IPGP3: Cancer Genome Tech Assist (CGTA)

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Introduction

The increasing incidence of cancer is a serious problem in our society. Usually, most types of cancer are difficult to diagnose. By using concepts from deep neural networks and supervised learning, Cancer Genome Tech Assist (CGTA) processes a lung image by segmentation, and determines normal or abnormal cellular regions. With this, we hope to assist doctors and patients in their fight against cancer.

現代社会において，癌発生率の増加は，深刻な問題となっている．一般的に，多くの癌は診断することが困難である．ディープ・ニューラルネットワークと教師あり学習を用いて，Cancer Genome Tech Assist (CGTA)は肺画像をセグメント処理し，病的な細胞部位かどうかを判断する．これに伴い，本研究では医者と癌患者の闘病生活を支援することを考える．

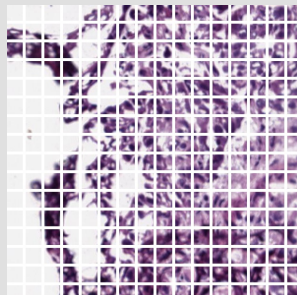## Training

Data from The Cancer Genome Atlas database were used for training.

1 Collect data of size 512x512 from the Cancer Genome Atlas Database
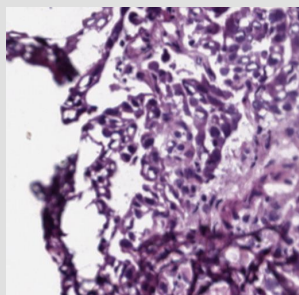
2 Segmentation into smaller regions

3 Train the data set using Deep Neural Network or Bayesian filter.

$$h_\theta(\mathbf{x}) = \frac{2}{1 + \exp(\theta^T \mathbf{x})}$$

$$\arg \max_{G \in \{N, B, C\}} P\left(G | \tilde{f}_1, \tilde{f}_2, \ldots, \tilde{f}_n\right)$$

Testing and Visualization

Images may be uploaded to the website for testing.

1 Upload biomedical images on the website's homepage.

Cancer Genome Technical Assist — Upload — About — Docs

Image Upload

STEP ONE
Type of Classification:
- ○ DNN
- ○ Bayes

STEP TWO
Select an image:
Choose File   No file chosen

STEP THREE
Upload Image

2 Test image is segmented accordingly and evaluated for each subregion.