

# ALMA Science

Knowledgebase > Offline Data Reduction and/or CASA > What should I do if scriptForPI breaks at scriptForImagingPrep step due to an error?

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## What should I do if scriptForPI breaks at scriptForImagingPrep step due to an error?

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For projects that were imaged using the pipeline after April 2017, scriptForPI.py may produce an error when trying to restore data.

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RuntimeError

Traceback (most recent call last)

```
/home/casa/packages/RHEL6/release/casa-release-4.7.2-el6/lib/python2.7/casapy.py in  
<module>()
```

```
----> 1  
      2  
      3  
      4  
      5
```

```
/home/casa/packages/RHEL6/release/casa-release-4.7.2-el6/lib/python2.7/casapy.py in  
<module>()
```

```
    341 if imprepresent:  
    342     print 'Executing scriptForImagingPrep.py ...'  
--> 343     execfile('./script/scriptForImagingPrep.py')  
    344  
    345 if (savingslevel>=3) and os.path.exists('calibrated.ms'):
```

```
/home/casa/packages/RHEL6/release/casa-release-4.7.2-el6/lib/python2.7/casapy.py in  
<module>()
```

```
    42 os.system('rm -rf ' + concatvis + '.flagversions')  
    43 concat(vis=vislist2,  
--> 44     concatvis=concatvis)  
    45  
    46
```

```
#####
```

```
/home/casa/packages/RHEL6/release/casa-release-4.7.2-el6/lib/python2.7/concat_cli.pyc in
```

```
__call__(self, vis, concatvis, freqtol, dirtol, respectname, timesort, cypointing,  
visweightscale, forcesingleephemfield)
```

```
269         #return False
```

```
270
```

```
--> 271         casac.casac.utils().verify(mytmp, trec['concat'], True)
```

```
272         scriptstr=[]
```

```
273         saveinputs = self.__globals__['saveinputs']
```

```
/home/casa/packages/RHEL6/release/casa-release-4.7.2-  
el6/lib/python2.7/_casac_/utils.pyc in verify(self, *args, **kwargs)
```

```
103
```

```
104         """
```

```
--> 105         return _utils.utils_verify(self, *args, **kwargs)
```

```
106
```

```
107     def setconstraints(self, *args, **kwargs):
```

RuntimeError: Parameter verification failed

-----

scriptForPI.py will not split out the calibrated science SPWs into uid\_\*.ms.split.cal if the imaging pipeline was used, which scriptForImagingPrep.py looks for, causing the scriptForPI.py to break.

If you only want the calibrated data, it is sufficient to stop here and use the uid\_\*.ms, keeping in mind that the calibrated data is stored in the CORRECTED data column, and all sources are in the ms.

If you want to run the imaging pipeline, you can start from here, without changing the uid\_\*.ms.

If you want to run scriptForPI.py all the way through, change <<usedimpipe = True>> to <<usedimpipe = False>> in L59 of scriptForPI.py and run.

```
if ( nummkim > 1 ):
```

```
    print "Imaging pipeline was used."
```

```
    usedimpipe = False
```