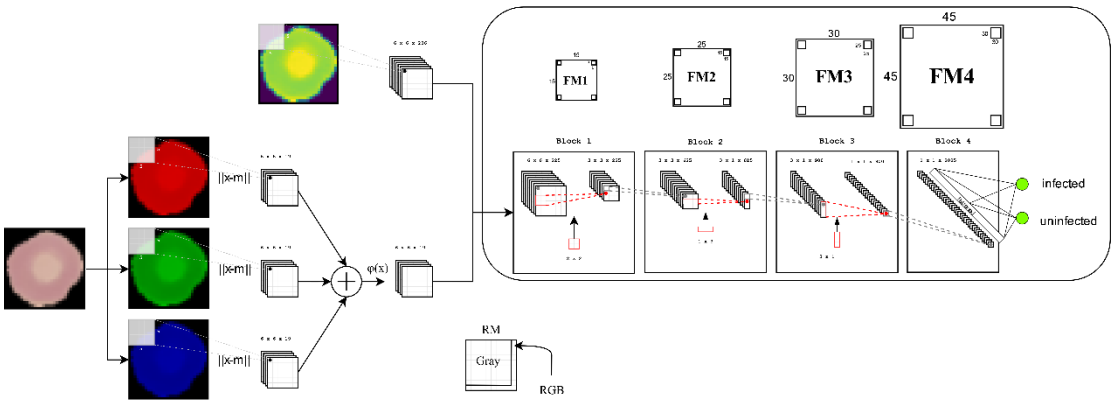
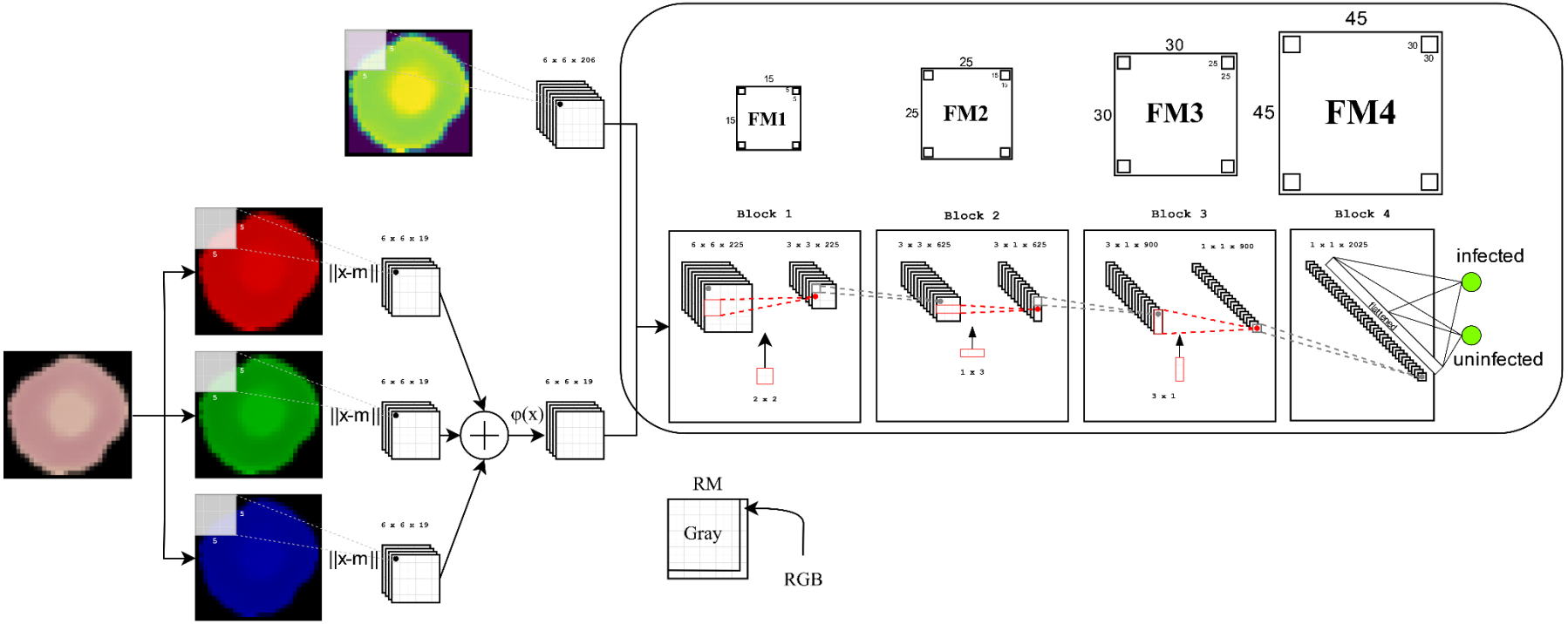
Malaria Analysis

```
model (
   (layer1): (
      (0): RBFConv2d(n_filters=225, kernel size=(5, 5))
      (1): cReLU(bias=0.4)
      (2): SFM(filter=(2, 2), alpha=0.9)
   )
   (layer2): (
      (0): RBFConv2d(n_filters=625, kernel size=(15, 15))
      (1): cReLU(bias=0.1)
      (2): SFM(filter=(1, 3), alpha=0.9)
   )
   (layer3): (
      (0): RBFConv2d(n_filters=900, kernel size=(25, 25))
      (1): cReLU(bias=0.01)
      (2): SFM(filter=(3, 1), alpha=0.9)
   )
   (layer4): (
      (0): RBFConv2d(n_filters=2025, kernel size=(30, 30))
      (1): cReLU(bias=0.01)
   )
   (fc1): Linear(in_features=2025, out_features=2, bias=True)
   (softmax): Softmax(dim=-1)
)
```

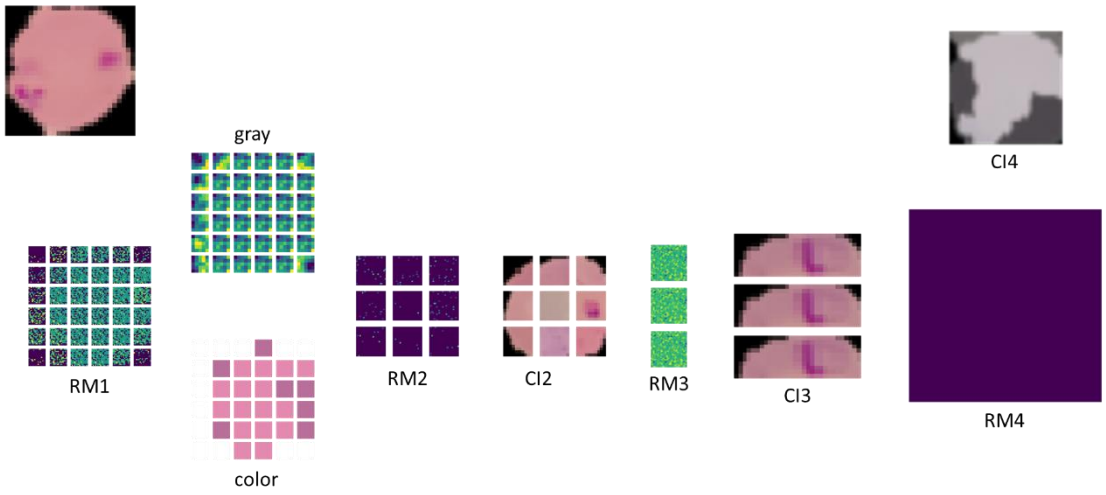
這張架構圖跟下一頁的架構圖是同一張，只是轉橫的比較大。



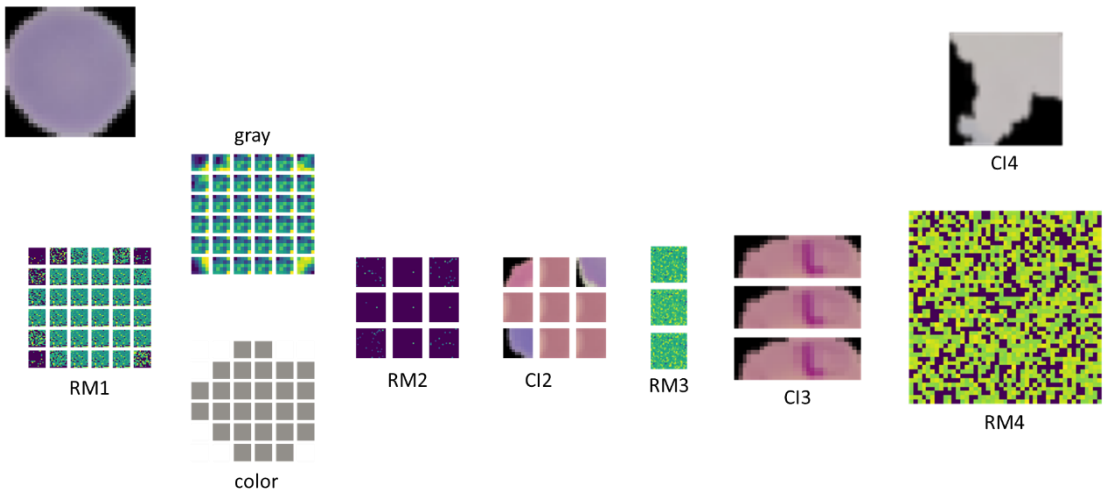

6 x 6 x 206
FM1
FM2
FM3
FM4
15
25
30
45
Block 1
Block 2
Block 3
Block 4
6 x 6 x 225
3 x 3 x 225
3 x 3 x 625
3 x 1 x 625
3 x 1 x 900
1 x 1 x 900
1 x 1 x 2025
2 x 2
1 x 3
3 x 1
flattened
infected
uninfected
6 x 6 x 19
||x-m||
φ(x)
RM
Gray
RGB

Correct case

infected

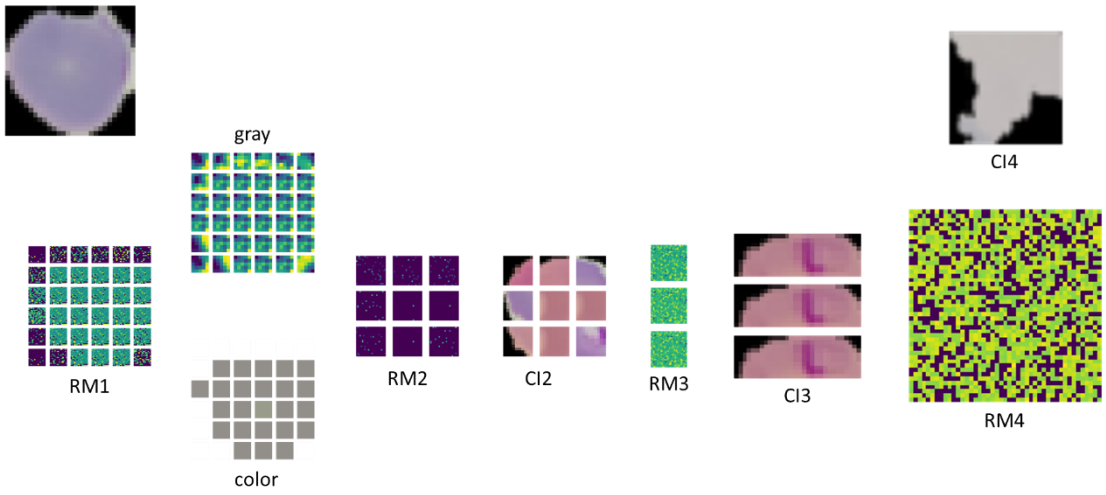


uninfected

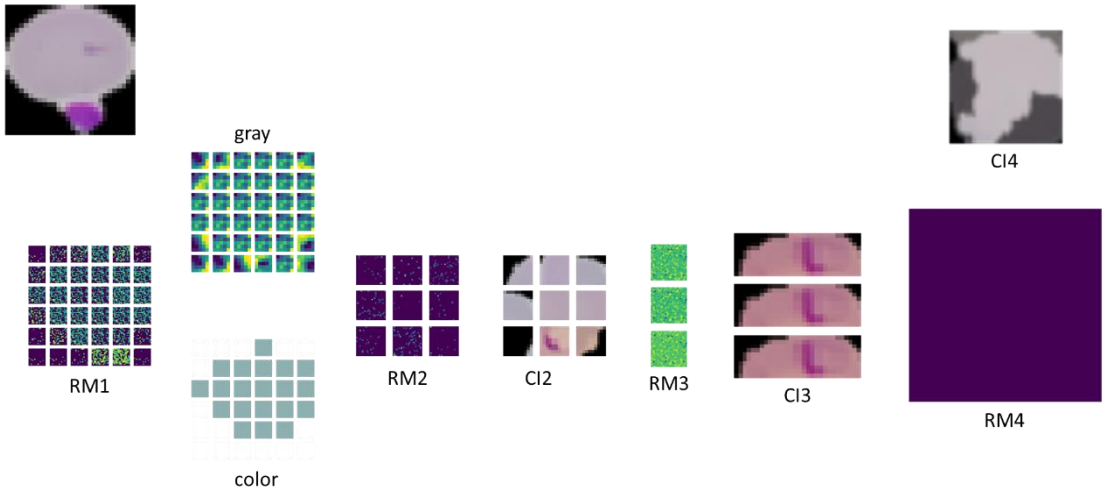


Misclassified case

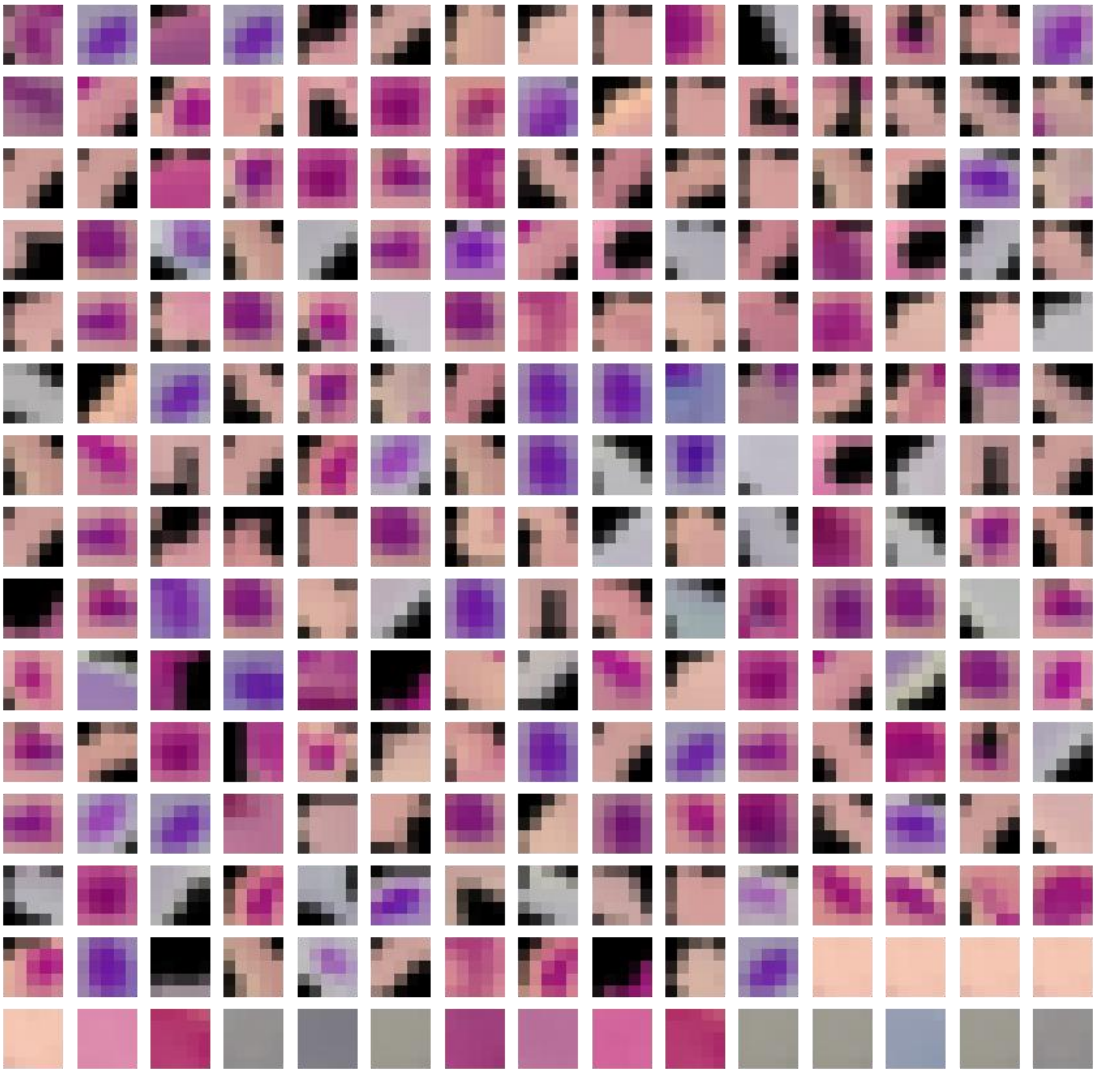
class : infected , pred : uninfected



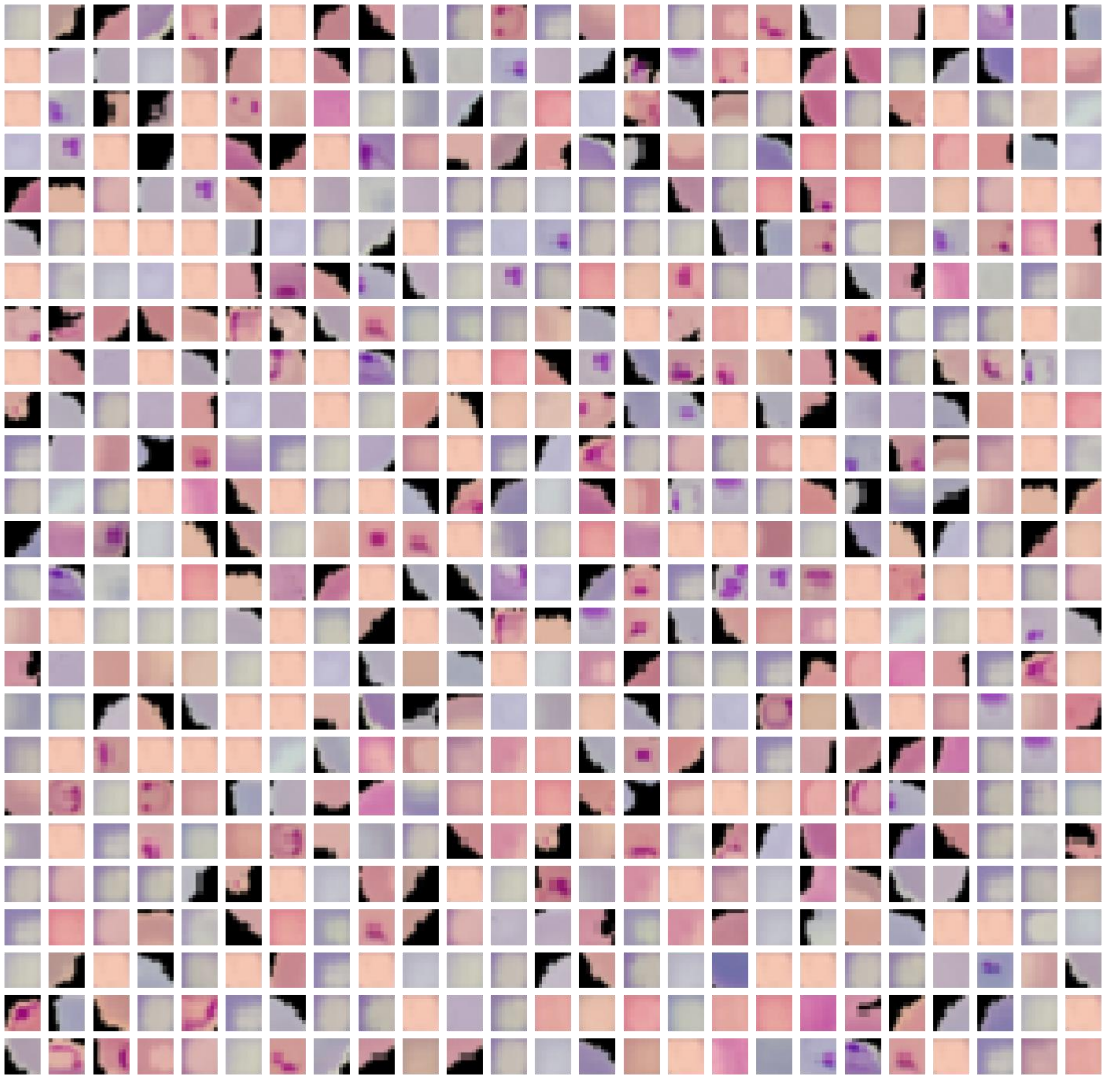
class : uninfected , pred : infected

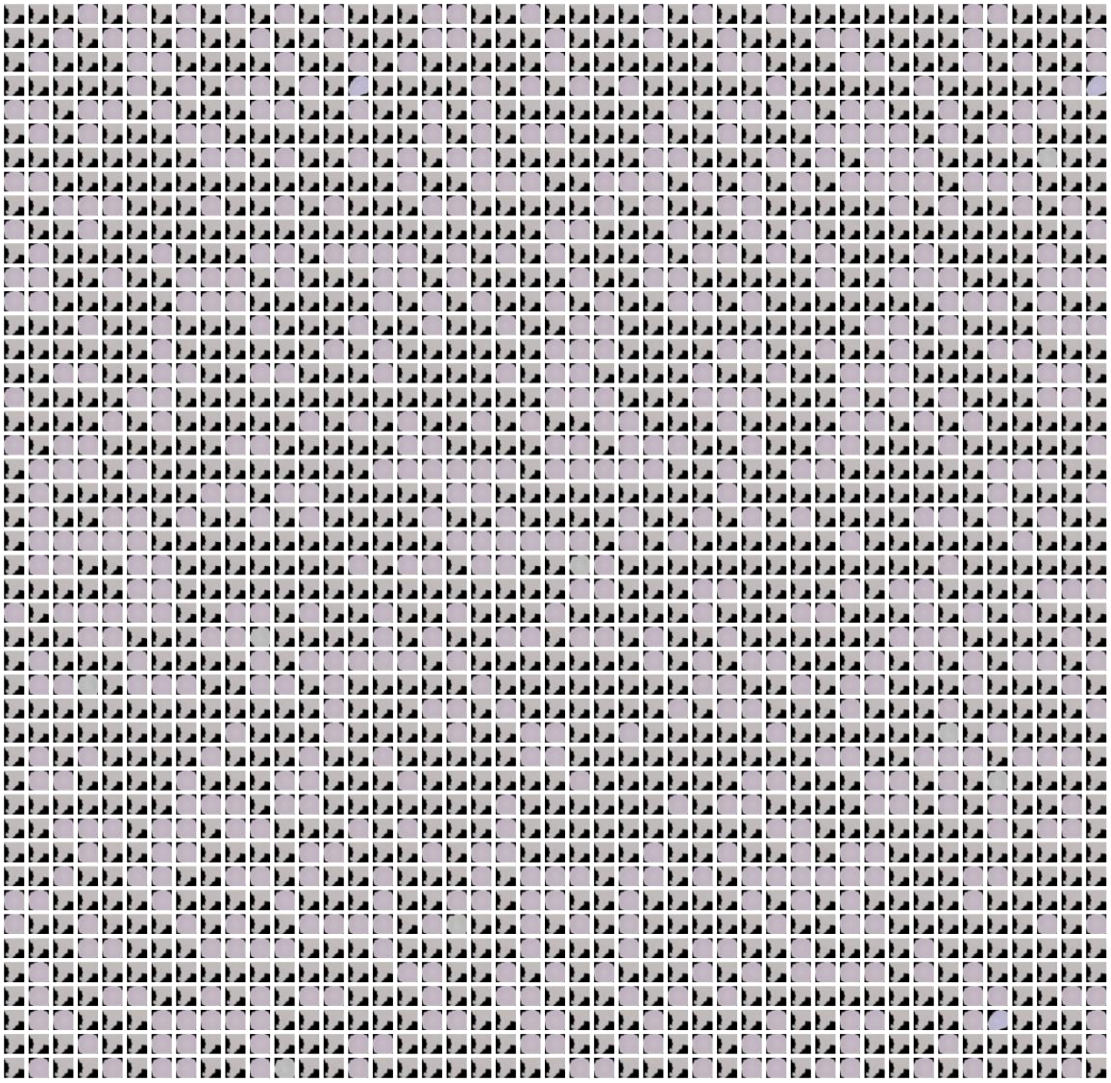


Cl1



Cl2



Cl3

CI4