

Ich_thresholds

Here we answer the question of the reviewer what if we change the threshold for Ich First we load the libraries

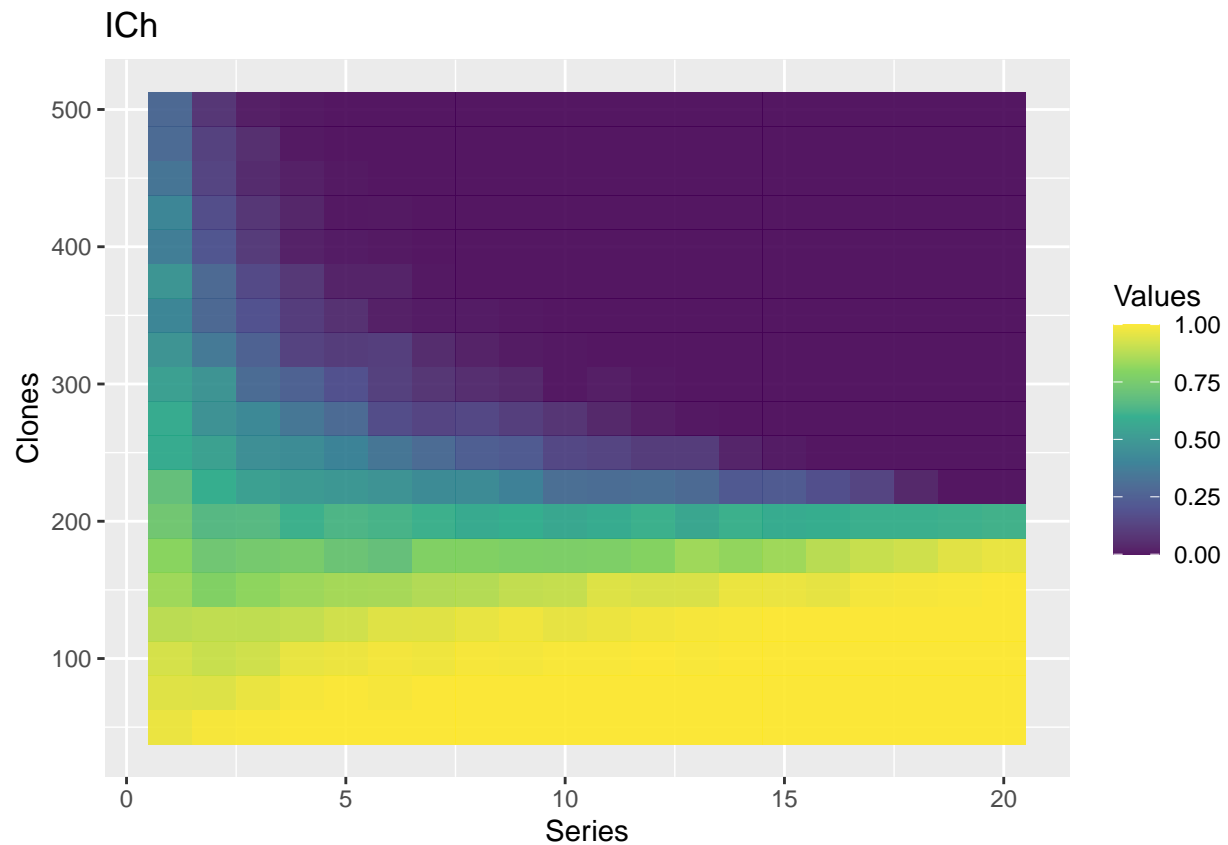
```
library(RColorBrewer) #for custom colors
library(reshape2) #for melt function
library(ggplot2) #for ggplot type heatmap
```

Since we will repeat calculations for Ich at several conditions we make the first part as a function

```
make_series<-function(start_n, end_n, step_n, series, thresh_Ich){
  Ich_series=c()
  for (clones in seq(start_n,end_n, step_n)){
    Ich=c()
    for (i in 1:series){
      values=rbeta(clones,i,series+1-i)
      fractions<-values/sum(values)
      selected<-fractions[fractions>=thresh_Ich]
      Ich=append(Ich,sum(selected))
    }
    Ich_series=cbind(Ich_series,Ich)
  }
  colnames(Ich_series)<-seq(start_n, end_n, step_n) #make proper col names
  return(Ich_series)
}
```

Now we can repeatedly use this function and look at the plots how they change

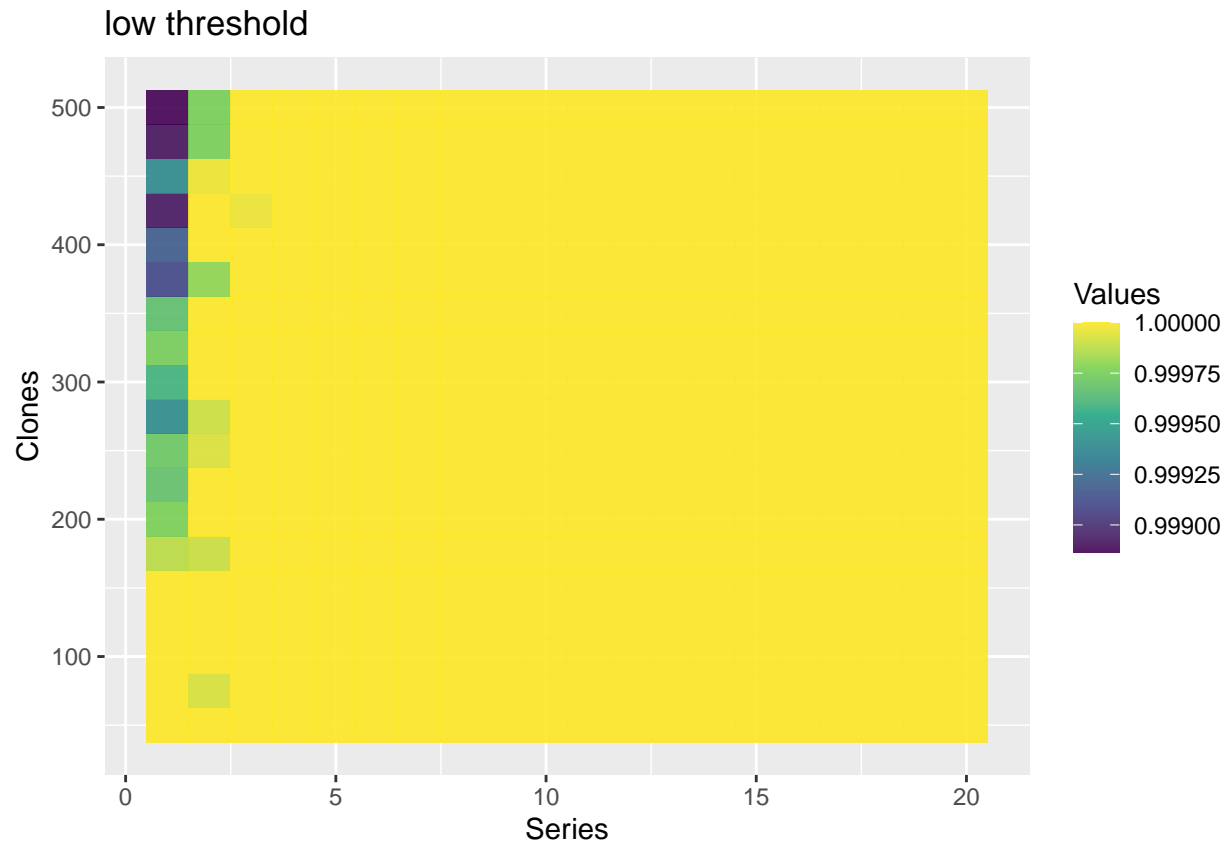
```
#define color palette for the heatmap
coul <- colorRampPalette(brewer.pal(8, "YlGnBu"))(20)
#generate data for the heatmap
#first a standard threshold used throuout the manuscript
Ich_series<-make_series(50,500,25,20, 0.005)
melted<-melt(Ich_series) #or any other series down the script
colnames(melted)<-c("Series","Clones","Values")
#note: theme_void() controls appearance of the scale values
ggplot(melted, aes(Series, Clones, fill=Values))+
  geom_tile()+
  labs(title="Ich", x="Series", y="Clones")+
  scale_fill_viridis_c(alpha=0.9) #+
```



```
# theme_void()
```

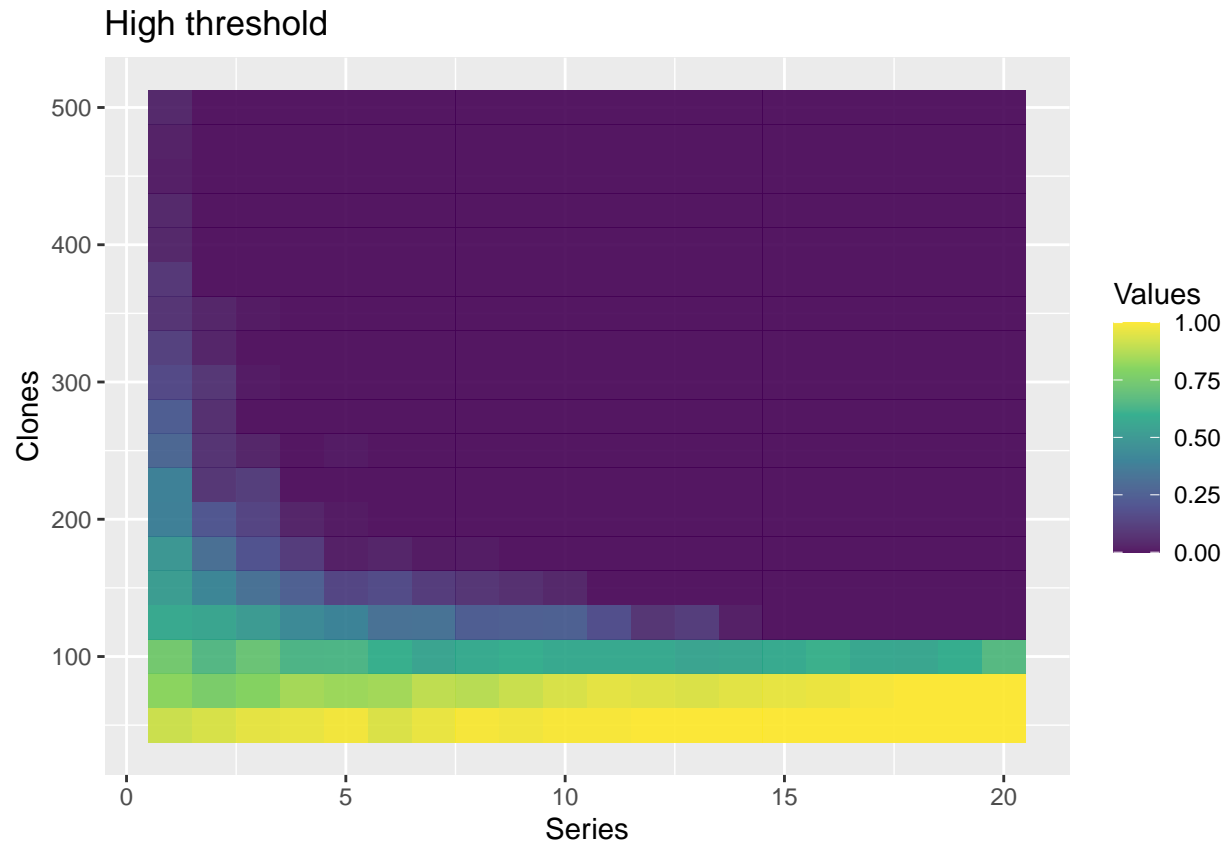
Note that the last line `theme_void()` controls appearance of the scales. If you set it on then the figure will be exactly like in the manuscript. What if we decrease the threshold?

```
Ich_series<-make_series(50,500,25,20, 0.0001)
melted<-melt(Ich_series) #or any other series down the script
colnames(melted)<-c("Series","Clones","Values")
ggplot(melted, aes(Series, Clones, fill=Values))+
  geom_tile()+
  labs(title="low threshold", x="Series", y="Clones")+
  scale_fill_viridis_c(alpha=0.9)
```



As expected the Ich value is shifted to its maximum because nearly all clones are counted. What if we increase the threshold?

```
Ich_series<-make_series(50,500,25,20, 0.01)
melted<-melt(Ich_series) #or any other series down the script
colnames(melted)<-c("Series","Clones","Values")
ggplot(melted, aes(Series, Clones, fill=Values))+
  geom_tile()+
  labs(title="High threshold", x="Series", y="Clones")+
  scale_fill_viridis_c(alpha=0.9)#+
```



This causes the opposite effect. Very few clones are counted and Ich value is mostly at zero.