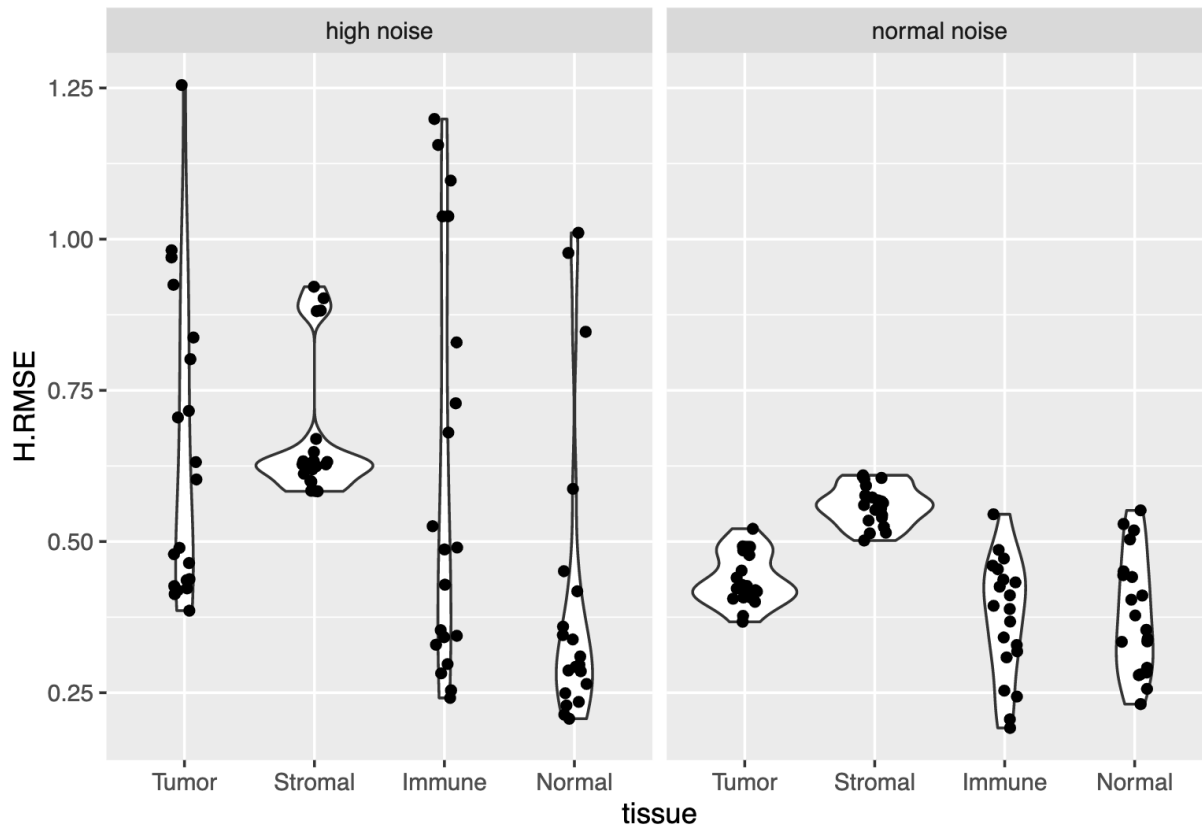
mydf <- rbind(x.a,x.b)
mydf <- mydf[,-1]
names(mydf) <- c("tissue", "H.RMSE", "condition")

p <- ggplot(data = mydf,
```

```

aes(y = H.RMSE,
    x= tissue))
p <- p + geom_violin()
p <- p + geom_jitter(width = 0.1)
p <- p + facet_grid(~condition)
print(p)

```



```

x.a <- melt(simresult.a[[4]])
x.b <- melt(simresult.b[[4]])
x.a$condition <- "normal noise"
x.b$condition <- "high noise"

mydf <- rbind(x.a,x.b)
mydf <- mydf[,-1]
names(mydf) <- c("tissue", "w_cos_dist", "condition")

p <- ggplot(data = mydf,
            aes(y = w_cos_dist,
                x= tissue))
p <- p + geom_violin()
p <- p + geom_jitter(width = 0.1)
p <- p + facet_grid(~condition)
print(p)

```

