MSA Heatmap

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```r
library(bio3d)

alignment <- read.fasta("new_msa_alignment.clw.fst")

seqidentity(alignment)
```

```
             Homo_sapiens Stoat Brown_bear Snow_leopard Canada_lynx Leopard
Homo_sapiens        1.000 0.951      0.954        0.966       0.966   0.966
Stoat               0.951 1.000      0.966        0.968       0.968   0.968
Brown_bear          0.954 0.966      1.000        0.983       0.983   0.983
Snow_leopard        0.966 0.968      0.983        1.000       1.000   1.000
Canada_lynx         0.966 0.968      0.983        1.000       1.000   1.000
Leopard             0.966 0.968      0.983        1.000       1.000   1.000
Jaguarundi          0.966 0.968      0.983        1.000       1.000   1.000
             Jaguarundi
Homo_sapiens      0.966
Stoat             0.968
Brown_bear        0.983
Snow_leopard      1.000
Canada_lynx       1.000
Leopard           1.000
Jaguarundi        1.000
```

```r
identity_matrix <- seqidentity(alignment)

heatmap(identity_matrix, Rowv = NA, Colv = NA, scale = "none", main = "Sequence Identity H
```

Sequence Identity Heatmap