Cell Counting
REPORT

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Repository Link: https://github.com/Pulkit-Marlin/Cell-Counting

VGG Cells

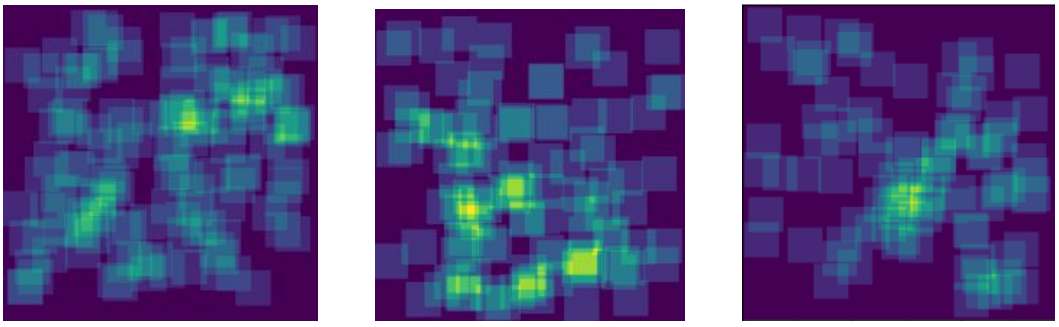
- Using Square Kernel:

  The model gave the best result for 300 epochs with a learning rate of 0.001 and a batch size of 2. There were 40 images for training, 40 images for validation, and 120 images for testing.

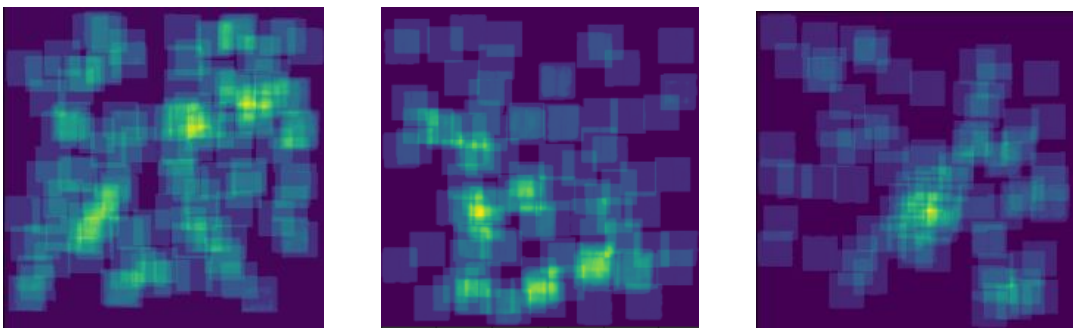
  We got **`Mean Difference in Counts = 2.83.`**

  `Few of the target Images 'T' along with the predicted images 'F(I)' is shown below:`

  `Actual Count Map (T):`



  `Corresponding Predicted Count Map(F(I)):`



(Mean Difference in Counts is taken over the whole test dataset in all)

Adipocyte Cells

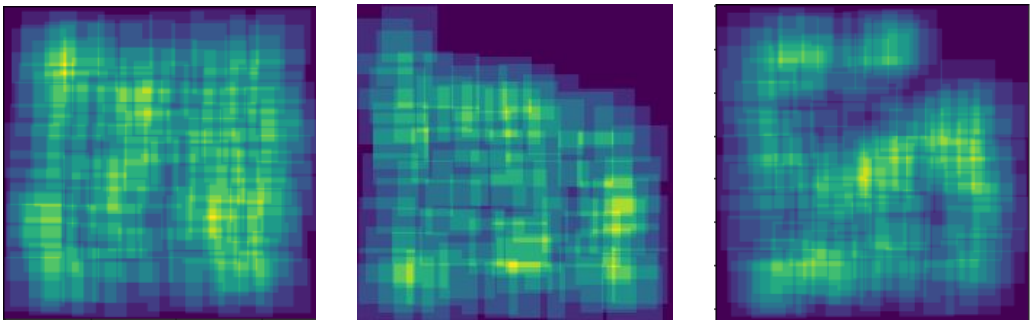
- Using Square Kernel:

  The model gave the best result for 1000 epochs with a learning rate of 0.005 and a batch size of 2. There were 38 images for training, 38 images for validation, and 116 images for testing. (We have removed a few images for whom we felt that the marked annotations did not match with the original image)

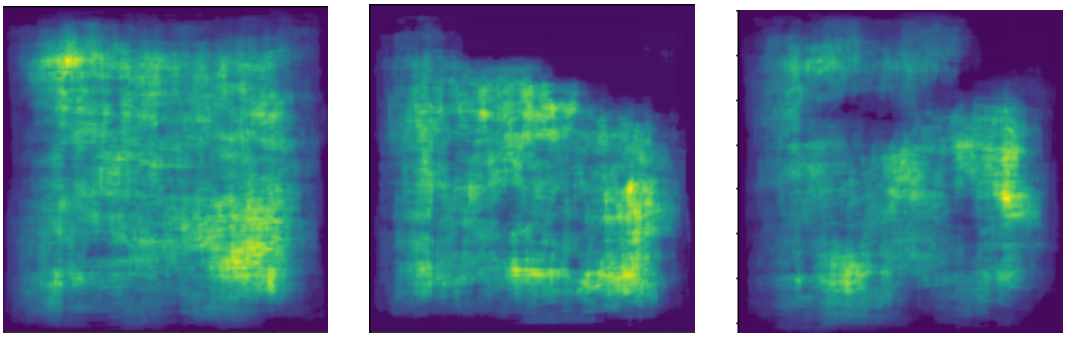
  We got **`Mean Difference in Counts = 13.85.`**
  (Adipocytes can vary in size dramatically (20-200μ) and given they are densely packed adjoining cells with few gaps, they represent a difficult test-case for automated cell counting procedures.)

  `Few of the target Images 'T' along with the predicted images 'F(I)' is shown below:`

  `Actual Count Map (T):`



  `Corresponding Predicted Count Map(F(I)):`



MBM Cells

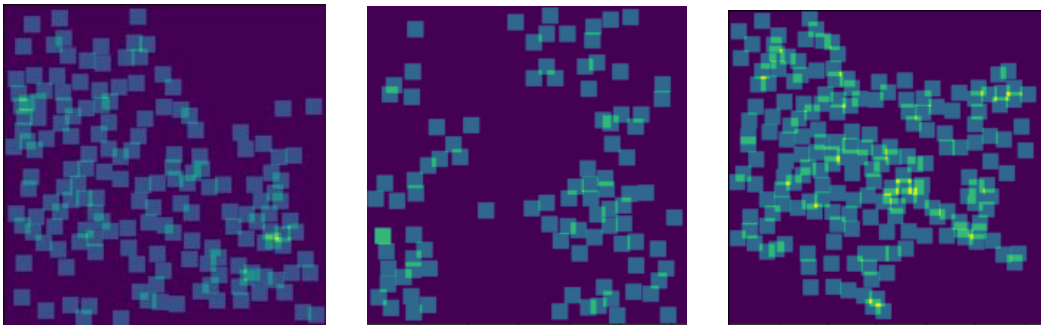
- Using Square Kernel:

  The model gave the best result for 300 epochs with a learning rate of 0.001 and a batch size of 2. There were 21 images for training, 5 images for validation, and 18 images for testing.

  We got **`Mean Difference in Counts = 9.55.`**
  (This prediction can be further improved with the availability of more data)

  `Few of the target Images 'T' along with the predicted images 'F(I)' is shown below:`

  `Actual Count Map (T):`



  `Corresponding Predicted Count Map(F(I)):`