

# XeonPhi\_logging

*SPONucleomics Core*

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## Test assembly results

A >6h assembly job was submitted to the thinkmate from IrysView and data collected at 30sec intervals on the Thinkmate server using a custom bash script and the basic command:

```
micsmc -c ${mic} -t ${mic} -f ${mic} | egrep "Device Utilization:Cpu Temp:Memory Temp:Total Power:"
```

## Xeon cards metrics during mapping

Because sampling leads to a lot of data scattering, smoothing was applied to only retain the average values over time. Each factor was used separately to build a plot for all 6 Xeon cards.

```
# move where the data is
path <-normalizePath("~/Downloads")
opts_knit$set(root.dir = path)
setwd(path)

# read log data in R
log <- read.delim("Xeon_usage_1458047940.log", sep = "\t", dec = ".",
                  header=TRUE, comment.char = "#", stringsAsFactors=FALSE)

colnames(log) <- c("logtime", "mic", "cpu.user", "cpuT", "memT", "totW" )

# subtract initial timestamp t0
init <- log[1,1]

# add column with spent time in hours
log$time <- (log$logtime-init)/3600

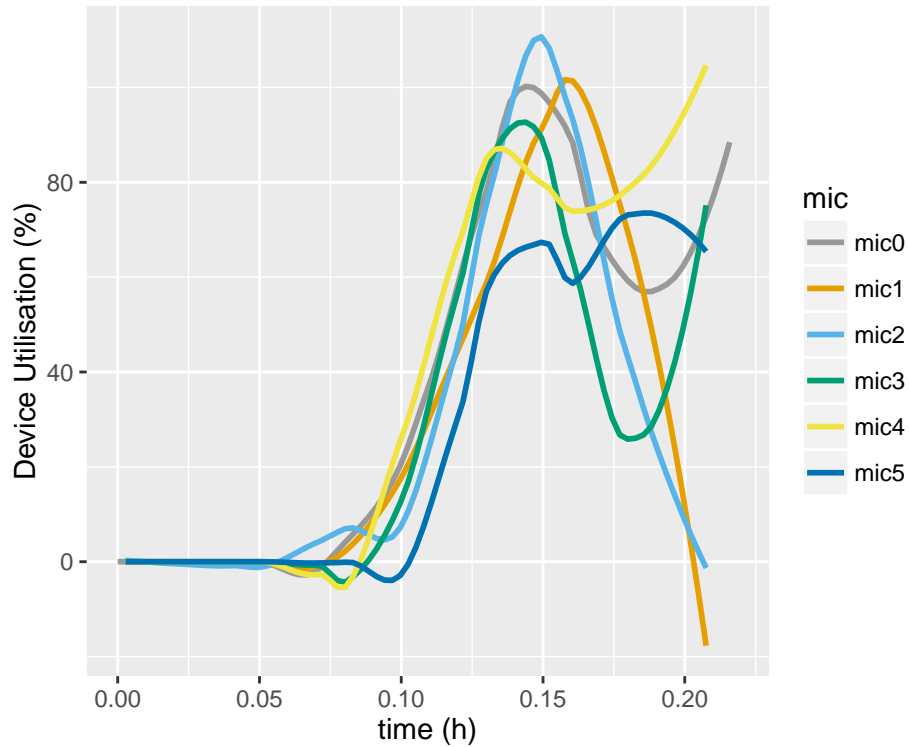
# keep only first 6.5h for that experiment
log <- subset(log, time<6.5)

# inspect
head(log)
```

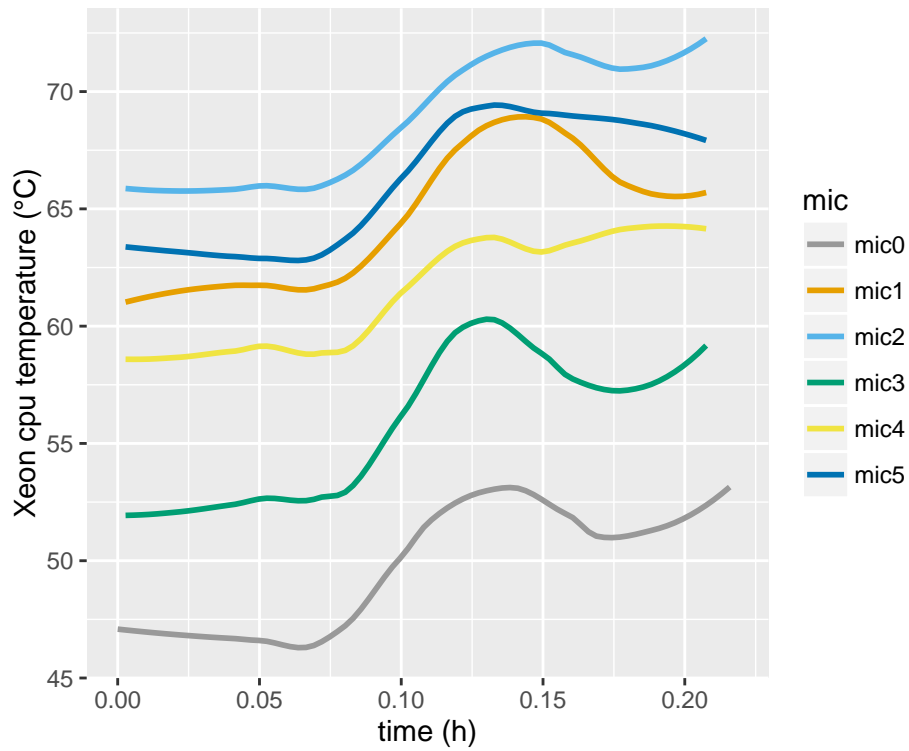
```
##      logtime  mic cpu.user  cpuT memT totW      time
## 1 1458047940 mic0      0   47   36  103 0.0000000000
## 2 1458047941 mic1      0   61   48  110 0.0002777778
## 3 1458047942 mic2      0   66   52  126 0.0005555556
## 4 1458047943 mic3      0   52   39  108 0.0008333333
## 5 1458047944 mic4      0   59   42  107 0.0011111111
## 6 1458047945 mic5      0   63   47  106 0.0013888889
```

```
# define a color-blind friendly palette
cbPalette <- c("#999999", "#E69F00", "#56B4E9", "#009E73",
               "#F0E442", "#0072B2", "#D55E00", "#CC79A7")
```

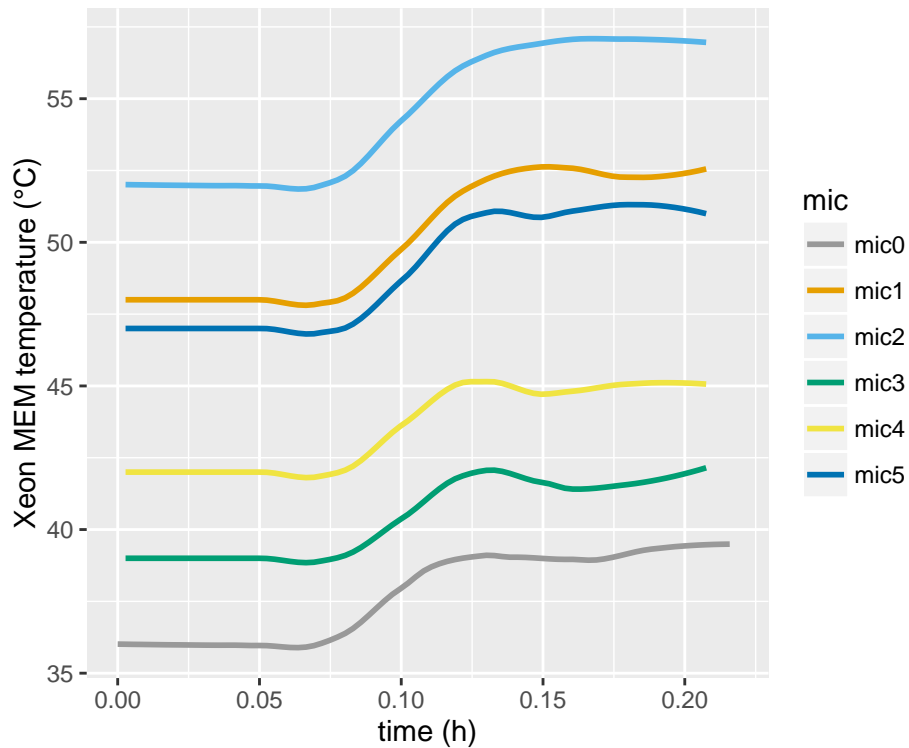
```
# plot cpu%
ggplot(log, aes(x=time, y=cpu.user, color=mic, group=mic)) +
  stat_smooth(size=1, method="loess", level=0.95, fullrange=TRUE, se=FALSE, span = 0.5) +
  ylab("Device Utilisation (%)") + xlab("time (h)") +
  scale_colour_manual(values=cbPalette)
```



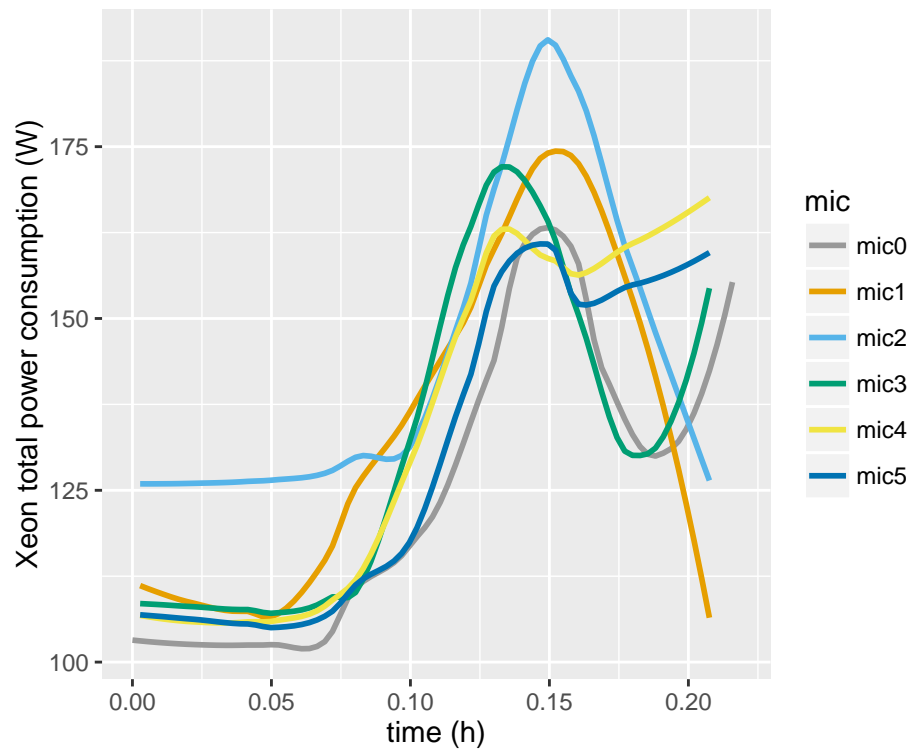
```
# plot cpuT
ggplot(log, aes(x=time, y=cpuT, color=mic, group=mic)) +
  stat_smooth(size=1, method="loess", level=0.95, fullrange=TRUE, se=FALSE, span = 0.5) +
  ylab("Xeon cpu temperature (°C)") + xlab("time (h)") +
  scale_colour_manual(values=cbPalette)
```



```
# plot memT
ggplot(log, aes(x=time, y=memT, color=mic, group=mic)) +
  stat_smooth(size=1, method="loess", level=0.95, fullrange=TRUE, se=FALSE, span = 0.5) +
  ylab("Xeon MEM temperature (°C)") + xlab("time (h)") +
  scale_colour_manual(values=cbPalette)
```



```
# plot totW
ggplot(log, aes(x=time, y=totW, color=mic, group=mic)) +
  stat_smooth(size=1, method="loess", level=0.95, fullrange=TRUE, se=FALSE, span = 0.5) +
  ylab("Xeon total power consumption (W)") + xlab("time (h)") +
  scale_colour_manual(values=cbPalette)
```



more at <http://www.nucleomics.be>