breast_victre - Installation #6527

Install version 20221013

2022-10-20 04:09 PM - Albert van Eck

Status:	Resolved		**Start date:**	2022-10-20
Priority:	Normal		**Due date:**	
Assignee:	Albert van Eck		**% Done:**	100%
Category:			**Estimated time:**	2.00 hours
Target version:			**Spent time:**	4.00 hours

Description

History

#1 - 2022-10-20 04:10 PM - Albert van Eck

- % Done changed from 0 to 100

- Status changed from New to Resolved

Dear HPC User

To make use of the VICTRE Breast pipeline, please follow the instructions below.

To install the pipeline, execute the following command, and follow the instructions provided by the command itself.
module help breast_victre

The pipeline requires that you have the Python code calling the pipeline, within the same directory where the pipeline is installed. When following the instructions as mentioned by the module help command, the default location will be in your home-directory under a directory called VICTRE_PIPELINE
Therefore, suppose you want to execute a file named example5.py, follow these instructions:
cp <Path where the file resides>/example5.py   ~/VICTRE_PIPELINE/

If you make use of the MCGPU projection function, you have to submit the job to a GPU node. The following example can be saved into a PBS submit file, to execute your pipeline on a node with a GPU:

```
#!/bin/bash
#PBS -N example5
#PBS -l nodes=1:ppn=10:gpus=1:gpu
#PBS -l walltime=40:00:00
#PBS -S /bin/bash

module purge &>/dev/null
module load hpc &>/dev/null
module load breast_victre
cd ~/VICTRE_PIPELINE

python example5.py
result=$?
exit $result ######################################
```

After the job completes, your results should be saved in a sub-folder called results under the pipeline directory, e.g.:
~/VICTRE_PIPELINE/results