

Feb 12th 2020.

Virtual environment setup:

Python 3.6.7 64-bit ("virpy3.6":venv)
Tensorflow-gpu==1.14.0

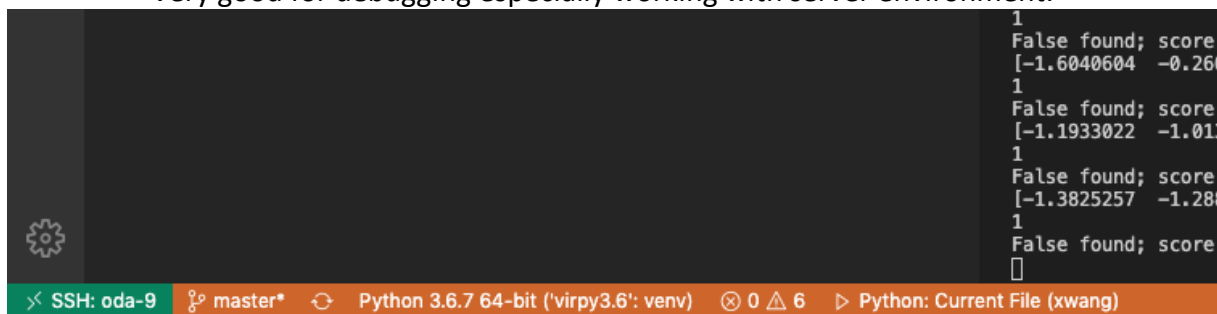
No more error when installing these.

Jupyter Binder <https://jupyter.org/binder>
<https://github.com/jupyterhub/binderhub>

- Similar to docker to make sure the correct version/environment when running/development programs.

VSCode (Visual Studio Code) <https://code.visualstudio.com/>

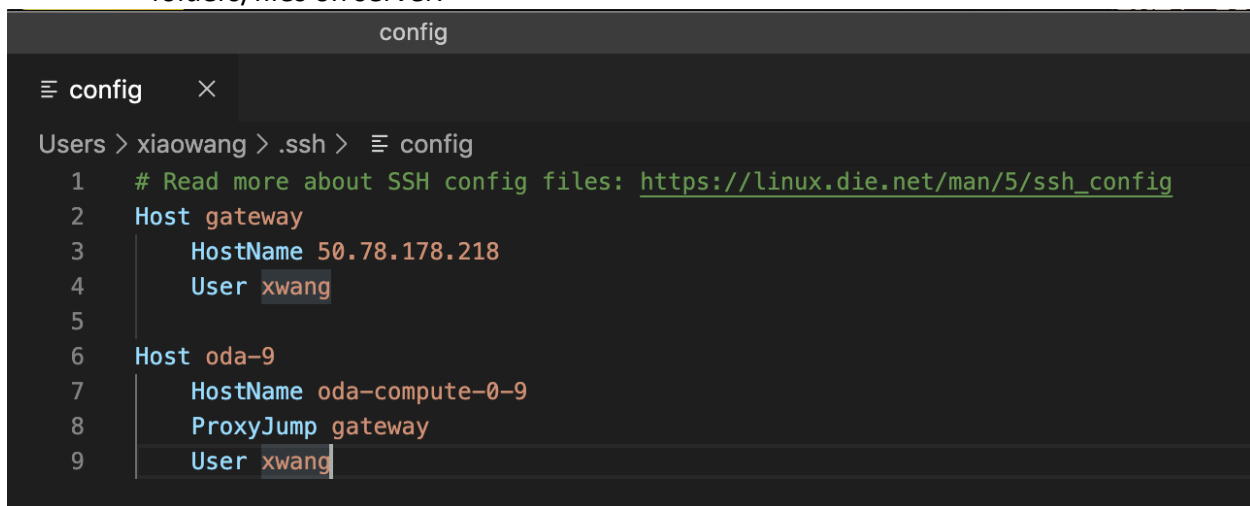
- Very good for debugging especially working with server environment.



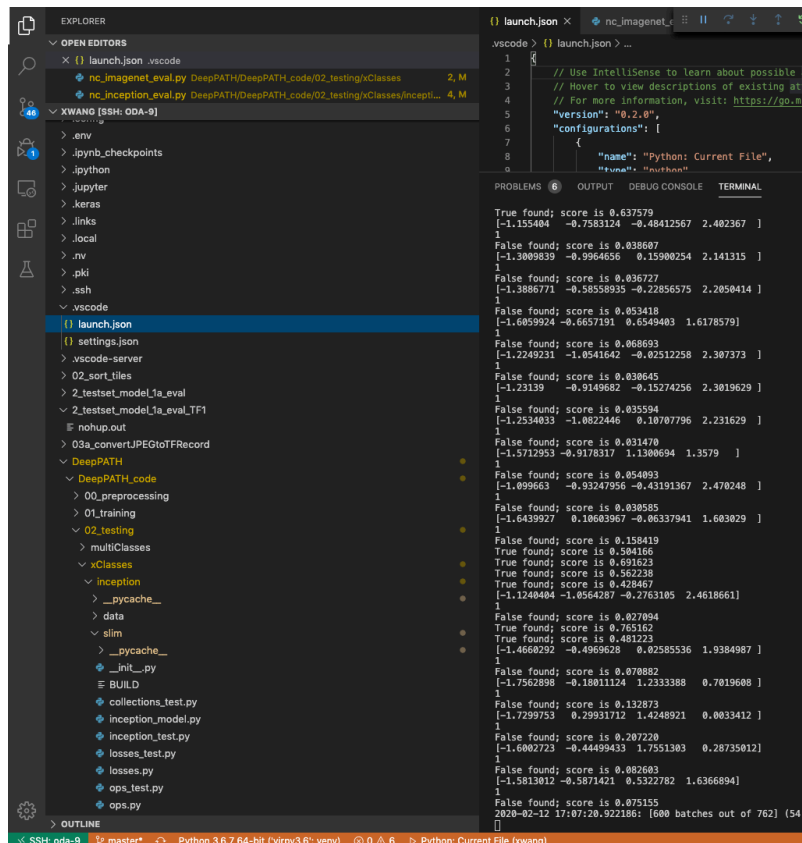
```
1
False found; score
[-1.6040604 -0.260
1
False found; score
[-1.1933022 -1.011
1
False found; score
[-1.3825257 -1.288
1
False found; score
[]
```

SSH: oda-9 master* Python 3.6.7 64-bit ('virpy3.6': venv) 0 6 Python: Current File (xwang)

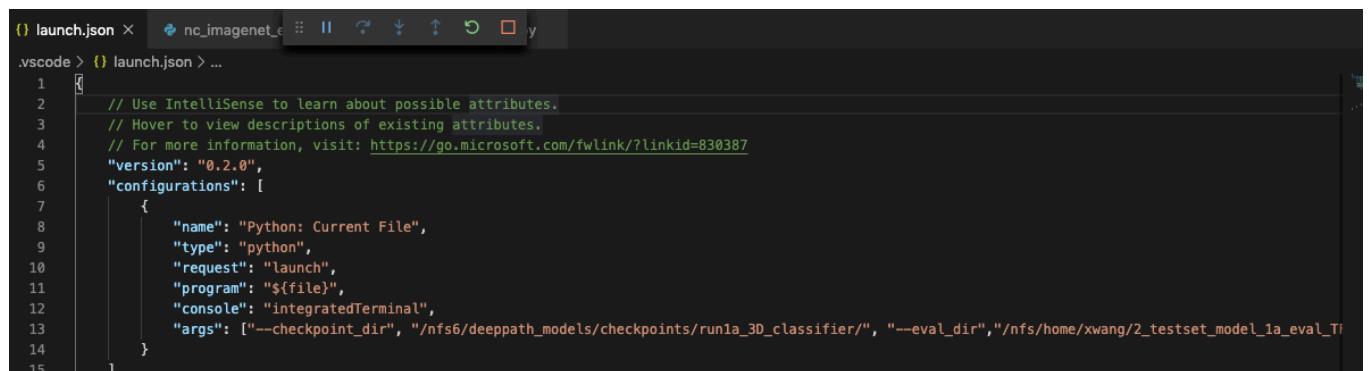
- Need to set up the config for Remote Explorer, you will see and work with all the folders/files on server.



```
config
Users > xiaowang > .ssh > config
1 # Read more about SSH config files: https://linux.die.net/man/5/ssh_config
2 Host gateway
3     HostName 50.78.178.218
4     User xwang
5
6 Host oda-9
7     HostName oda-compute-0-9
8     ProxyJump gateway
9     User xwang
```



- When debugging, use step in, step over, step out and continue. You can also use DEBUG console to print out every line or variables of desire.
- Use launch.json file to feed in command line argument for python script.

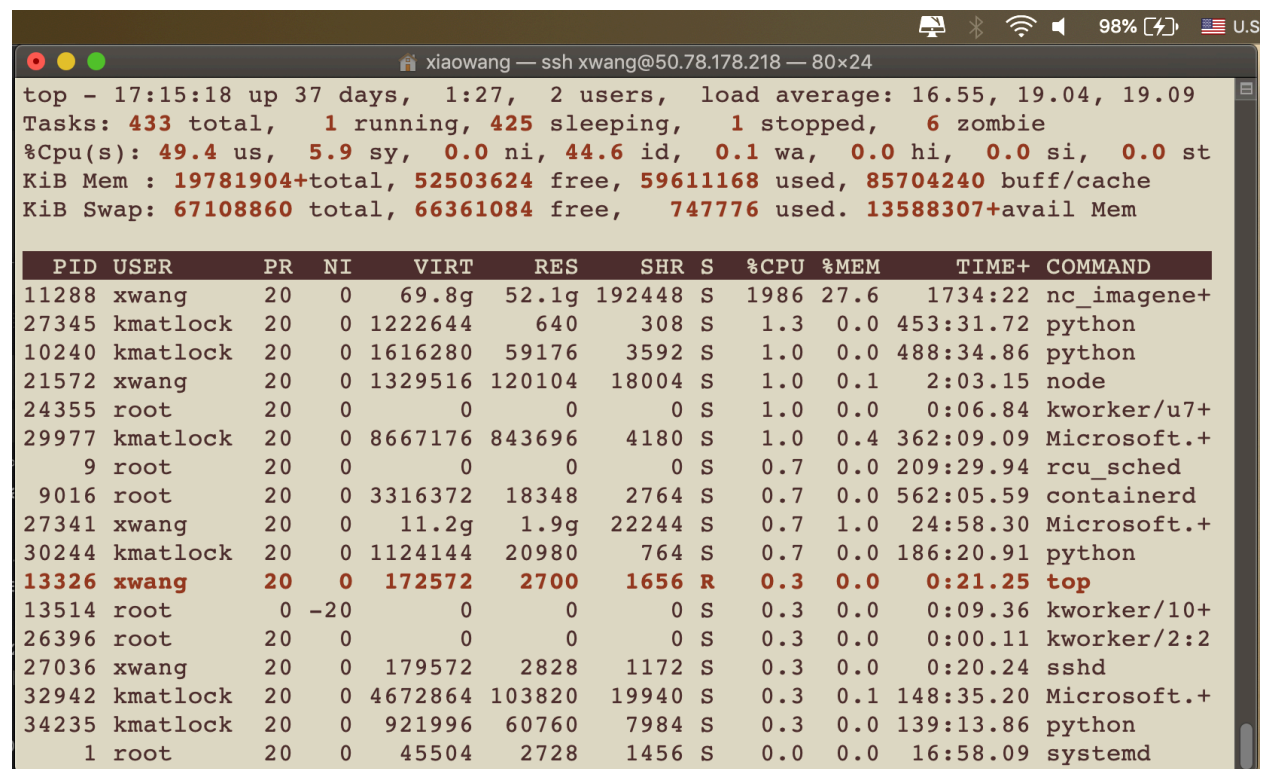


Solved the error problem:

Need to set the num of class to 3. DeepPATH 1a model is using 3 class (normal/LUAD/LUAD). The DeepPATH scripts nc_imagenet_eval.py is not fixable with number of classes I think. And because we are loading the previous saved model, our parameters for number of classes should match with their save model, otherwise, Invalid Argument. https://github.com/ncoudray/DeepPATH/tree/master/DeepPATH_code/example_TCGA_lung/c_checkpoints

```
oint_path)
pl.InvalidArgumentError: Restoring from checkpoint fail
en the current graph and the graph from the checkpoint.
graph expected based on the checkpoint. Original error:

s to match. lhs shape= [2048,3] rhs shape= [2048,4]
ed at nfs/home/xwang/DeepPATH/DeepPATH_code/02_testing/
```



The screenshot shows a terminal window with the following content:

top - 17:15:18 up 37 days, 1:27, 2 users, load average: 16.55, 19.04, 19.09
Tasks: 433 total, 1 running, 425 sleeping, 1 stopped, 6 zombie
%Cpu(s): 49.4 us, 5.9 sy, 0.0 ni, 44.6 id, 0.1 wa, 0.0 hi, 0.0 si, 0.0 st
KiB Mem : 19781904+total, 52503624 free, 59611168 used, 85704240 buff/cache
KiB Swap: 67108860 total, 66361084 free, 747776 used. 13588307+avail Mem

PID	USER	PR	NI	VIRT	RES	SHR	S	%CPU	%MEM	TIME+	COMMAND
11288	xwang	20	0	69.8g	52.1g	192448	S	1986	27.6	1734:22	nc_imagenet+
27345	kmatlock	20	0	1222644	640	308	S	1.3	0.0	453:31.72	python
10240	kmatlock	20	0	1616280	59176	3592	S	1.0	0.0	488:34.86	python
21572	xwang	20	0	1329516	120104	18004	S	1.0	0.1	2:03.15	node
24355	root	20	0	0	0	0	S	1.0	0.0	0:06.84	kworker/u7+
29977	kmatlock	20	0	8667176	843696	4180	S	1.0	0.4	362:09.09	Microsoft.+
9	root	20	0	0	0	0	S	0.7	0.0	209:29.94	rcu_sched
9016	root	20	0	3316372	18348	2764	S	0.7	0.0	562:05.59	containerd
27341	xwang	20	0	11.2g	1.9g	22244	S	0.7	1.0	24:58.30	Microsoft.+
30244	kmatlock	20	0	1124144	20980	764	S	0.7	0.0	186:20.91	python
13326	xwang	20	0	172572	2700	1656	R	0.3	0.0	0:21.25	top
13514	root	0	-20	0	0	0	S	0.3	0.0	0:09.36	kworker/10+
26396	root	20	0	0	0	0	S	0.3	0.0	0:00.11	kworker/2:2
27036	xwang	20	0	179572	2828	1172	S	0.3	0.0	0:20.24	sshd
32942	kmatlock	20	0	4672864	103820	19940	S	0.3	0.1	148:35.20	Microsoft.+
34235	kmatlock	20	0	921996	60760	7984	S	0.3	0.0	139:13.86	python
1	root	20	0	45504	2728	1456	S	0.0	0.0	16:58.09	systemd

Next Step:

1. Waiting for this 1a model to finish and check the result. Current result is running test TFRecords for inference.
2. We could change parameters in previous pre-processing steps to larger value for background filtering, so that the quality of these image may result in better accuracy.
3. Clarifying how DeepPATH calculate the results / accuracy with softmax.

nohup python

```
/nfs/home/xwang/DeepPATH/DeepPATH_code/02_testing/xClasses/nc_imagenet_eval.py --  
checkpoint_dir=/nfs6/deeppath_models/checkpoints/run1a_3D_classifier/ --  
eval_dir=/nfs/home/xwang/2_testset_model_1a_eval_TF1/ --  
data_dir=/nfs/home/xwang/03a_convertJPEGtoTFRecord/03a_TFRecord_test/ --batch_size 30 -  
-ImageSet_basename='test_' --run_once --ClassNumber 3 --mode='0_softmax' --TVmode='test'
```

Image Processing Project:

Cross correlation registration

Watershed

During interview meeting, the introductions of oda:

OpenMrs (reference schema for EHR dataset) <https://openmrs.org/>

OpenMRS 是一个协作性开源项目，旨在开发软件以支持发展中国家的医疗保健。

OpenMRS 建立在开放性和共享思想，软件以及部署和使用策略的原则之上。该系统设计为可在资源非常匮乏的环境中使用，并且可以通过添加新的数据项，表格和报告进行修改，而无需进行编程。

Design[edit]

The OpenMRS code is based on a "concept dictionary" that describes all the data items that can be stored in the system such as clinical findings, laboratory test results or socio-economic data. This approach avoids the need to modify the database structure to add new diseases, for example, and facilitates sharing of data dictionaries between projects and sites.^[12] An important feature of OpenMRS is its modular construction which allows the programming of new functions without modifying the core code. OpenMRS is web based but can be deployed on a single laptop or on a large server and runs on Linux, Windows or Mac OS X.^[3]

Other key features of OpenMRS:

- Built on the MySQL database^[2] (but uses Hibernate allowing it to be ported to other databases)
- Programmed in Java^[2]
- Includes tools for data export and reporting
- Versions currently exist for HIV/AIDS, Drug resistant TB, primary care and oncology
- Supports open standards for medical data exchange including HL7,^[2] FHIR, LOINC and IXF
- Form-based tools, such as the Form Entry module^[12] and XForms module^[2]
- Provides access to between-release code through "Continuous Deployment"^[13]
- Bidirectional synchronization with systems such as MoTeCH^[expand acronym] and TRACnet^[expand acronym]
- The Atlas module, which gives information on all OpenMRS facilities using a visual map
- Can be integrated with SMS messaging

https://en.wikipedia.org/wiki/List_of_open-source_health_software

GenomicsDB <https://www.genomicsdb.org/>
<https://github.com/GenomicsDB/GenomicsDB/wiki>

-> UCLA ib2b

This is also part of GATK pipeline use for multivariant prediction.