

A large, stylized molecular structure in the top-left corner, featuring several large red spheres and one smaller black sphere connected by thin red lines.

Cancer Metastases Detection

COMS W4995 Applied Deep Learning
Hanjun Li

A smaller, stylized molecular structure in the bottom-right corner, featuring a central red sphere and several black spheres connected by thin black lines.

Outline

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INTRODUCTION

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and Motivation

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Data Preprocessing
and Model Training

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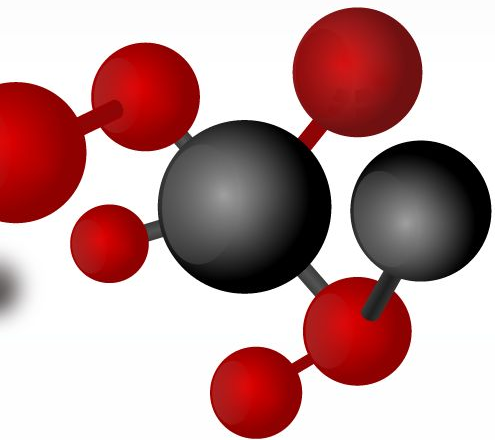
RESULTS ANALYSIS

Model Testing and
Metrics Evaluation

04

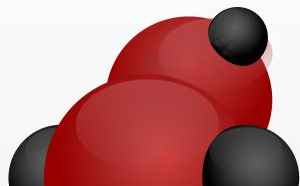
CONCLUSIONS

Limitation and Future
Improvement



01

INTRODUCTION



INTRODUCTION


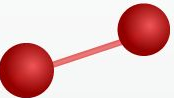


- **Motivation:** The process of manually performing metastasis detection is labor intensive and error-prone [1]. To relieve the workload of pathologists, scholars proposed utilizing deep learning models i.e. Convolution Neural Network (CNN), to assist pathologists by providing second opinions.
- **Objective:** Leverage deep learning model to detect tumor cells on gigapixel pathology image and experiment with multi-scale zoom levels



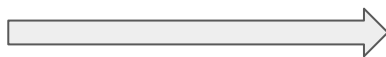


BACKGROUND

- Based on “*Detecting Cancer Metastases on Gigapixel Pathology Images*” (see reference for detail)
 - **KEY TAKEAWAYS:**
 - Utilize Inception (V3) architecture
 - Input patch size (299, 299, 3) and label of this patch is determined by the central 128*128 region; classify as **tumor** if at least one pixel in the central region is a tumor pixel
 - Use two levels of magnification
 - Data Augmentation helps
- 
- 

WORKFLOW

Data Preparation and
Visualization

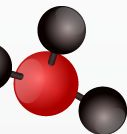


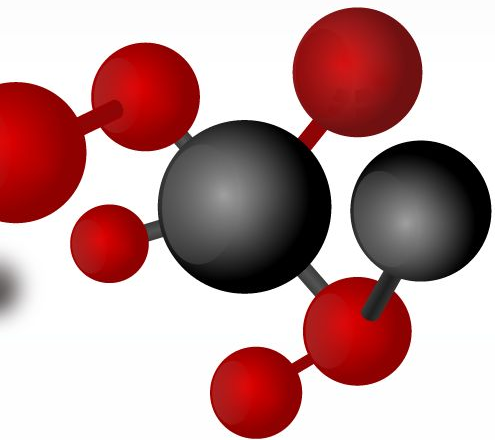
Train/Test Split, Patch
Generation

Model Testing and
Generate Heatmap



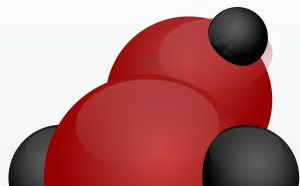
Model Building





02

METHODOLOGY



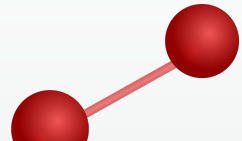


Data Content

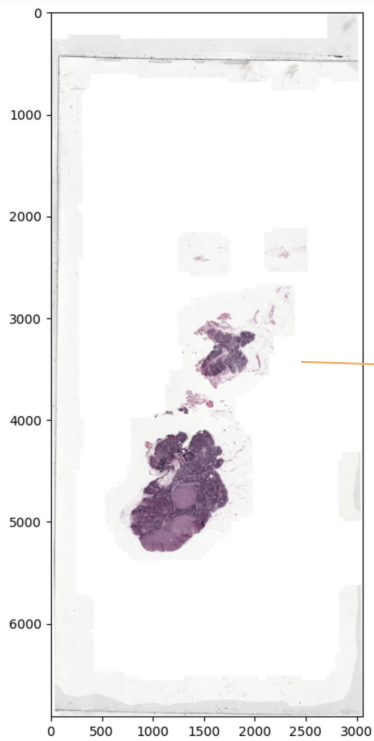


- **Dataset:** Camelyon16
- **Input:** lymph node digitized images, tumor mask
- Different zoom level associates with different dimension and downsample factor (lower level has higher resolution)

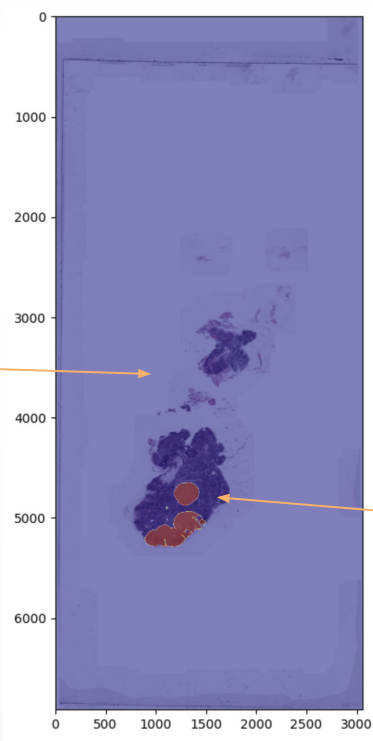
```
Read WSI from /content/gdrive/MyDrive/ADL_Project/slides/tumor_016.tif with width: 97792, height: 221184
Read tumor mask from /content/gdrive/MyDrive/ADL_Project/slides/tumor_016_mask.tif
Slide includes %d levels 10
Level 0, dimensions: (97792, 221184) downsample factor 1
Level 1, dimensions: (48896, 110592) downsample factor 2
Level 2, dimensions: (24448, 55296) downsample factor 4
Level 3, dimensions: (12224, 27648) downsample factor 8
Level 4, dimensions: (6112, 13824) downsample factor 16
Level 5, dimensions: (3056, 6912) downsample factor 32
Level 6, dimensions: (1528, 3456) downsample factor 64
Level 7, dimensions: (764, 1728) downsample factor 128
Level 8, dimensions: (382, 864) downsample factor 256
```



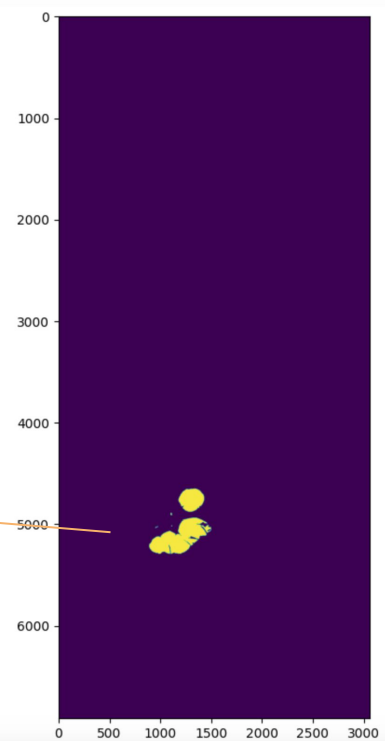
VISUALIZATION



Slide 016 at zoom level 5

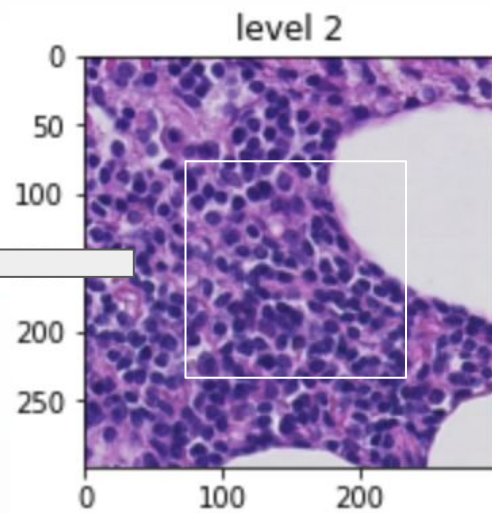
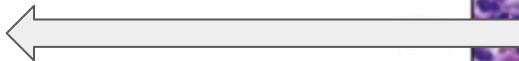
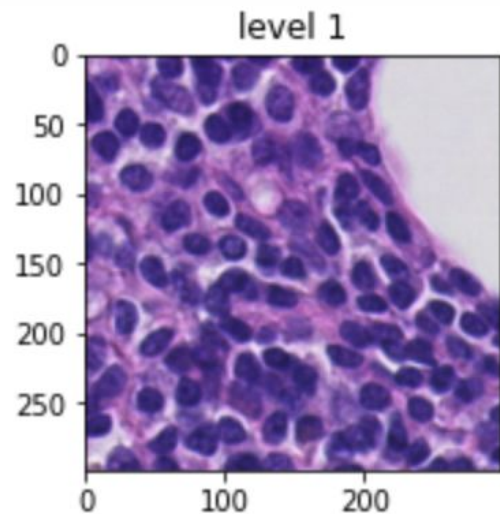


Overlay Slide 016



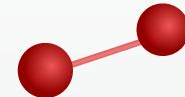
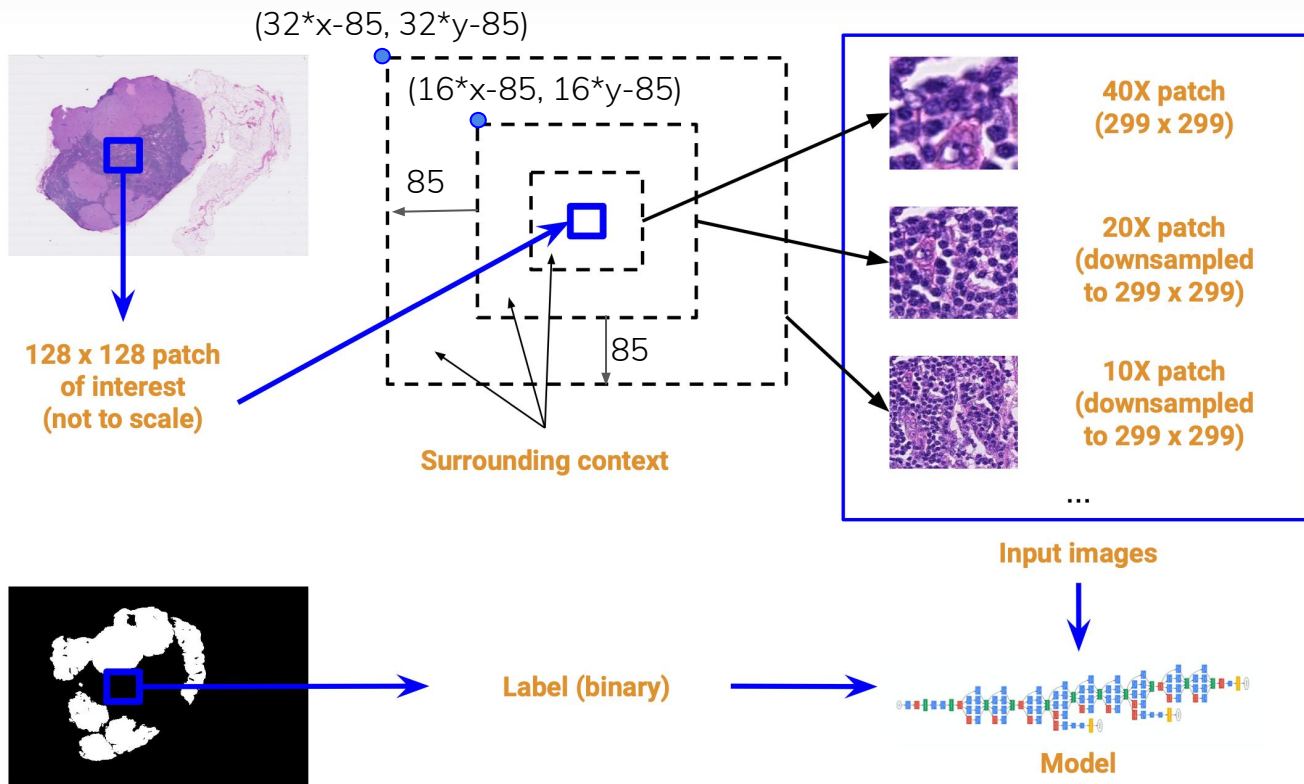
Mask 016 at zoom level 5

VISUALIZATION





PIPELINE





PATCH GENERATION

```
patch_generator(slides, tumor_masks, zoom_level_1, zoom_level_2,  
                tissue_percentage=30, base_zoom_level=5, center_size=128, patch_size=299, n_sample=250)
```

1.

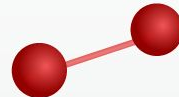
For each slide image, get all the normal pixels and tumor pixels i.e.(x, y) pairs, and retrieve the center of this patch

2.

Repeatedly generate normal patches by locating the central region until n_sample is met

3.

Repeatedly generate tumor patches by locating the central region until n_sample is met

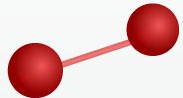





PATCH GENERATION


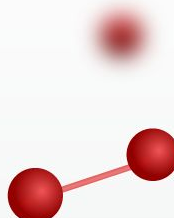
- Training Slide: 016, 075, 101, 110
- Validation Slide: 064, 094
- Testing Slide: 084, 091

	Tumor	Normal
Training Data	1017	983
Validation Data	506	494



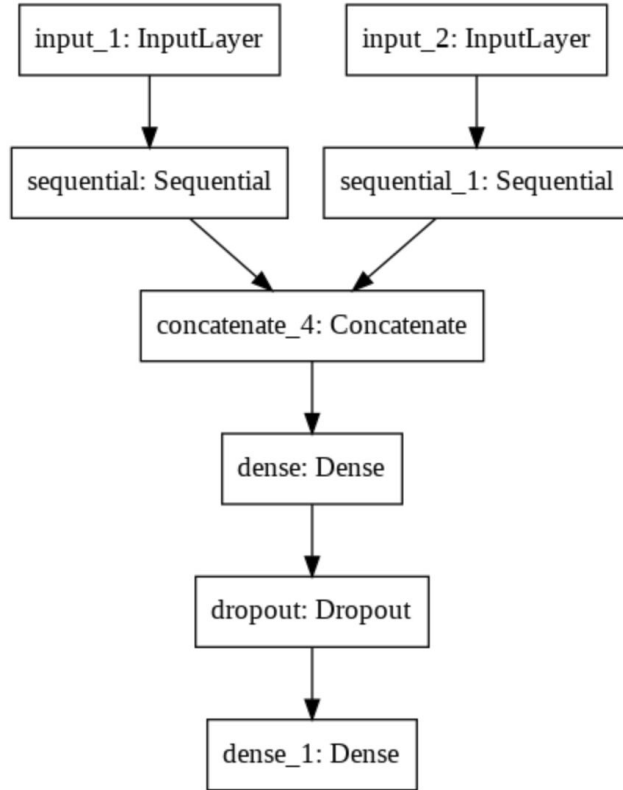



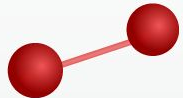
DATA AUGMENTATION

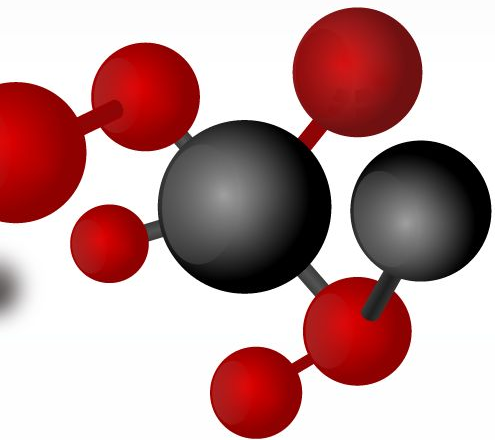
- Horizontal Flip
 - Vertical Flip
 - Rotation 90 degree
 - Shear range 0.2
 - Brightness: [0.7, 1.3]
- 
- 



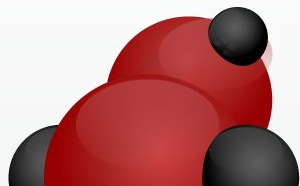
MODEL BUILDING



- InceptionV3 as base model
 - Concatenate model using zoom level 0 and model using zoom level 1
 - 0.2 Dropout is used
 - A dense layer with sigmoid activation function is built on top
- 
- 

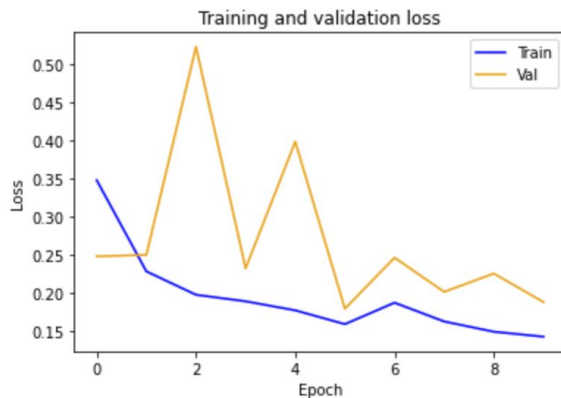
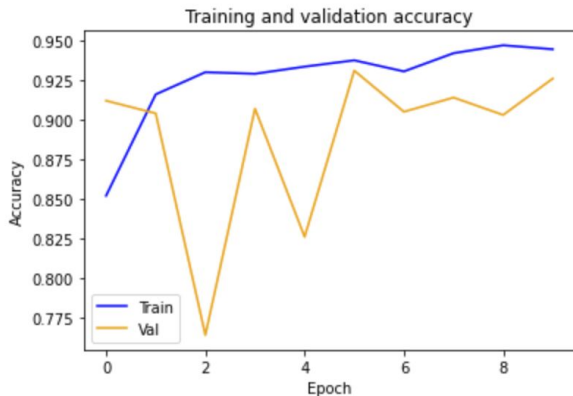


03
RESULT

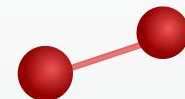




TRAINING MODEL RESULT

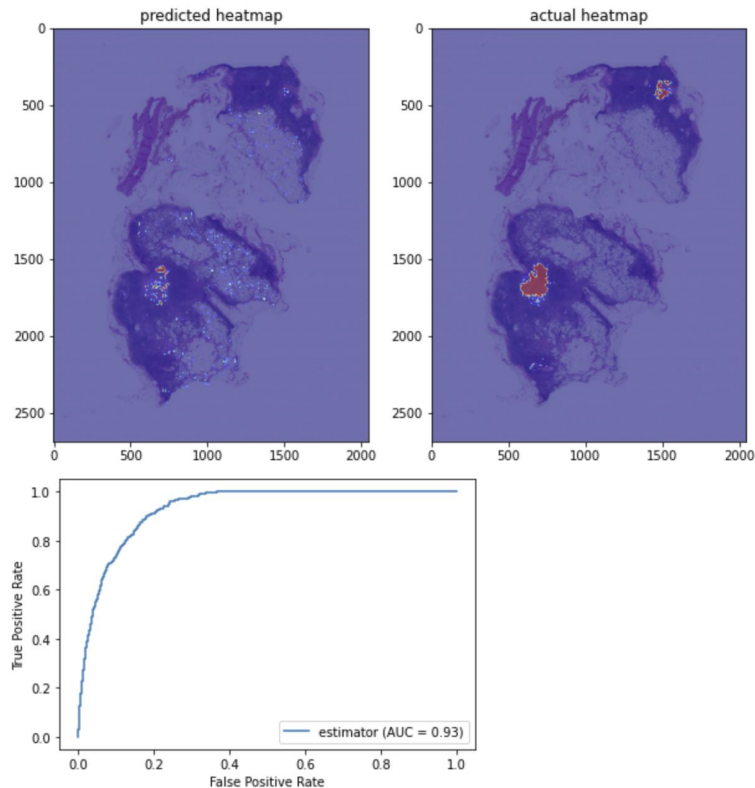


	loss	accuracy
training	0.1309	0.9460
validation	0.1882	0.9260



TESTING SLIDE 084

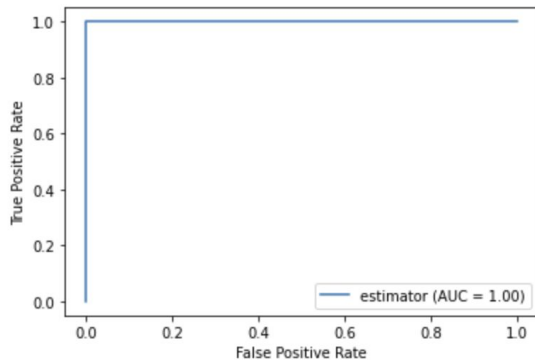
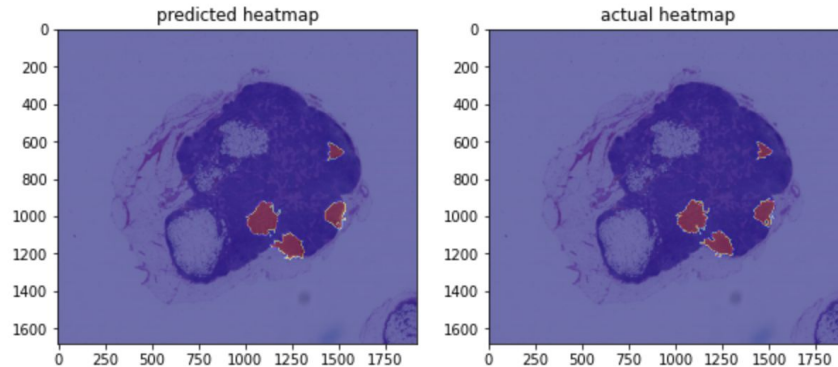
AUC: 0.9305, F1 Score: 0.1791, Precision: 0.1338, Recall: 0.2712, ROC AUC Score: 0.9305



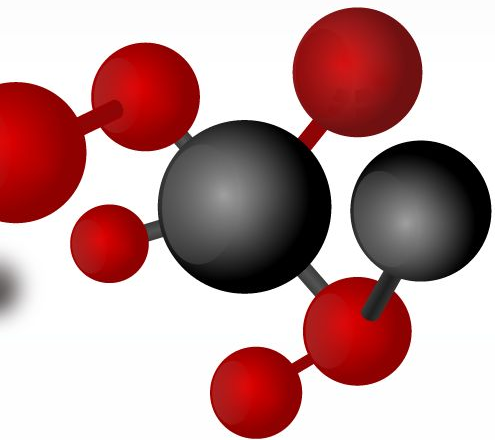
- Using 0.7 as threshold while predicting labels

TESTING SLIDE 091

AUC: 1.0000, F1 Score: 1.0000, Precision: 1.0000, Recall: 1.0000, ROC AUC Score: 1.0000

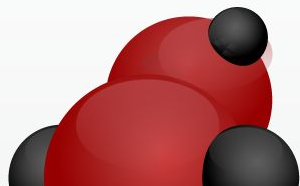


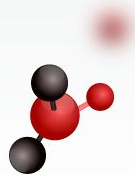
- Using 0.7 as threshold while predicting labels



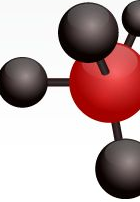
04

CONCLUSION

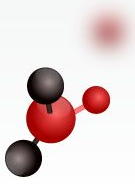




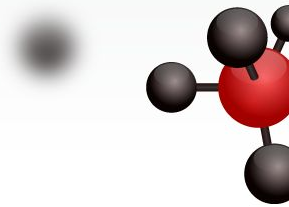
CONCLUSION



- This model performs surprisingly well on slide 091, but not as well on slide 084
- **Limitation:** limited dataset and the model requires excessive amount of RAM, which makes it unrealistic to train and test on local machine
- **Next step:**
 - Get more data
 - handle margin while finding pixels in a slide
 - Better model and threshold tuning



Reference



- [1] [Detecting Cancer Metastases on Gigapixel Pathology Images](#)

The slide features several decorative molecular models. In the top left, there is a small molecule with two red spheres connected by a thin red line, and another red sphere below it. In the top center, there is a large, dense cluster of many red spheres. To the right of this cluster, there is a single red sphere. On the far right edge, there is a molecule with two black spheres and one red sphere. The word "THANKS" is centered in a large, bold, red font.

THANKS

For more details: <https://github.com/BrianHJLi/Tumor-Tissue-Detection>

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