Bounding boxes for Type_1

posted in Intel & MobileODT Cervical Cancer Screening 10 months ago

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Disclaimer

I am not an MD, but I have a masters in biology and I'm doing a PhD in oncology (bioinformatics side). I annotated on all images what looked like epithelial lesions, but I cannot guarantee perfect labelling.

Script to annotate

I edited this script for the natural conservancy fish so that I could label more than one object per image. I'm not sure that it's super helpful here but I kept it this way. My python script using OpenCV2 is also attached, use, edit or share as permitted by the licenses of sqshemet.

Results

Format

The file is space separated with columns:

Filenames | number of rectangles | min(x1) | min(y1) | width1 | height1 (addtional coordinates if more than one rectangle).

x,y ,width, height

x,y, width and height are pixel divided by two compared to the full size image (this was only due to the fact that some images did not fit my screen otherwise). Please take this into account when resizing.

Additional notes:

1. The paths are "Windows" style, so you may want to change "\" to "/" for Unix users
2. Feel free to comment or suggest improvements in the annotations.

Skipped images

I skipped some images when I had no idea about what should be annotated. I wanted to information as accurate as possible.

Type_1_bbox.tsv (8.82 KB)
ObjectMarker2.py (7.78 KB)
Type_2_bboxes.tsv (27.3 KB)
Type_3_bbox.tsv (15.52 KB)

XuleiYang • 10 months ago • Options • Reply 1

Thanks Paul for the great efforts to come out the bounding box. Will you continue the annotations for the rest?

Paul • 10 months ago • Options • Reply 3

Hi,

I have just added bounding boxes for type 3 also. I don't plan on using and annotating the additional dataset so far if that was your question.

XuleiYang • 10 months ago • Options • Reply 1

Hi Paul, type 3 is exactly what I asked for, thank you very much.

XuleiYang • 10 months ago • Options • Reply 1

Thanks Paul, type 3 is exactly what I asked for, really appreciated!

Neha • (20th in this Competition) • 10 months ago • Options • Reply 0

Hi Paul, Thanks for doing annotations. I have a question regarding x, y, width, and height values. You mentioned that these values are pixel divided by two, so in order to get actual bounding box on original image we have to multiply these values by 2 ?

Paul • 10 months ago • Options • Reply 0

Hi Neha,

I wanted to post a notebook to display the bounding boxes, but I cannot find how to import the annotation files. To answer your question, the resize only impacts the window size, but not the output. So what you have are the original size.

Paul • 10 months ago • Options • Reply 0

Just to let you know, I tried to upload the notebook I used to check boxes here: https://www.kaggle.com/deveaup/intel-mobileodt-cervical-cancer-screening/checking-bounding-boxes I don't see anything so I don't know if the error is on my side or Kaggle or anything. Let me know if needed.

authman • 9 months ago • Options • Reply 0

Seeking clarification:

> I annotated on all images what looked like epithelial lesions, but I cannot guarantee perfect labeling.

Epithelial lesions consist of squamous and columnar cells; what I'm seeing in these annotations for the *most* part seems like the bboxes are for the squamocolumnar junction, although occasionally they are for the entire cervical border. Can you confirm your original intent? Was it for the cervical border, the SJ or the OS?

Thank you!

Paul • 9 months ago • Options • Reply 0

Hi,

I annotated everything that did not look like smooth epithelial tissue. I have to say that it's much harder than annotating animal images, since I'm much more familiar with the latter. I have annotated anything that seemed abnormal, for example presence of blood.

I you think that something has to be corrected, can you give an example (image number and what you would have annotated instead)?

Han199214chen • 8 months ago • Options • Reply 0

Thanks for your annoation. I have refined some annoations of yours and support for everybody. The file is in "https://github.com/ChenhanXmu/Cervical_Cancer". But I can't ensure that the work shall be done in the right way.