1.2 Brucella/Salmonella Ellipses

Nicolas Bennett

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The following investigation should shed a light on the quesion whether cell location within an image has an influence on its features. If such an influence is visible, it may have to be considered to remove some cells (e.g. in image or well corners). As an extension to previous investigations, not a single ellipse is used to bin cells, but five ellipses of equal area.

```
features <- c("^Cells.Location_Center_X$",
              "^Cells.Location_Center_Y$",
              "^Cells.AreaShape_Perimeter$",
              "^Cells.Texture_InfoMeas1_CorrActin_3$",
              "^Cells.Texture_InfoMeas2_CorrActin_3$",
              "^Cells.Intensity_MeanIntensity_CorrDNA$")
plates   <- list(PlateLocation("KB2-01-1W"),
                 PlateLocation("KB01-2L"),
                 PlateLocation("J107-2D"),
                 PlateLocation("KB2-02-1C"),
                 PlateLocation("KB01-1B"),
                 PlateLocation("J104-2L"))
data     <- getSingleCellData(plates, features)
```

```
## reading plate chache file.
## assuming 9 images per well:
## max legnth: 3456, fraction of full length features: 0.995
## removing 602 unmatched features.
## reading plate chache file.
## assuming 6 images per well:
## max legnth: 2304, fraction of full length features: 0.995
## removing 602 unmatched features.
## reading plate chache file.
## assuming 9 images per well:
## max legnth: 3456, fraction of full length features: 0.995
## removing 602 unmatched features.
## reading plate chache file.
## assuming 9 images per well:
## max legnth: 3456, fraction of full length features: 0.995
## removing 555 unmatched features.
## reading plate chache file.
## assuming 9 images per well:
## max legnth: 3456, fraction of full length features: 0.995
## removing 555 unmatched features.
## reading plate chache file.
## assuming 9 images per well:
## max legnth: 3456, fraction of full length features: 0.995
## removing 555 unmatched features.
```

```
augm  <- lapply(data, augmentCordinateFeatures, ellipse=5, facet=NULL,
                center.dist=FALSE)
```

```
## ellipse sizes: 289536, 579072, 868608, 1158144
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```
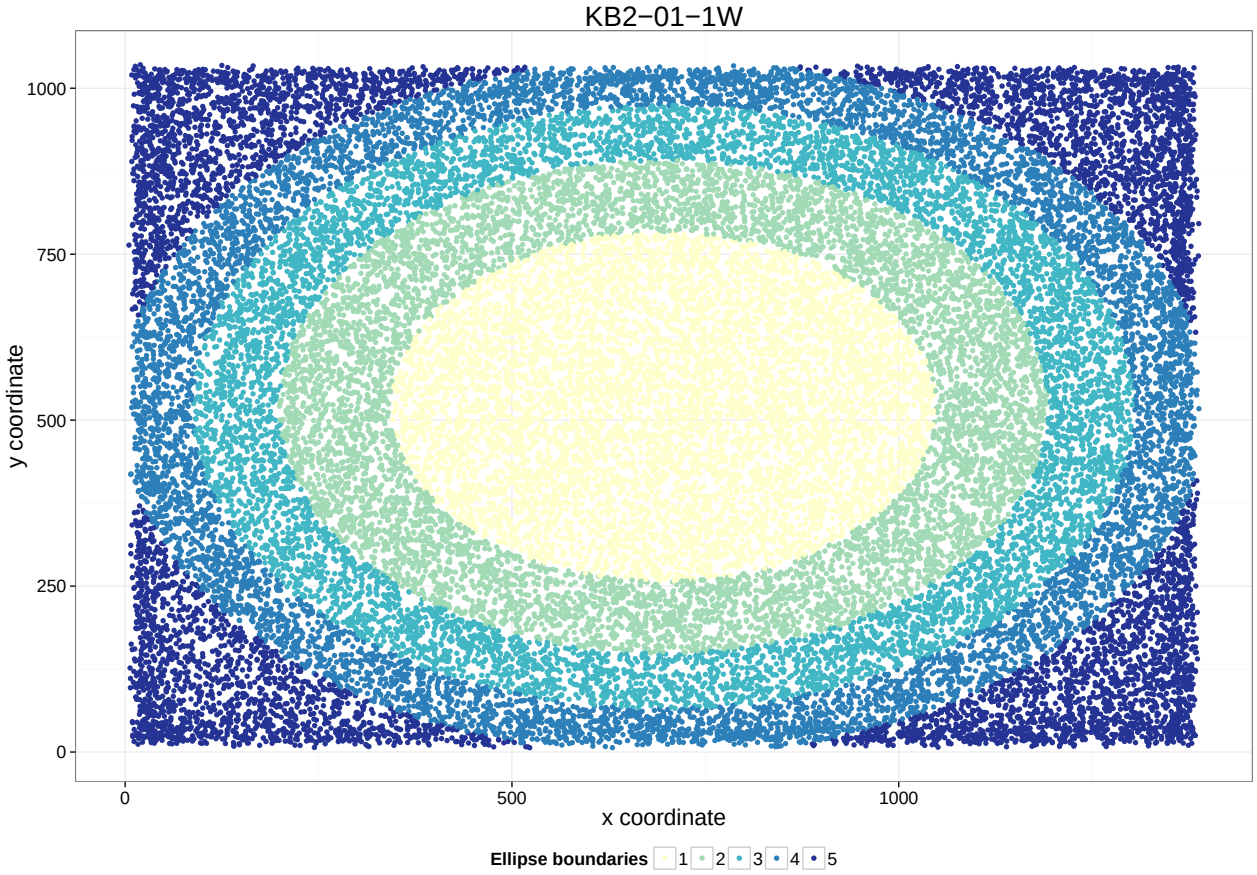
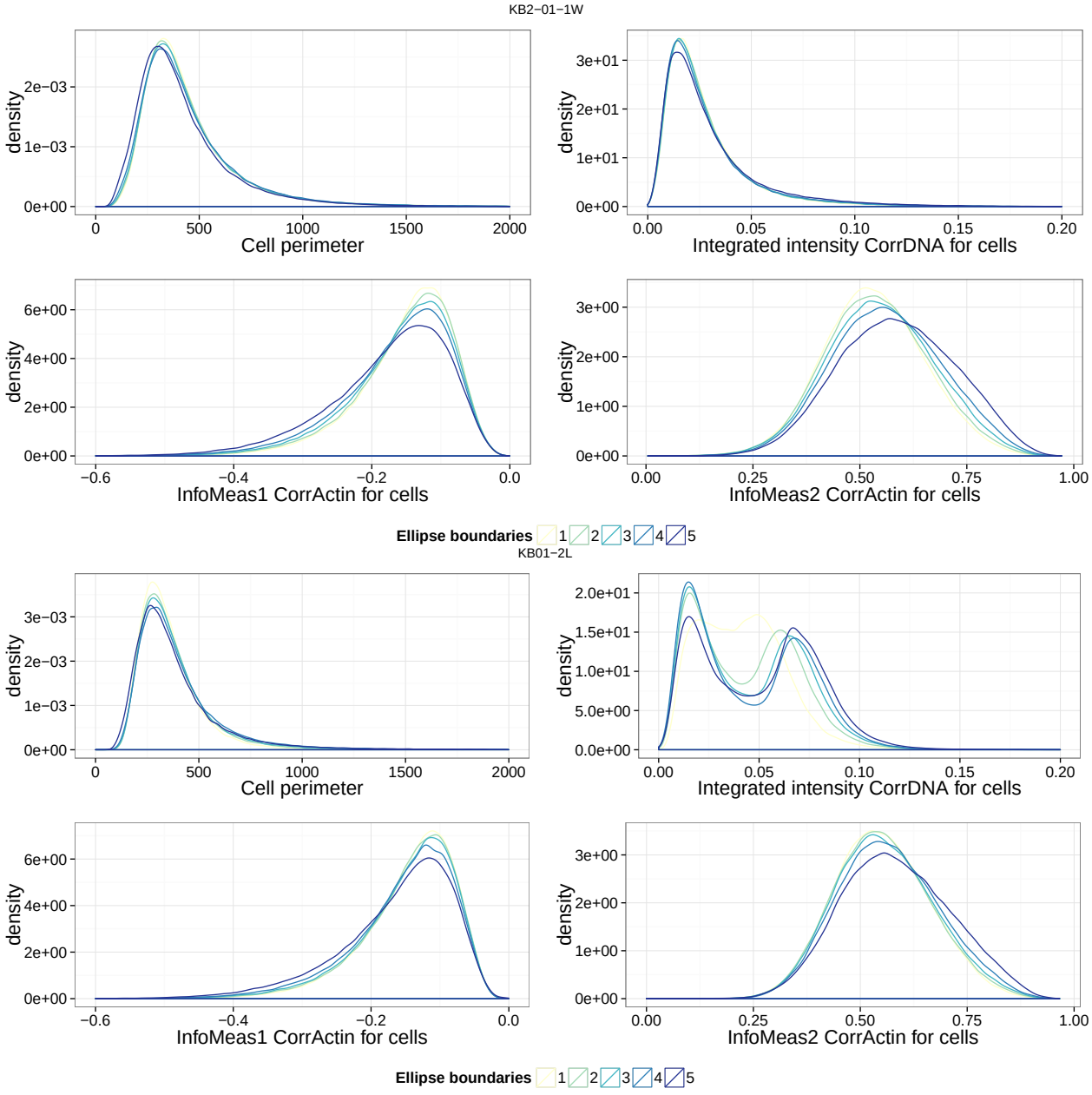

```
melt  <- lapply(augm, meltData)
cells <- lapply(melt, function(x) return(x$mat$Cells))
rm(features, plates, data, augm, melt)
colnames(cells[[1]])
```

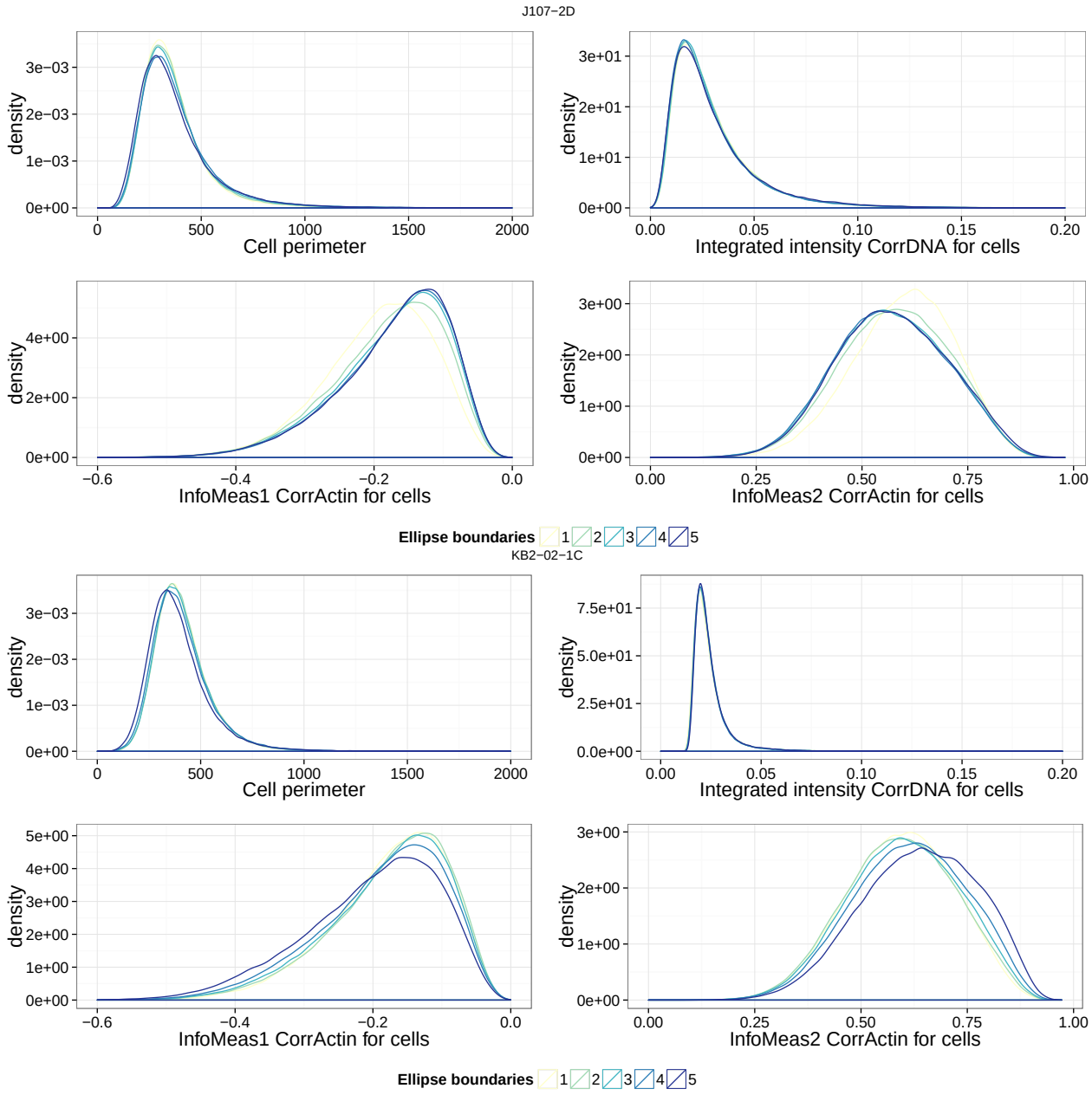
```
##  [1] "Cells.AreaShape_Perimeter"
##  [2] "Cells.Intensity_MeanIntensity_CorrDNA"
##  [3] "Cells.Location_Center_X"
##  [4] "Cells.Location_Center_Y"
##  [5] "Cells.Texture_InfoMeas1_CorrActin_3"
##  [6] "Cells.Texture_InfoMeas2_CorrActin_3"
##  [7] "Cells.Location_In_Ellipse"
##  [8] "Image.Index"
##  [9] "Well.Index"
## [10] "Well.Name"
## [11] "Plate.Barcode"
```

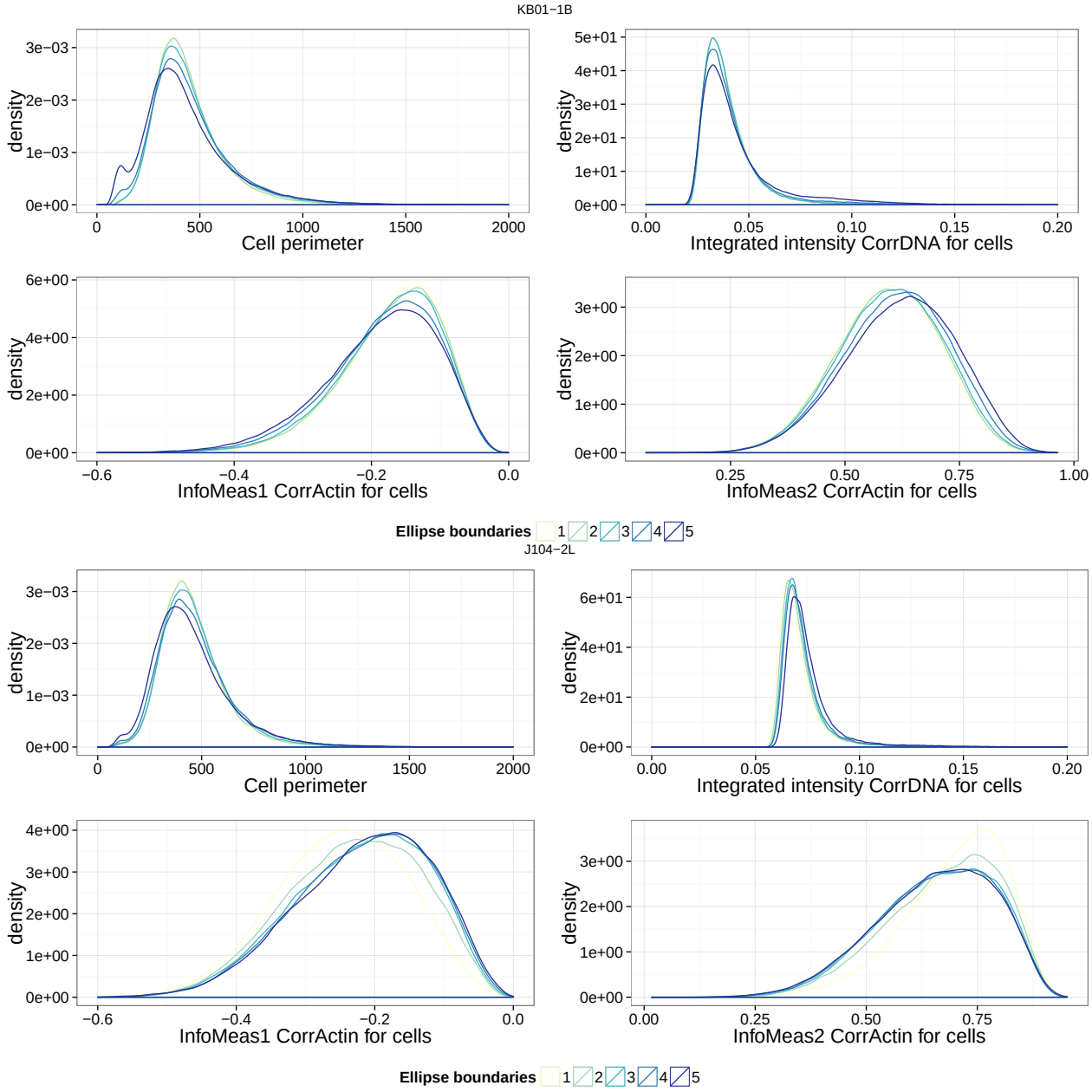
The image sizes are identical for 6 image per well (x coord in 4.84, 1387.81] and y coord in [3.96, 1387.81]) and 9 image per well datasets (x coord in [3.96, 1388.08] and y coord in [4.19, 1036.33]).



To see if the separation of cells along the ellipse boundary is performed correctly, the previous plot shows x vs. y coordinates and cells are colored by their membership to an ellipse. Only a randomly selected subset of size 1/20 is printed.




J107−2D
density
Cell perimeter
Integrated intensity CorrDNA for cells
InfoMeas1 CorrActin for cells
InfoMeas2 CorrActin for cells
Ellipse boundaries 1 2 3 4 5
KB2−02−1C
density
Cell perimeter
Integrated intensity CorrDNA for cells
InfoMeas1 CorrActin for cells
InfoMeas2 CorrActin for cells
Ellipse boundaries 1 2 3 4 5



For each plate, the four available features are shown in separate plots as densities with separate lines for cells in different regions. The border region does not appear to systematically behave much different than the more central ones, despite some individual deviations.