Some tools in bioimagetools

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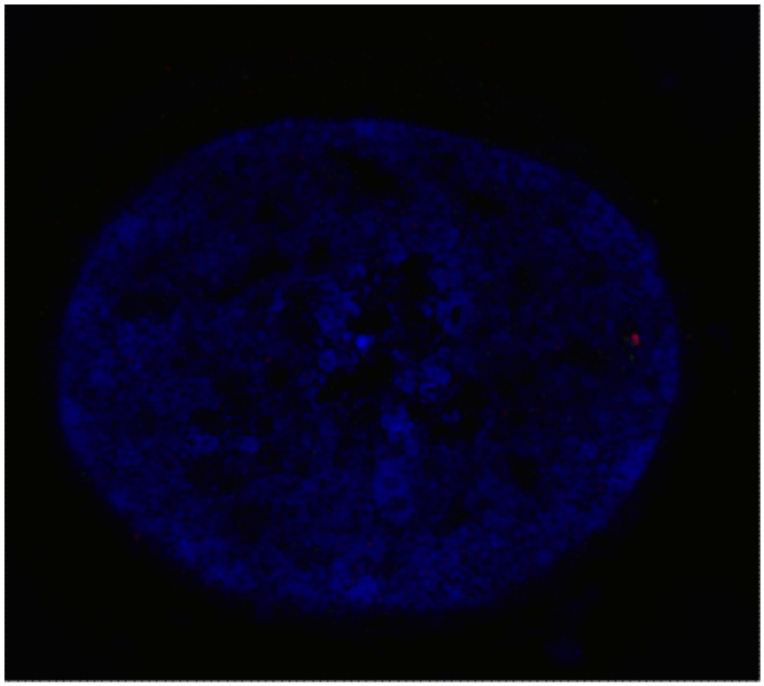
Contents

1 Basis operations: Read and write tiff and bmp.

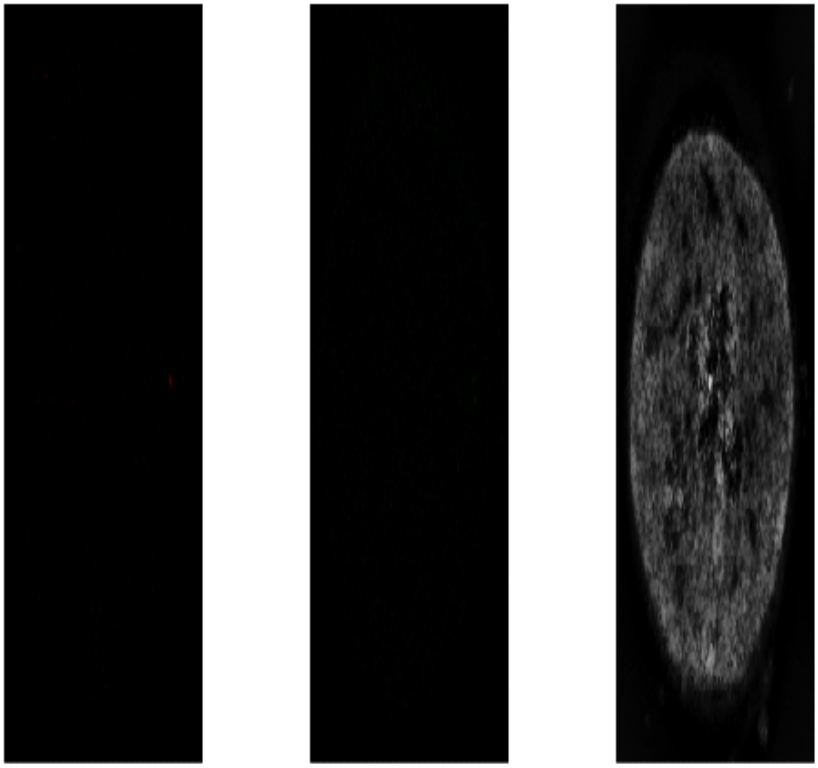
`readTIFF()` and `writeTIFF()` in the `tiff` package do not handle 3d stacks the right way. `bioimagetools` uses `readTIF()`.

```
library(bioimagetools)

## Loading required package:  EBImage
## Bioimagetools ver.0.3.22

cell <- readTIF("http://ex.volkerschmid.de/cell.tif")

## Warning in readTIFF(file, all = TRUE, info = TRUE, as.is = as.is,
native = native):  TIFFReadDirectory:  Unknown field with tag 50838
(0xc696) encountered
## Warning in readTIFF(file, all = TRUE, info = TRUE, as.is = as.is,
native = native):  TIFFReadDirectory:  Unknown field with tag 50839
(0xc697) encountered

print(dim(cell))

## [1] 512 512   3  52

img(cell, z=25 ,col="rgb")
```

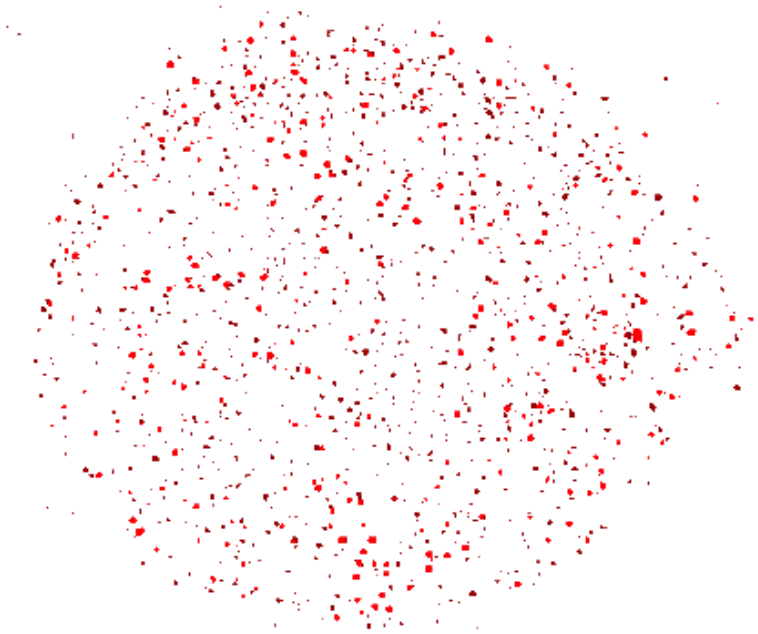


`img()` is a plotting function. It expects a 2d array, unless `col="rgb"`, which produces a color plot.

```
par(mfrow=c(1,3))
img(cell, z=25, col="r")
img(cell, z=25, col="g")
img(cell, z=25, col="grey")
```



```
writeTIF(cell, file="my_cell.tif")

## [1] 52

red <- cell[,,1,]
green <- cell[,,2,]
simple <- 2*EBImage::thresh(red)+EBImage::thresh(green)
writeTIF(simple, file="simple.tif")

## [1] 52

mysimple <- readClassTIF("simple.tif")
img(mysimple[,,25],col="red",up=3)
```



```
## [1] TRUE
## [1] TRUE
```

Unrelated, Bitmap files can be read

```
bi<-readBMP("http://www.statistik.lmu.de/institut/ag/bioimg/bit/ratbert.bmp")
img(bi,col="greyinvert")
```