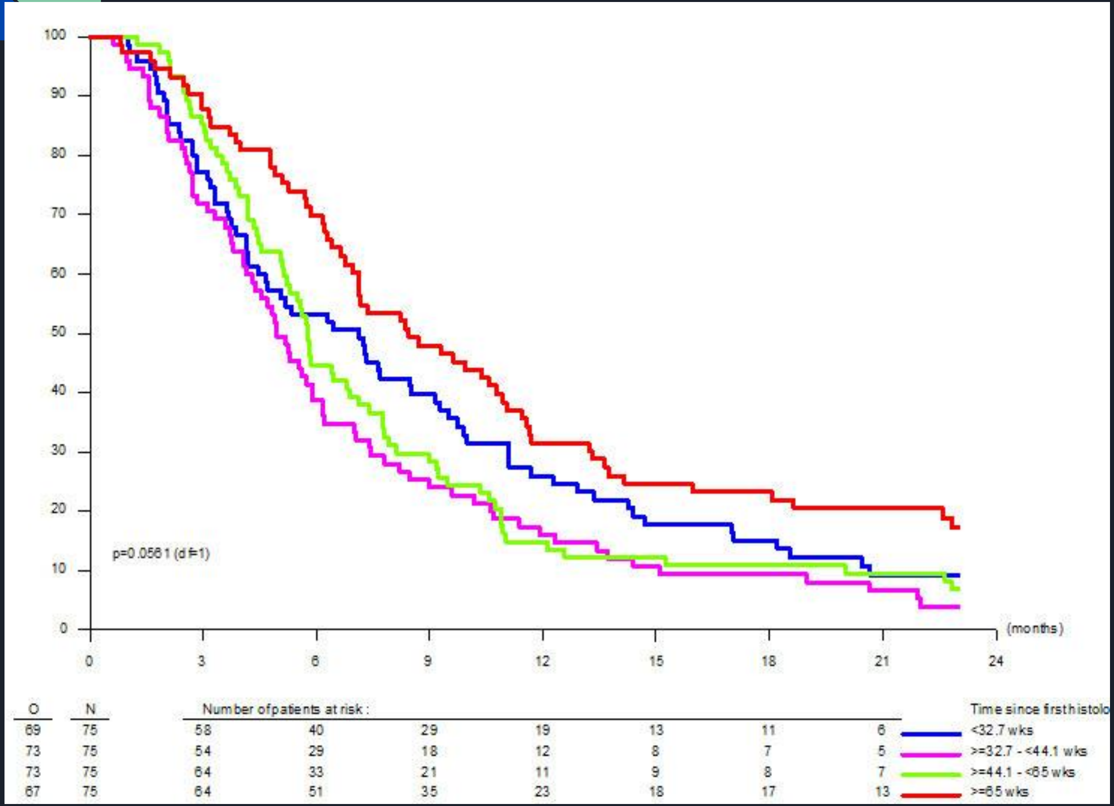
AstraZeneca AI Challenge

Team Russia
E Santhosh Kumar (SHA02921) (CS16B107)

Shaastra 2021

General Properties of Kaplan Meier Charts

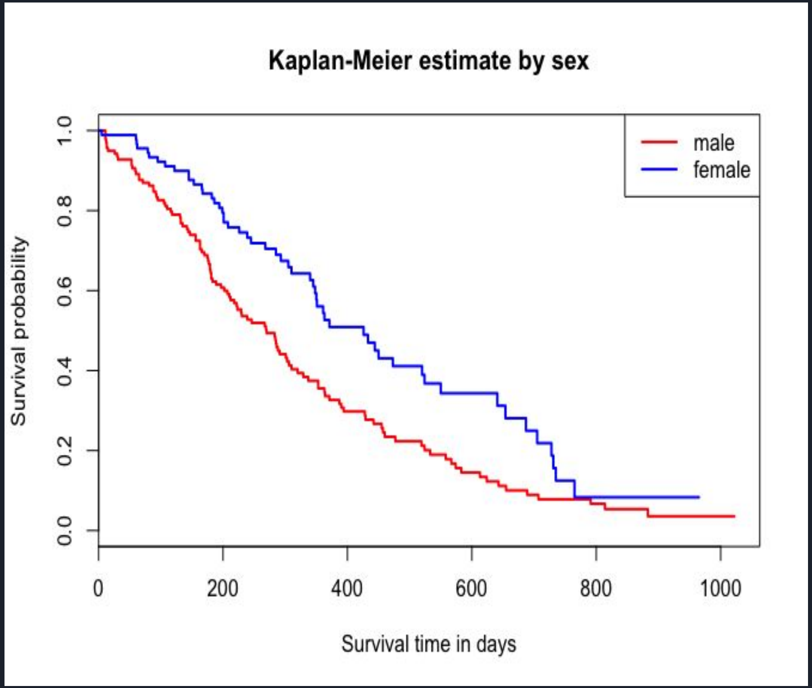


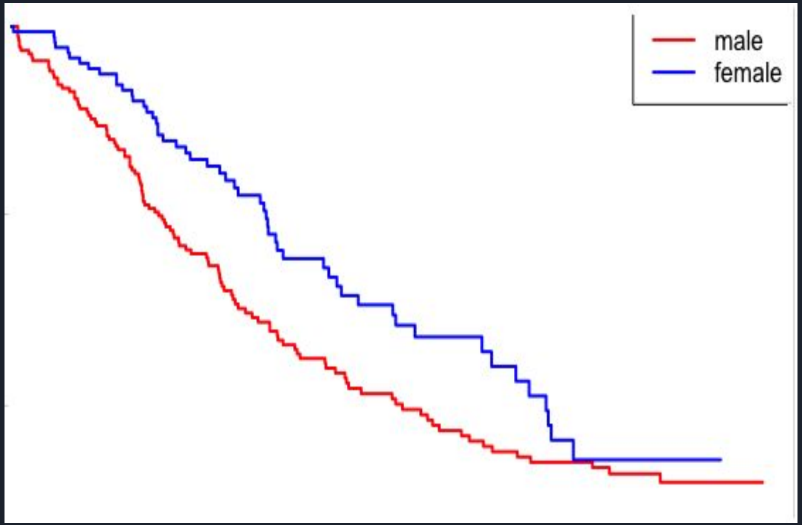
- Y axis is probability -> range [0, 1]
- Monotonically increasing or decreasing curves
- All curves in a chart begin at the same point

Key Processing Phases

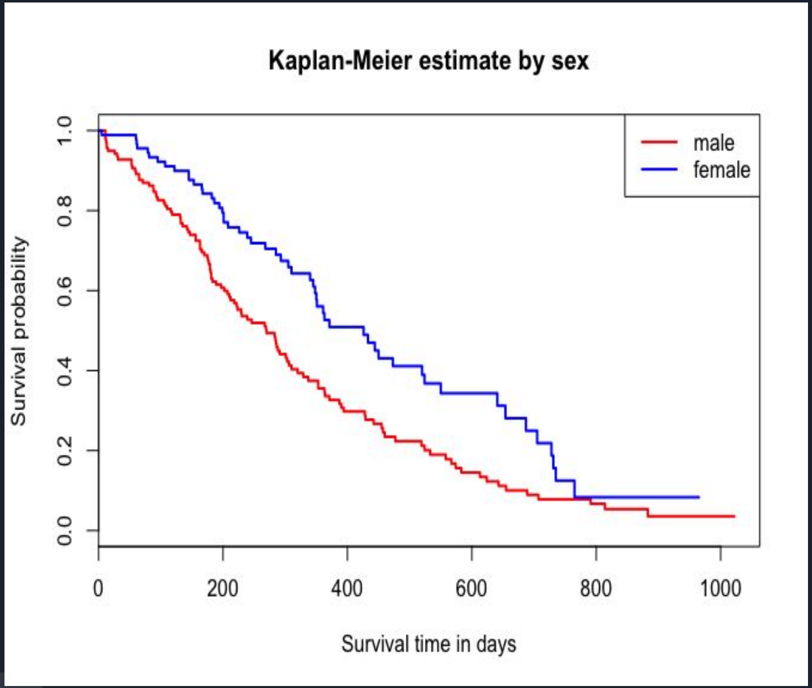
1. Identifying axes / ROI
2. Segmenting Plots
3. Interpolating Coordinates

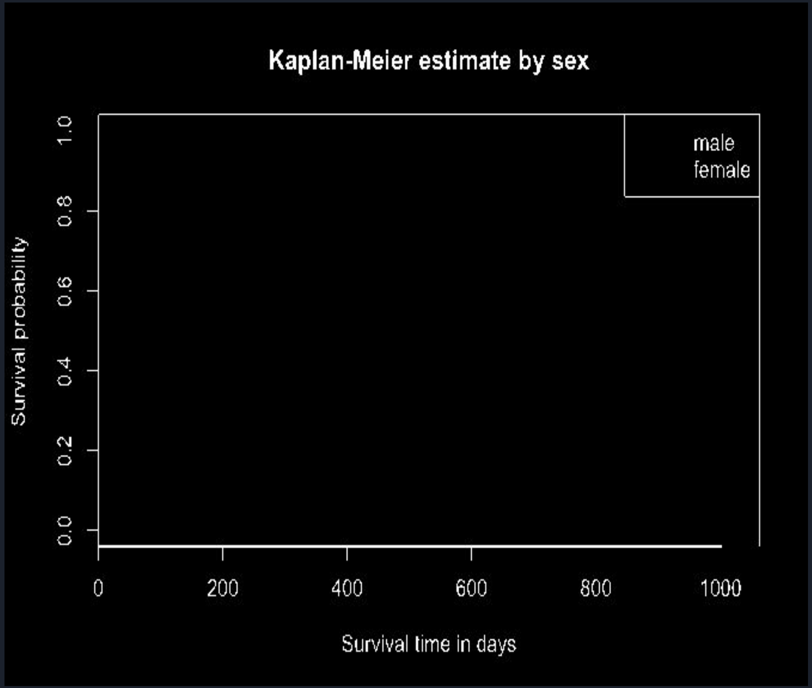
1. Identifying Axes / ROI





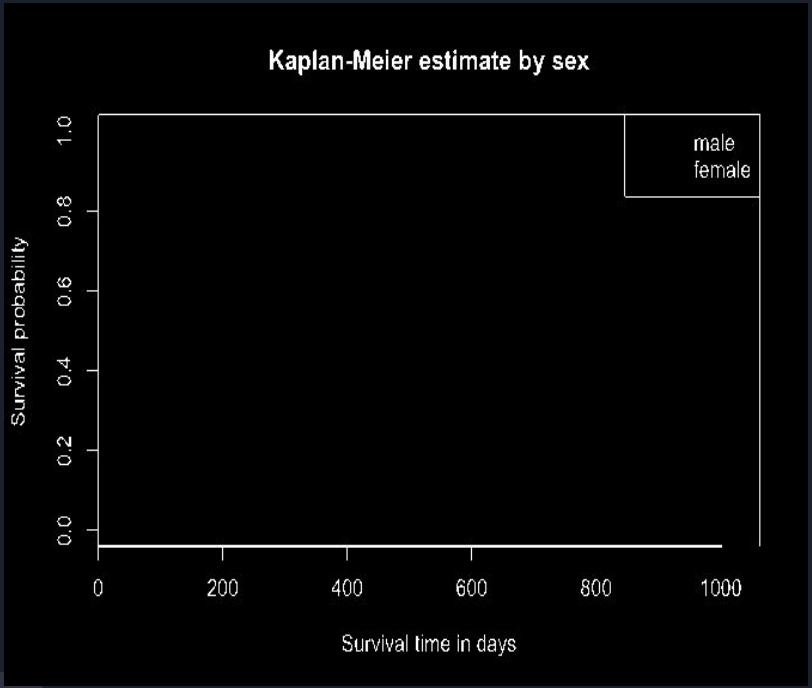
Step 1:
Mask only black areas by thresholding with HSV value

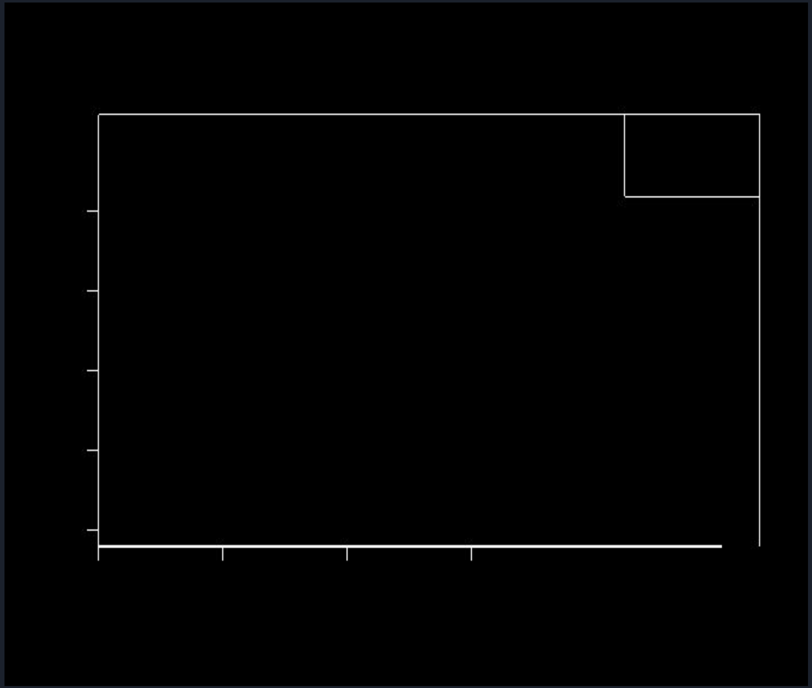




Assumption: axes are always black/dark

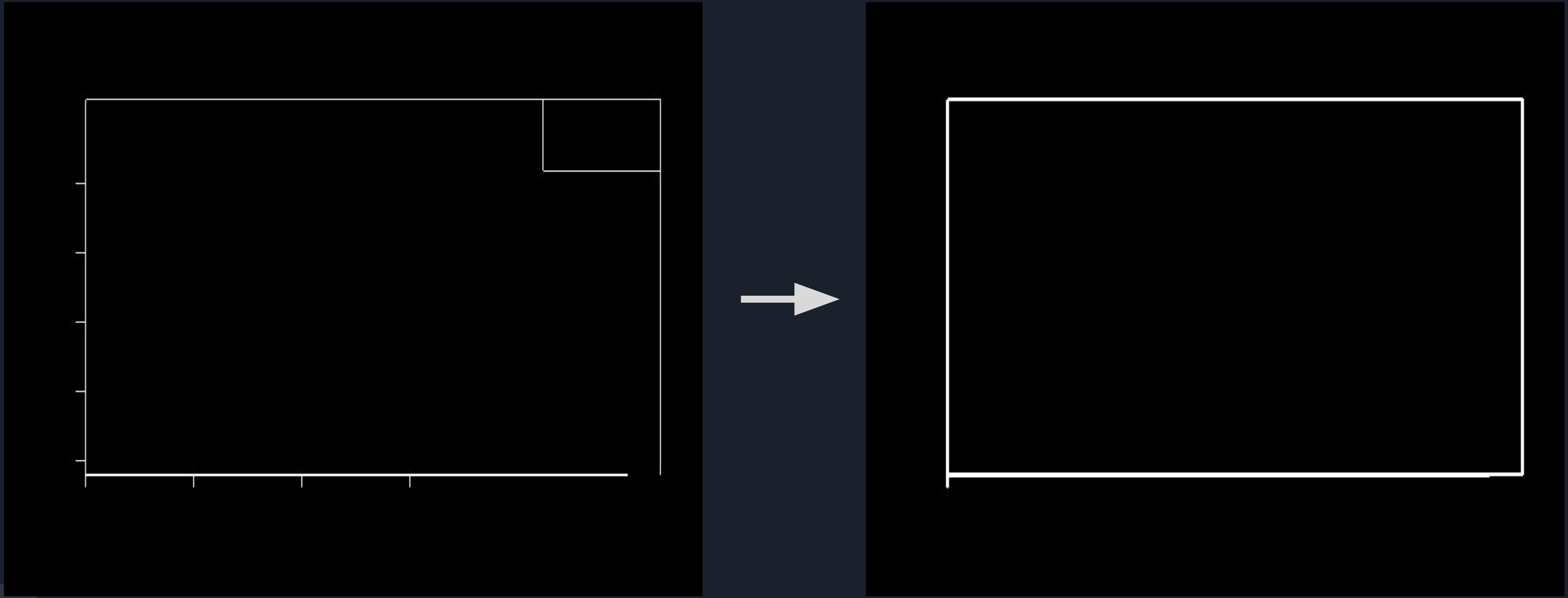
Step 2:
Remove connected components that are neither tall nor wide





Assumption: Y and X axes are among the tallest and widest components of the image respectively

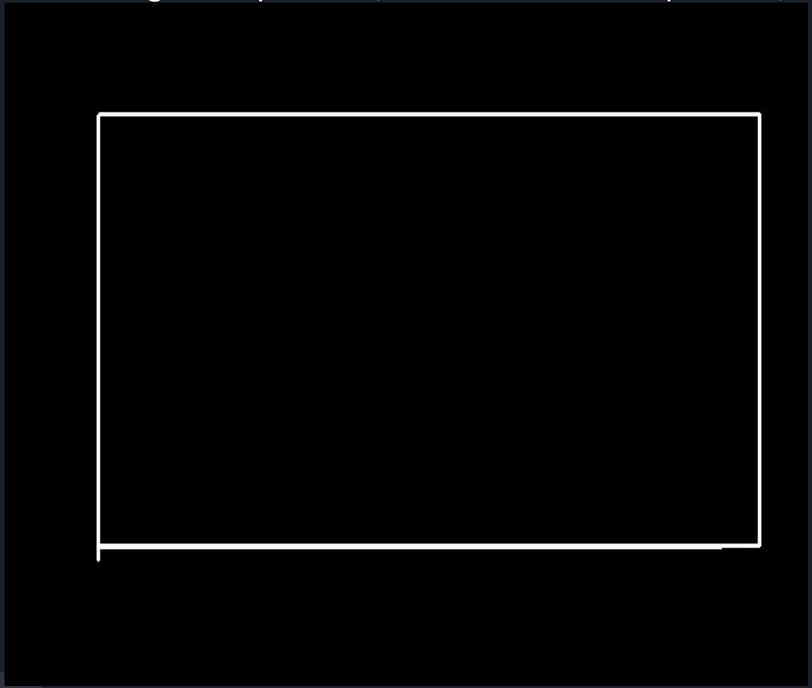
Step 3:
Identify line segments in mask using HoughLinesP



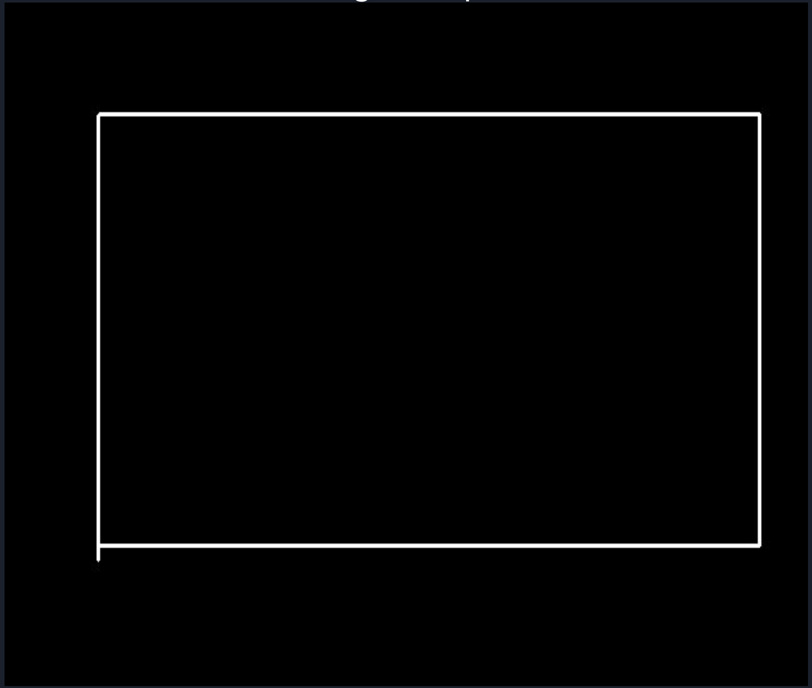
Assumption: Axes are ideally single straight lines. In practice, they are at least piece-wise straight

Step 4:
Merge line segments that are end-to-end or close-by duplicates

5 line segments present (x axis broken and duplicated)

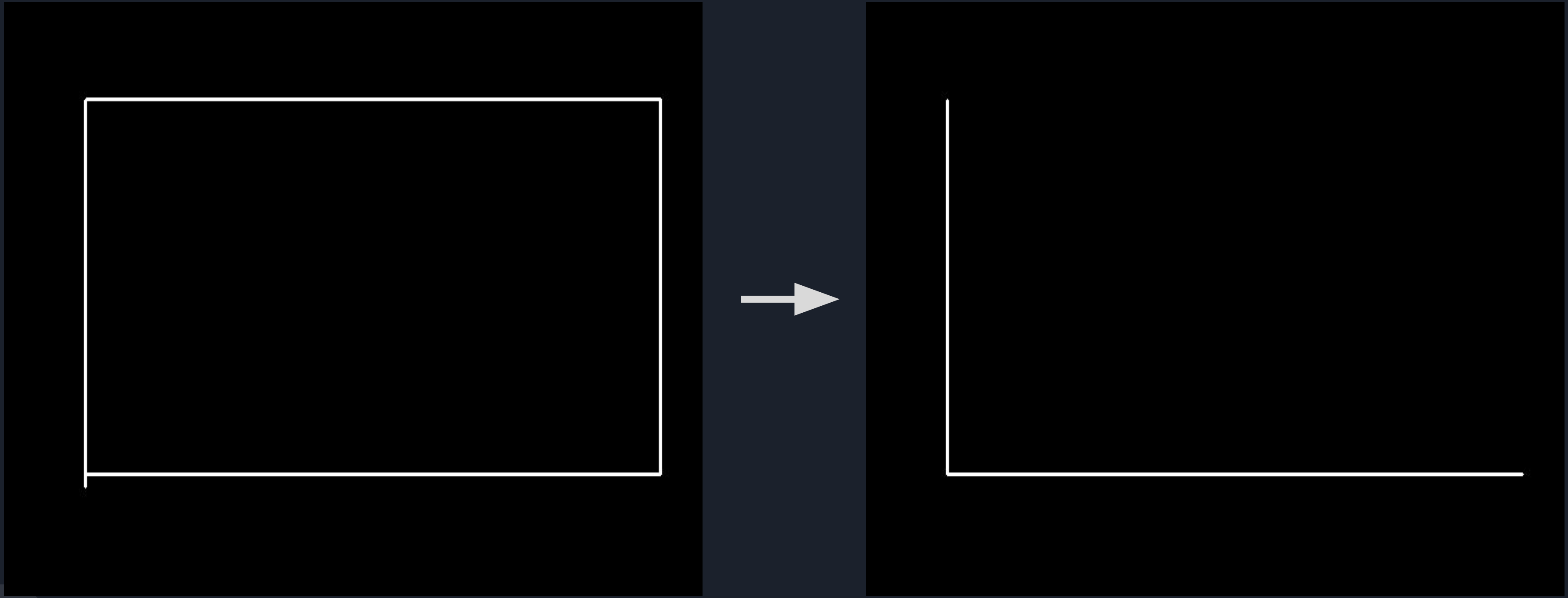


4 line segments present



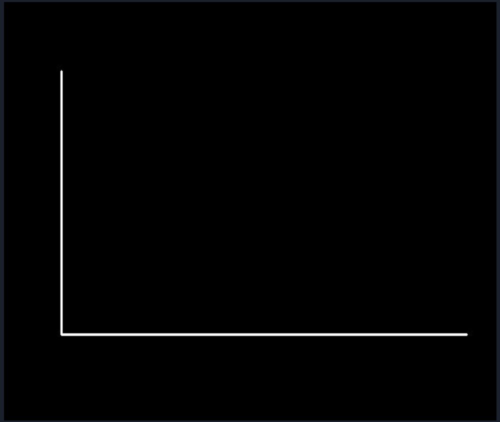
Reason: HoughLinesP may detect duplicate (because of thickness) or broken lines
Source: https://stackoverflow.com/questions/45531074/how-to-merge-lines-after-houghlinesp

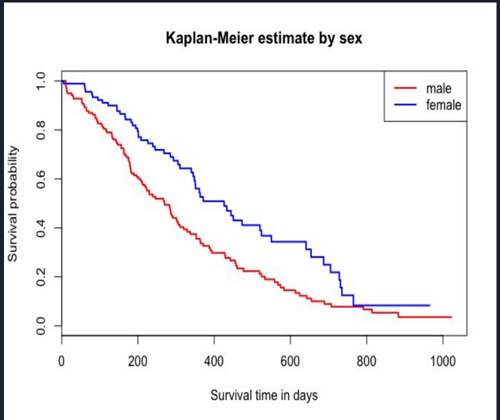
Step 5:
Identify X and Y axes from identified long lines

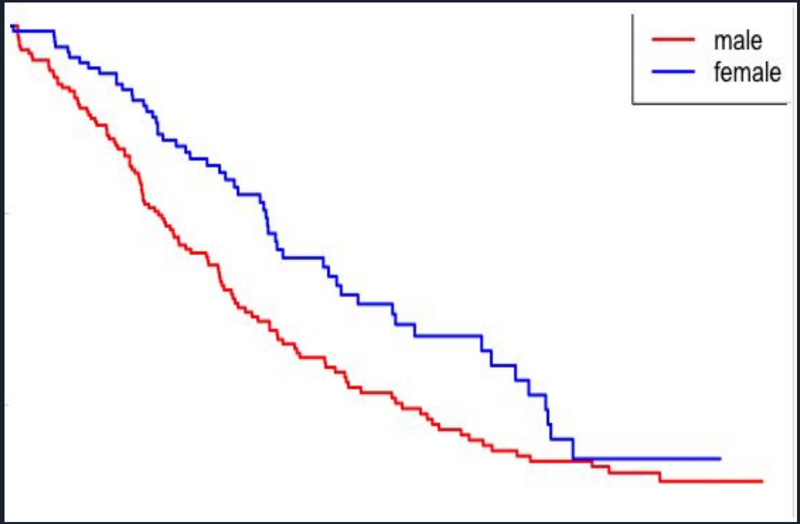


Assumptions: 1) axes can only be horizontal or vertical
2) Plots always have axes at least in the left and bottom
3) The actual chart has to be in the central area of the image

Step 6:
Crop image. Filter out black axes from the foreground of ROI



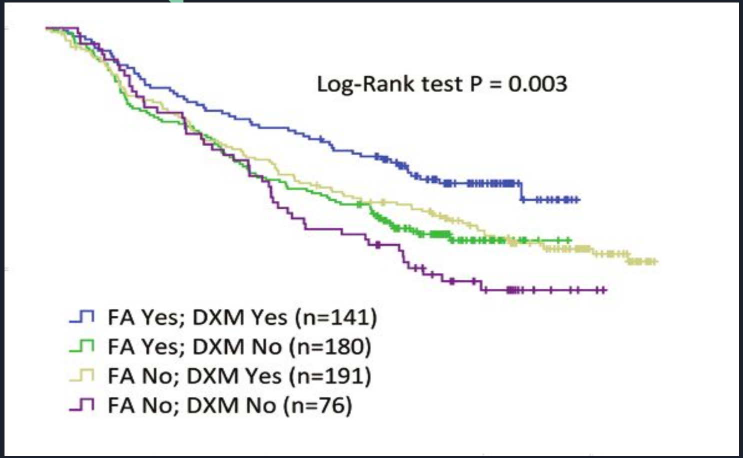




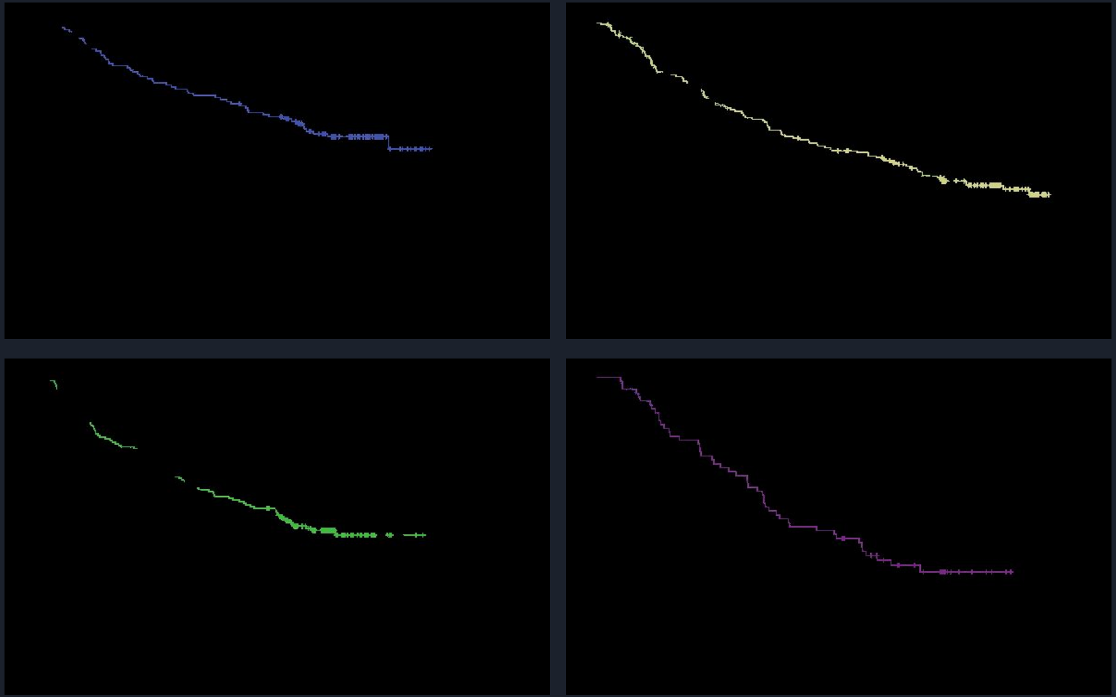
(Notice that the black axes have been filtered out)

Reason: The axes themselves should not be misinterpreted as plots in the next steps
Assumption: Axes are dark (low value in HSV)

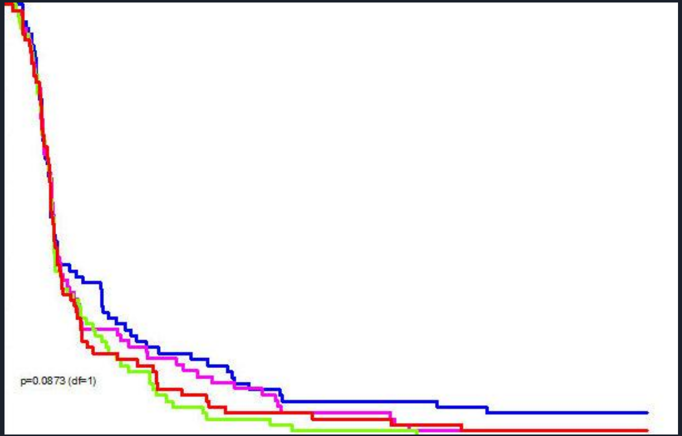
2. Segmenting Plots

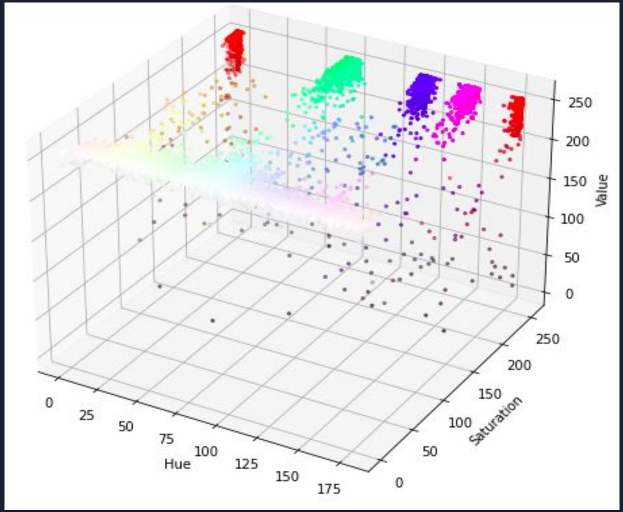


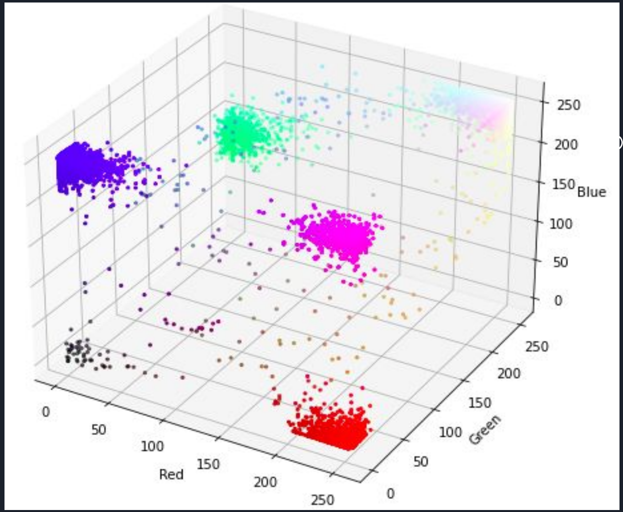
(Cropped ROI)



(Boolean masks for each label)



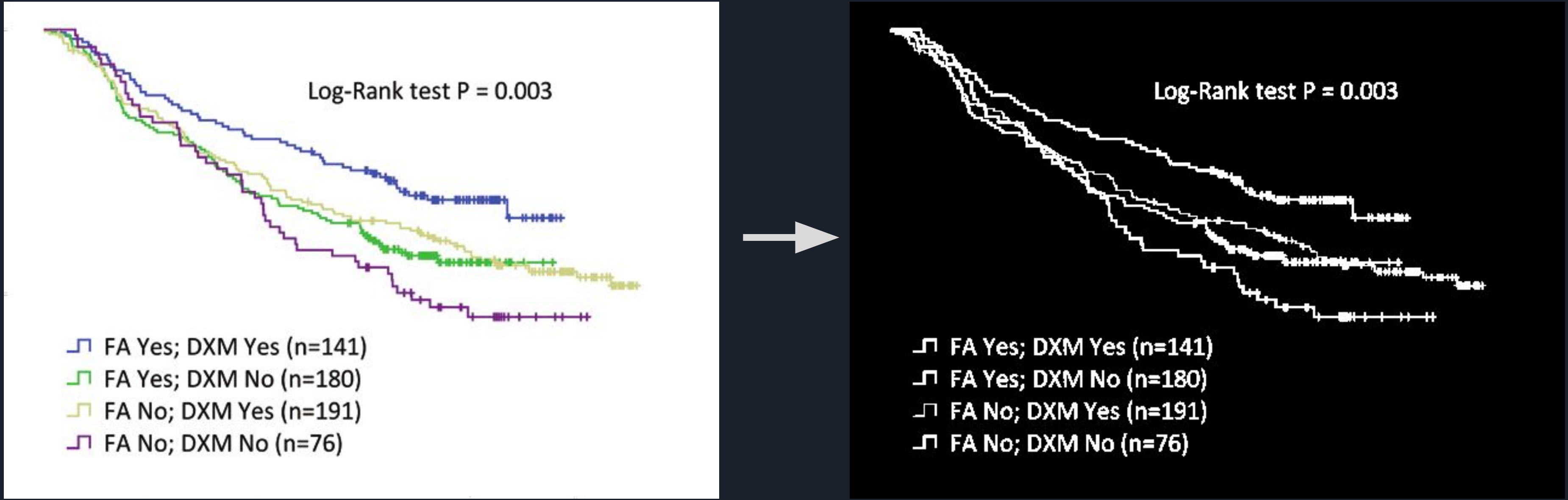




- Expectation:
    - few (k) unique pixel values apart from black and white, each corresponding to a label
- Reality:
    - Each label associated with a cluster of noisy pixel values
    - Specks of colours of one label present in unexpected locations like
        - legend of chart
        - other plots
        - black areas like text, axes
    - Other unexpected colours occurring with non-negligible frequency

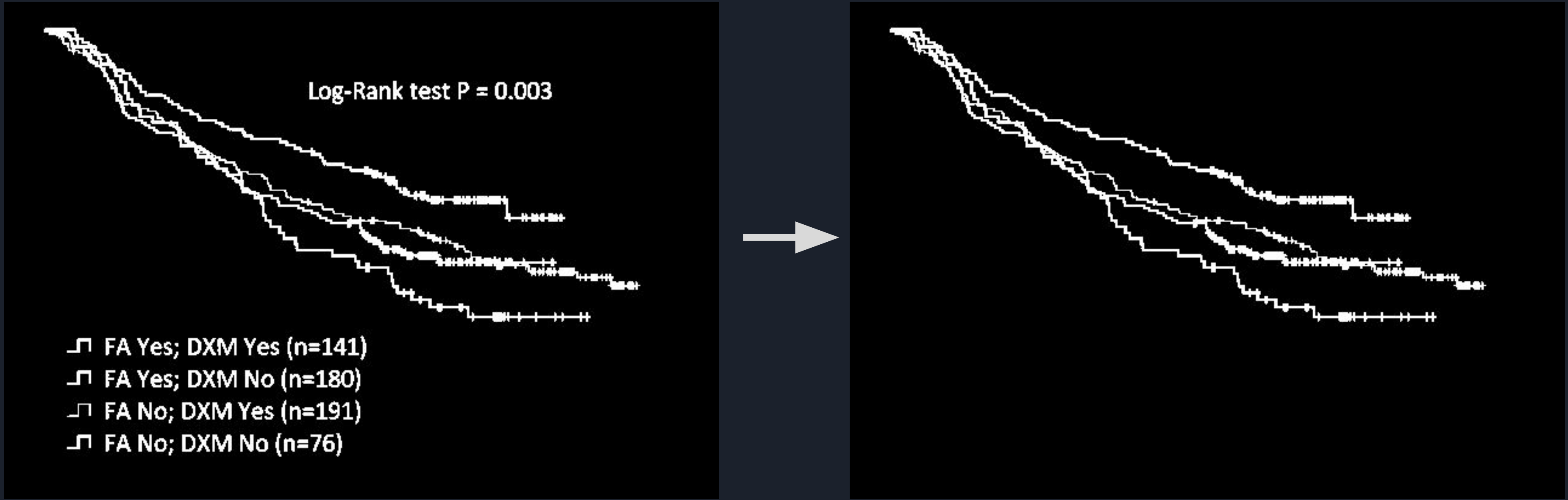
Step 1: Preprocessing for Clustering

- Denoise using an <u>edge-preserving</u> bilateral filter
- Mask out white background by thresholding with HSV value



Assumption: Background is the one and only white area

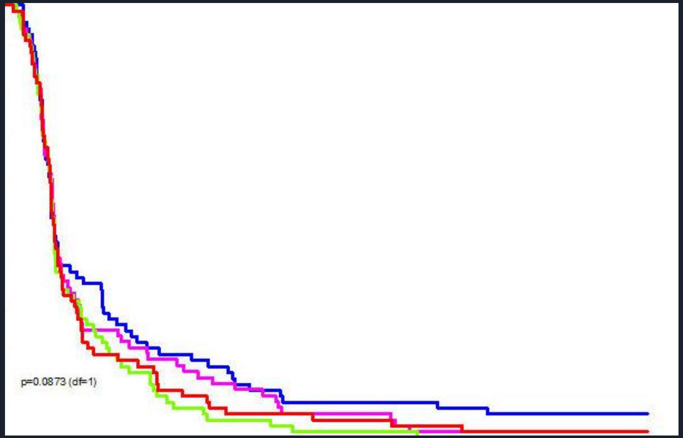
Step 2: Preprocessing for Clustering
Retain only the connected component with largest area in foreground

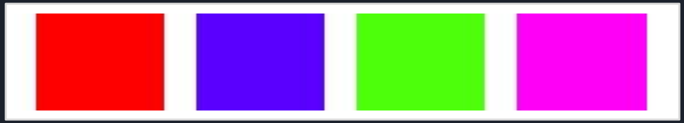


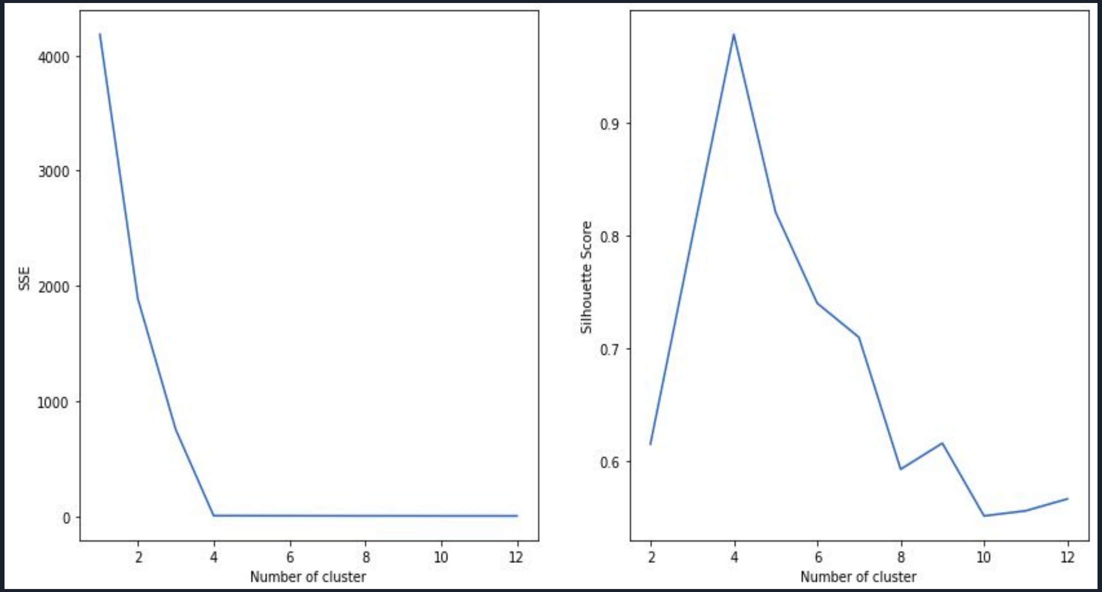
Reason: Expected to take away the legend, other text, random noise
Assumptions: 1) All curves in a chart begin at the same point
2) the union of all plots is the largest connected component in the non-white foreground

Step 3: K - means clustering on RGB Pixel values

- Perform clustering using a range of k values
- Choose the k with max Silhouette Coefficient of random sample





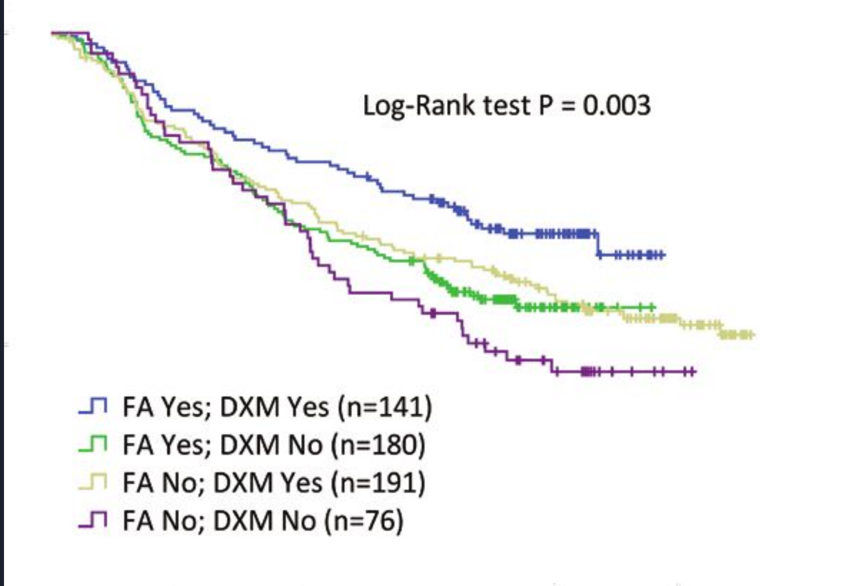


- Clustering doesn't use HSV as visually close shades (red) can be farther apart in space
  - Coefficient is computed with a random sample as it is an $O(n^2)$ algo
    - We may still end up with extra clusters that need pruning

Step 4: Filter Clustering Predictions

Image may contain extra pixel clusters (apart from the ones corresponding to valid plots) because of reasons like

- plot lines having shadows / border effects
- Pixel value approximations while rendering the chart as image. E.g,
  - Varying shades of the plot's colour in the edges between plot and white background
  - Completely random colours in edges between plots of different colours



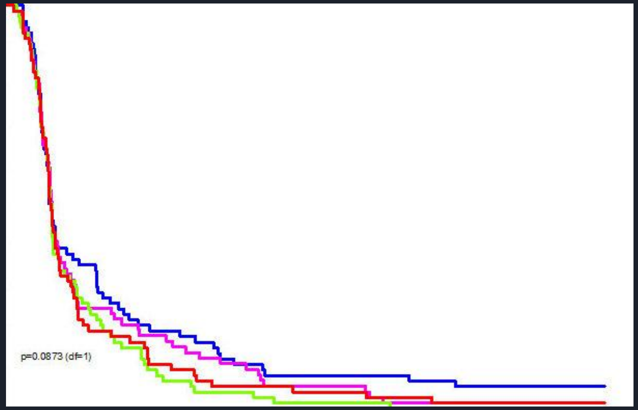
Steps to eliminate these extra clusters

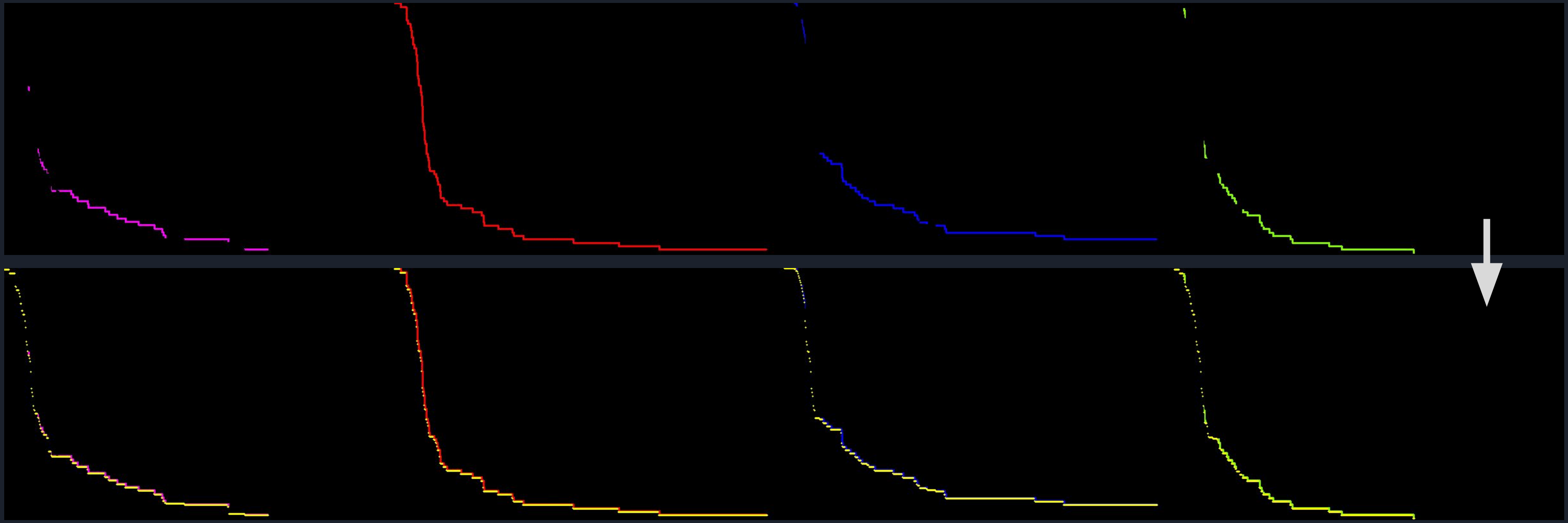
- In the mask of each cluster, remove components of size smaller than a minimum threshold (removes noisy blobs)
- Eliminate clusters with No. of pixels less than a minimum threshold. Threshold is a fraction of size of the largest cluster.

(Initial Clusters)

(Filtered Clusters)

3. Interpolating Coordinates

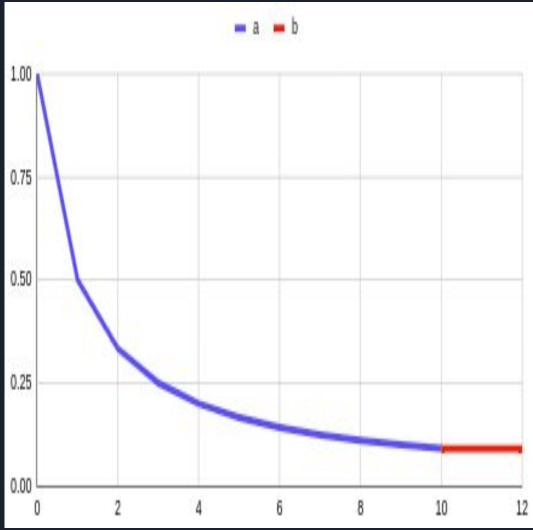


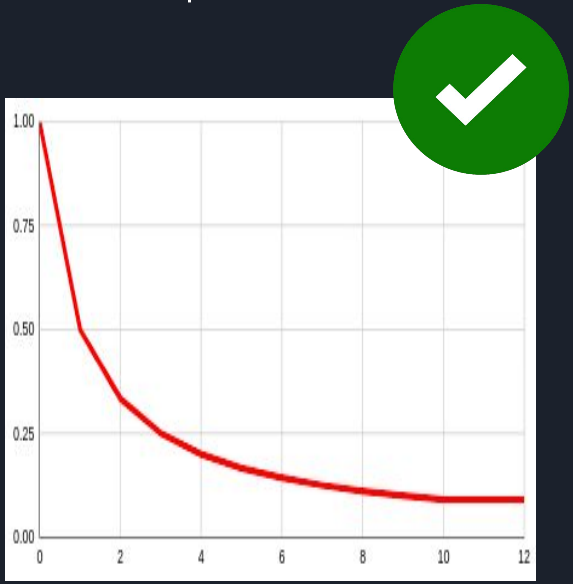


Why is simple linear interpolation in incomplete areas incorrect?

Assumptions:

- The various plots in the chart are superimposed (overlapped) in a fixed (unknown) order
- All plots begin from the same point



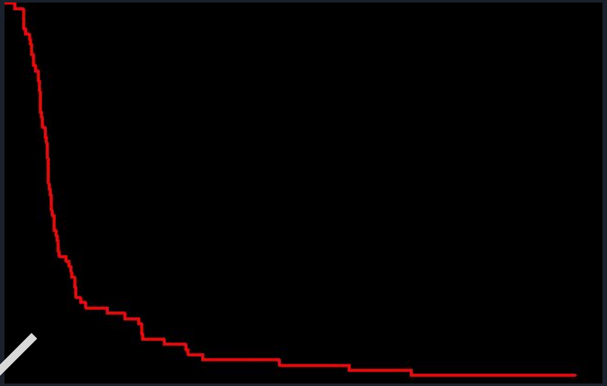


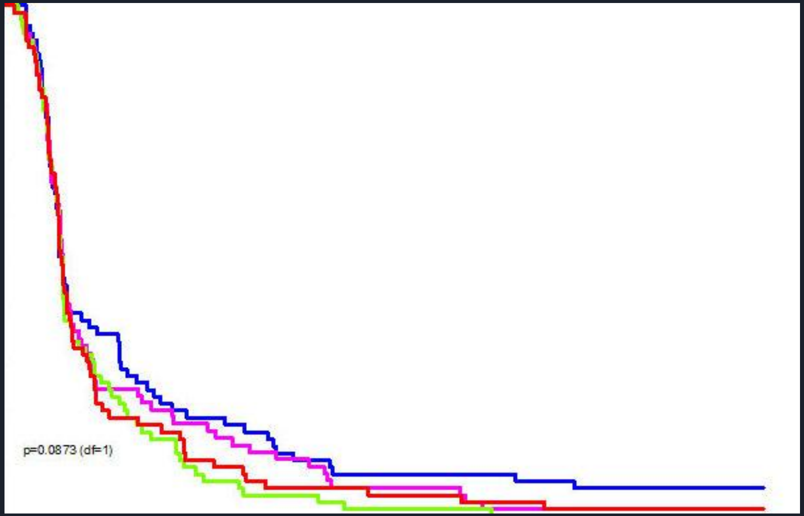
Algorithm

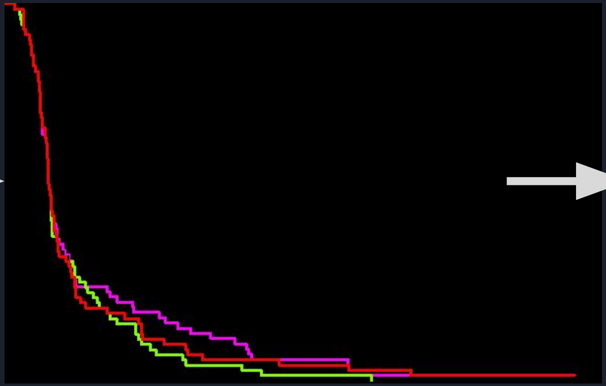
- Logic: Keep interpolating plots from top-most colour to bottom-most colour (in order of overlapping)
- Steps:
  - Identify top-most colour
    - It is the colour visible at the starting point (over all other colours)
    - Its plot is a single connected component
  - Initialize current_overlap_mask as the mask of top colour
  - While there are colours yet to be added,
    - Iterate over all remaining colours
    - The next colour to be added is the one who's incomplete sections can be connected through monotonically decreasing paths in the current_overlap_mask.
    - Once the next colour is chosen, add its mask to current_overlap_mask

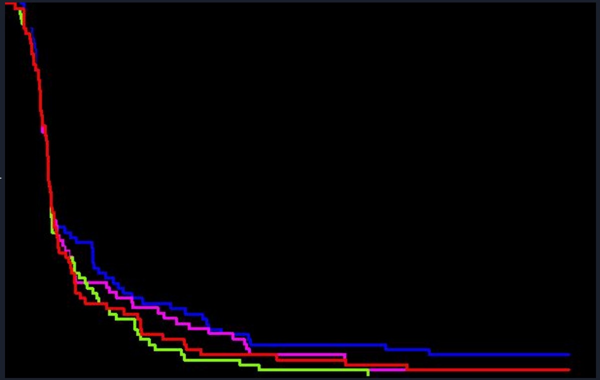
Note: This algorithm is for monotonically decreasing plots. For monotonically increasing plots, we flip the input

Algorithm - Example run



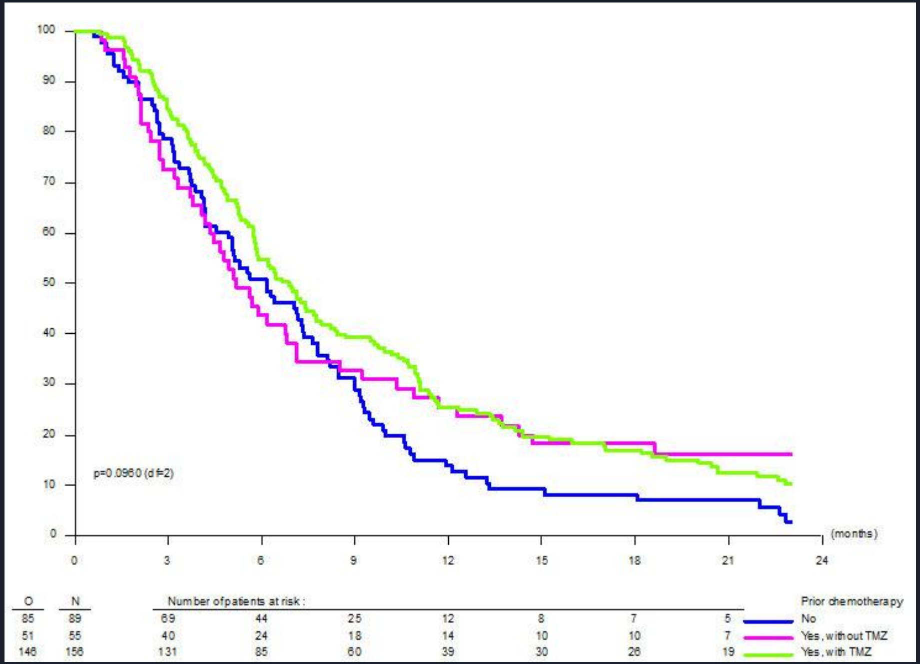




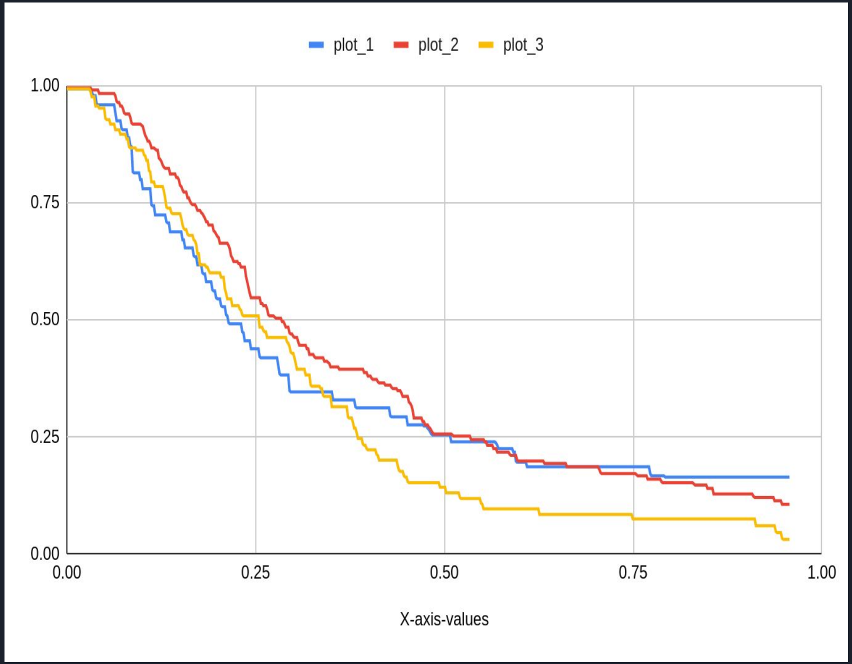


Results

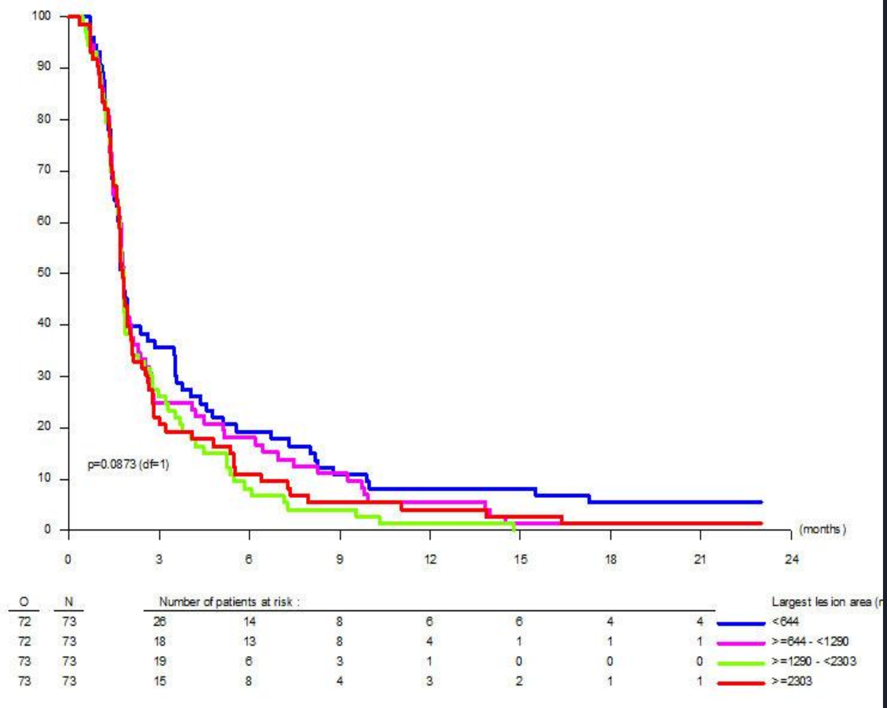
- Comparing input charts with charts generated on Google Sheets using generated data
- X axis coordinates have been normalized to [0, 1]



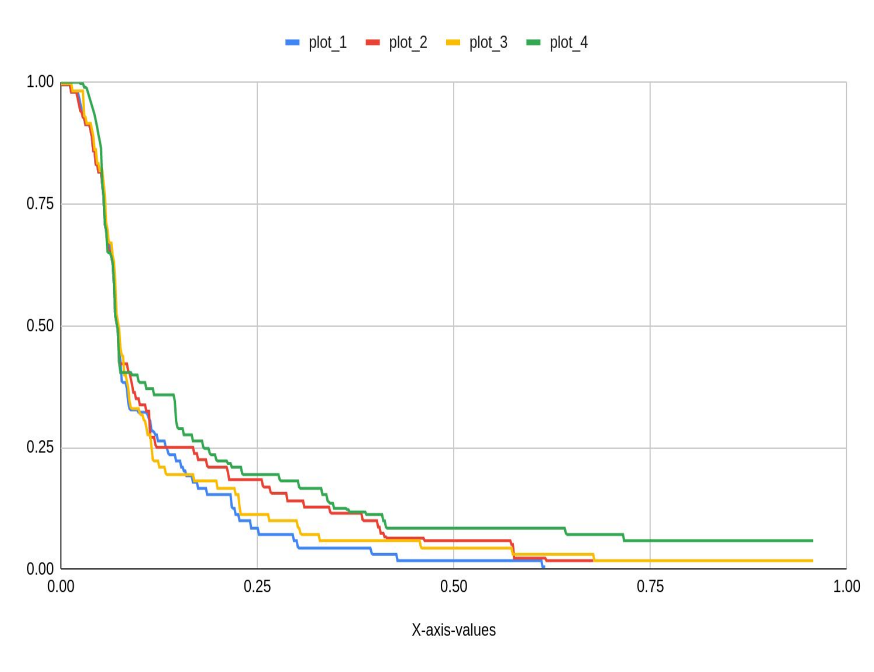
100
90
80
70
60
50
40
30
20
10
0
p=0.0960 (df=2)
0
3
6
9
12
15
18
21
24
(months)
O
N
Number of patients at risk :
Prior chemotherapy
85 89 69 44 25 12 8 7 5 No
51 55 40 24 18 14 10 10 7 Yes, without TMZ
146 156 131 85 60 39 30 26 19 Yes, with TMZ



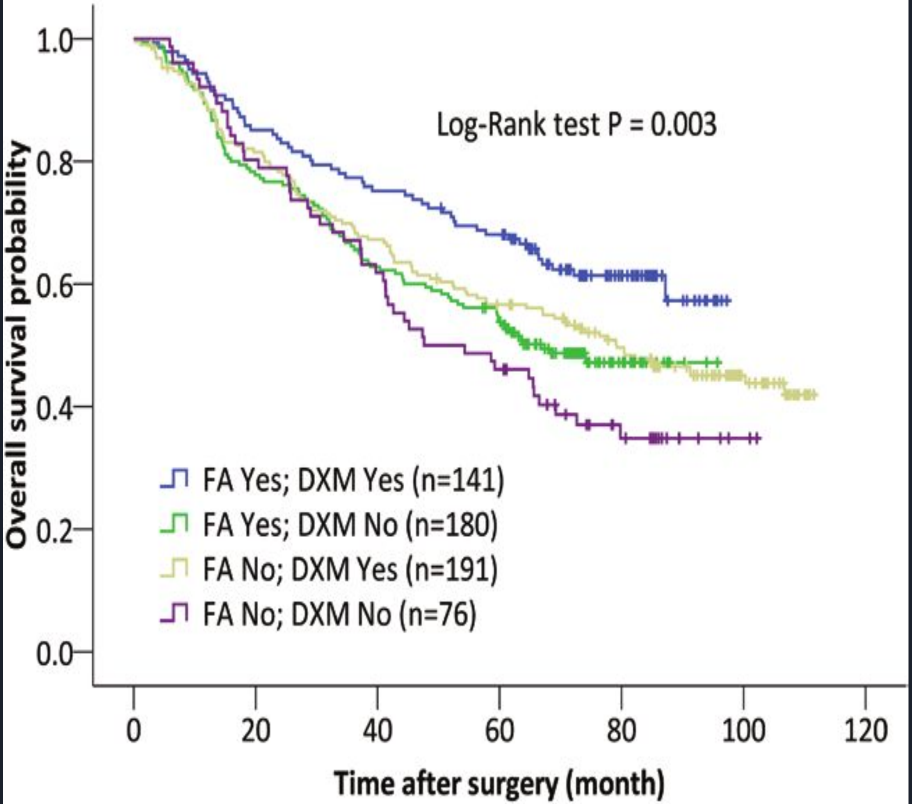
plot_1
plot_2
plot_3
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
X-axis-values

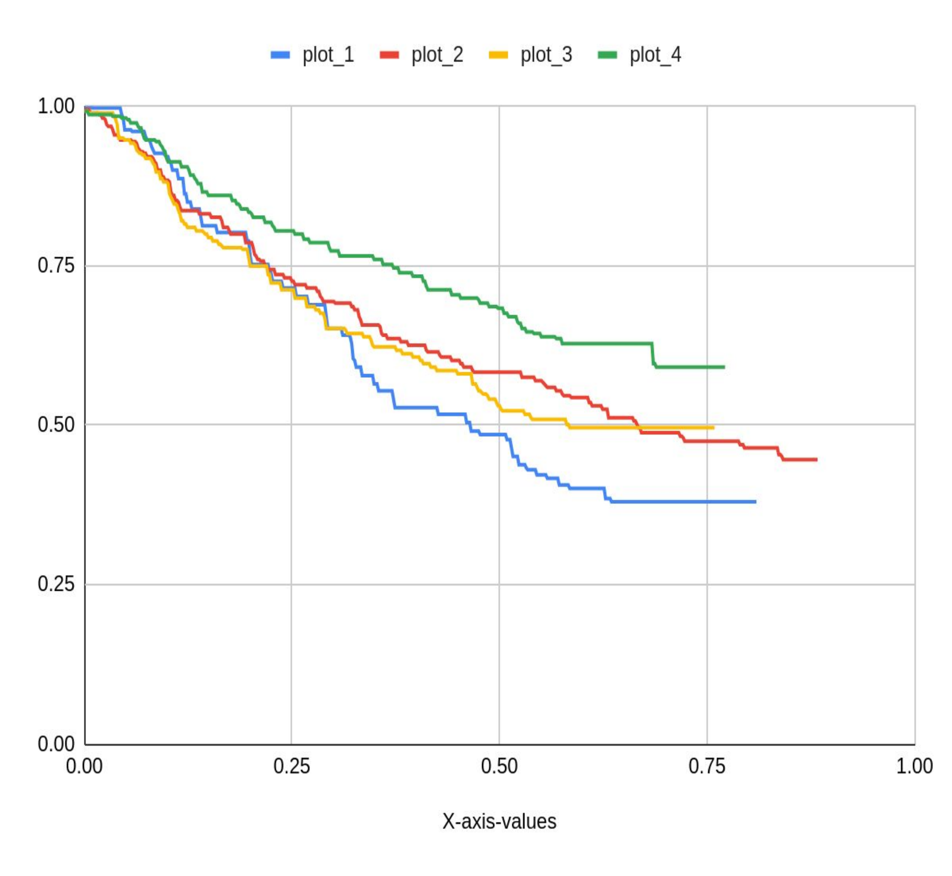


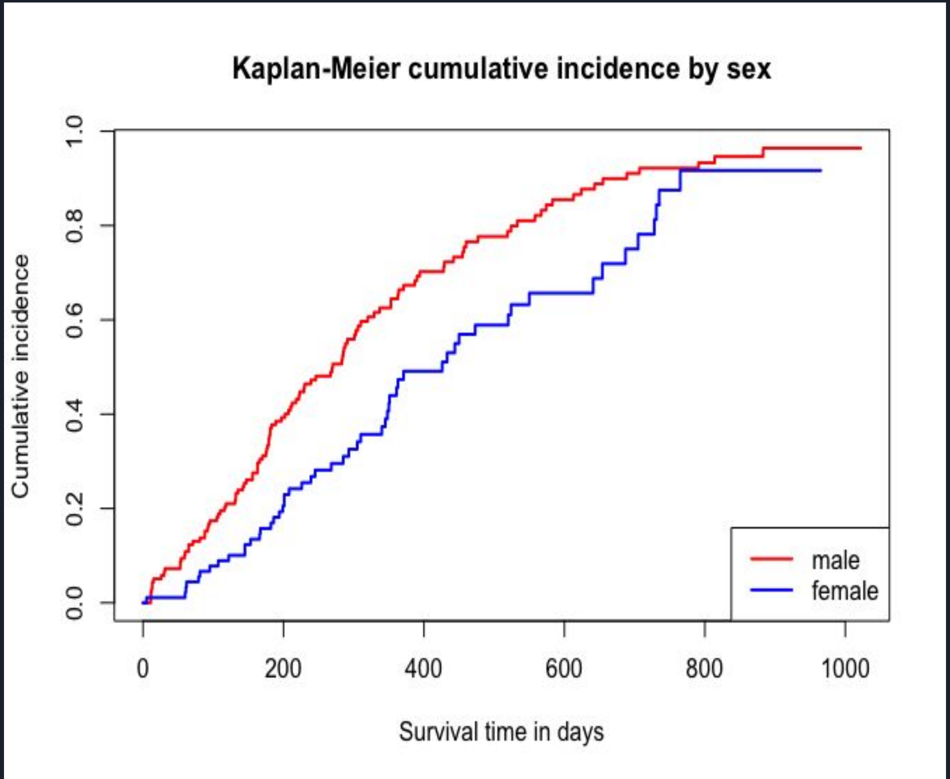
100
90
80
70
60
50
40
30
20
10
0
p=0.0873 (df=1)
(months)
0
3
6
9
12
15
18
21
24
O N Number of patients at risk :
72 73 26 14 8 6 6 4 4
72 73 18 13 8 4 1 1 1
73 73 19 6 3 1 0 0 0
73 73 15 8 4 3 2 1 1
Largest lesion area
<644
>=644 - <1290
>=1290 - <2303
>=2303



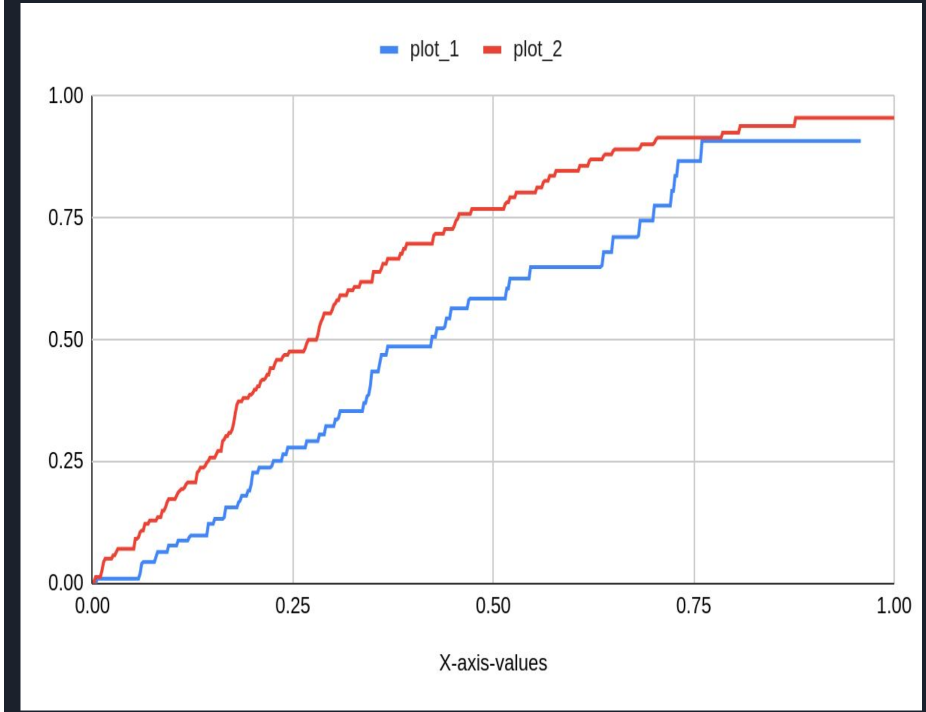
plot_1
plot_2
plot_3
plot_4
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
X-axis-values


Log-Rank test P = 0.003
Overall survival probability
1.0
0.8
0.6
0.4
0.2
0.0
FA Yes; DXM Yes (n=141)
FA Yes; DXM No (n=180)
FA No; DXM Yes (n=191)
FA No; DXM No (n=76)
0
20
40
60
80
100
120
Time after surgery (month)

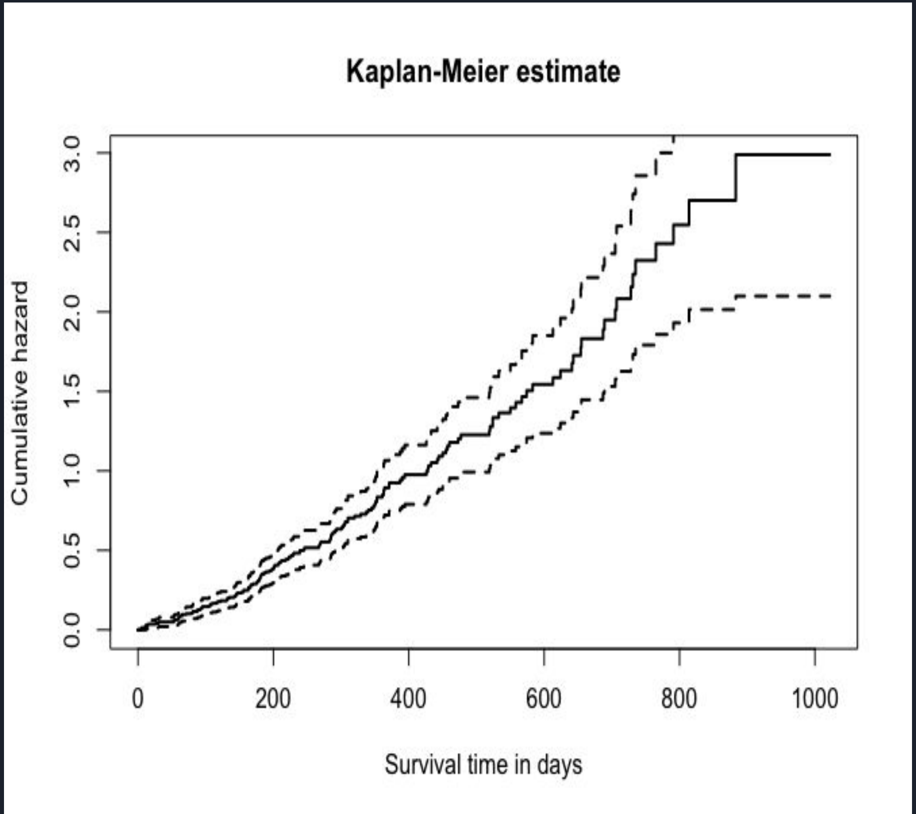

plot_1
plot_2
plot_3
plot_4
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
X-axis-values

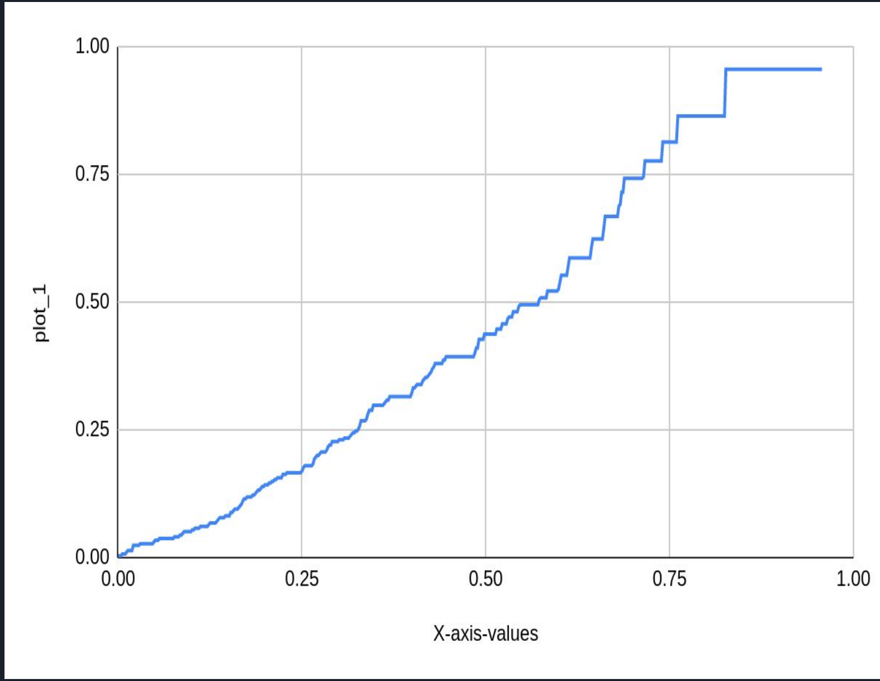


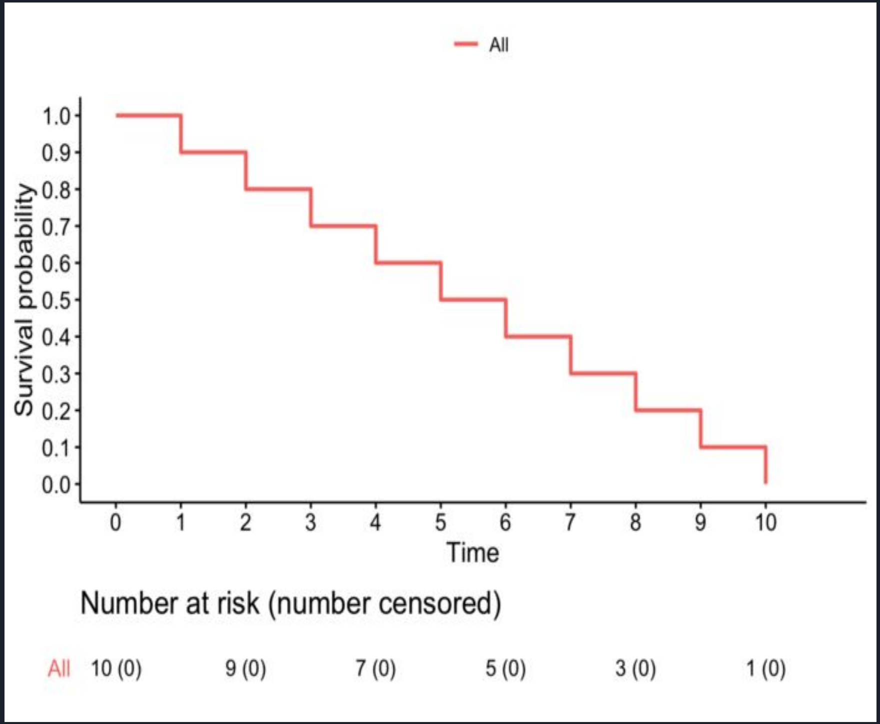
Kaplan-Meier cumulative incidence by sex
Cumulative incidence
0.0
0.2
0.4
0.6
0.8
1.0
0
200
400
600
800
1000
Survival time in days
male
female

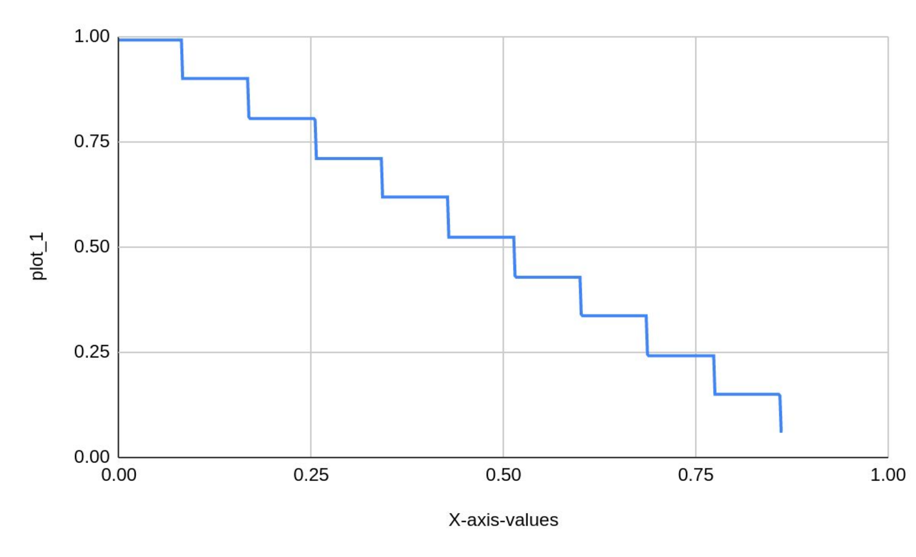


plot_1
plot_2
0.00
0.25
0.50
0.75
1.00
0.00
0.25
0.50
0.75
1.00
X-axis-values


Kaplan-Meier estimate
Cumulative hazard
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0
200
400
600
800
1000
Survival time in days


plot_1
0.00
0.25
0.50
0.75
1.00
0.00
0.25
0.50
0.75
1.00
X-axis-values


All
Survival probability
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0 1 2 3 4 5 6 7 8 9 10
Time
Number at risk (number censored)
All 10 (0) 9 (0) 7 (0) 5 (0) 3 (0) 1 (0)


plot_1
1.00
0.75
0.50
0.25
0.00
0.00 0.25 0.50 0.75 1.00
X-axis-values

Next Steps

- X axis scale identification
    - Current implementation identifies the x axis, and normalizes its range to [0,1]
    - Need to perform OCR in region below the x axis to identify the range to scale to.

- Handling dashed lines in plot
    - The current implementation relies on plots being large connected components for the following
        - Filtering out areas like the legend where smaller sections of the same colours may be found
        - Identifying the starting point of all plots
    - Once these logics are reworked, the same coordinate interpolation code is capable of handling dashed lines as well.

THANK YOU