HomogenMSI

Mridula Prasad

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1 Introduction

HomogenMSI package contains function calculateDHI that derives drug homogeneity index value from the MSI data, using following formula:

$$DHI = \frac{\frac{\sum_{i=1}^{N} g \sum_{j=Nu}^{N} zjP(i,j)}{\sum_{i=1}^{N} g \sum_{j=Nu}^{N} zP(i,j)}}{TumorArea}$$
 (1)

Here, P is the gray level size-zone matrix(GLSZM)

Ng is number of gray levels/rows in GLSZM

Nz is number of size zones/columns in GLSZM

P(i,j) is the frequency for particular gray level i occupided size zone j

j is the absolute size zone value

Tumor Area is the size of the tumor tissue

To derive DHI value from our synthetic imaging datasets, run following commands:

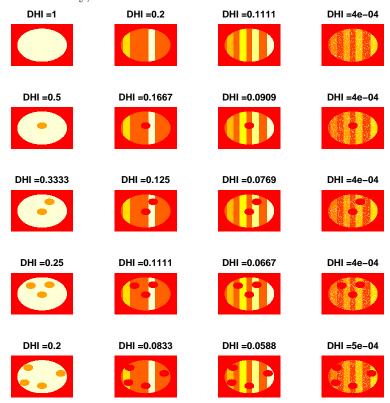
- > data("DHIimages")
- > drugImg = DHIimages[[20]]
- > maskImg = DHIimages[[1]]
- > maskImg[maskImg !=0] =1
- > print(CalculateDHI(drugImg,maskImg= maskImg))

[1] 0.0004664179

> print(CalculateDHI(drugImg,maskImg= maskImg,QuantLevel=0,Nu=5))

[1] 0.0339908

In similar way, DHI can be calculated for the rest of the images.



Note: our DHI formula will not work for image 1, as only single gray level present.