
Subject: Looking for IDL Structures to Python compatible HDF5 Examples

Posted by [eben.pendleton](#) on Tue, 01 Sep 2015 17:33:03 GMT

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Hi all,

I'm looking for code examples of writing ODL structures to HDF5 tables that can be read in Python (2.7). Filenames are removed

I've tried the following approach using the IDL coyote guide to create the file in IDL 7.1:

```
pro write_idl_struct_to_hdf5,struct,dir_out,outfile

file = dir_out+outfile+'.h5'
fid = H5F_CREATE(file)

datatype_id = H5T_IDL_CREATE(struct)
dataspace_id=H5S_CREATE_SIMPLE(1) ; not so simple..

dataset_id = H5D_CREATE(fid,'o',datatype_id,dataspace_id)
H5D_WRITE, dataset_id, struct

H5S_CLOSE, dataspace_id
H5T_CLOSE, datatype_id

H5F_CLOSE, fid

print,'---Finished Writing IDL struct to HDF5---'
end
```

Python code and Error

```
import pandas as pd
dir_in=r'C:\D_Drive\Python\hdf5'
infile=...

mynewdf = pd.HDFStore(dir_in+'\\'+infile)
print(mynewdf)

print(mynewdf.select('o',columns='TASK_NAME'))
```

resulting in:

```
<class 'pandas.io.pytables.HDFStore'>
```

```
File path: ...
```

```
/o      frame_table [0.0.0] (typ->generic,nrows->1,ncols->63,indexers->[index],dc->
[TASK_CODE,TASK_NAME,EVENT,SYS_LOC_CODE,SUBFACILITY_CODE,ARE
A,RIVER_STREAM_MILE,MILES_FROM_NC_MOUTH,X_COORD,Y_COORD,COORD
```

D_TYPE_CODE,REFERENCE_POINT,ELEV,ELEV_UNIT,ELEV_COLLECT_METHOD_CODE,ELEV_DATUM_CODE,WATER_COLUMN_DEPTH,WATER_COLUMN_DEPTH_UNIT_CODE,SYS_SAMPLE_CODE,PARENT_SAMPLE_CODE,MATRIX_CODE,LAB_MATRIX_CODE,SAMPLE_TYPE_CODE,SAMPLE_DATE,START_DEPTH,END_DEPTH,DEPTH_UNIT,DEPTH_INTERVAL,SEDIMENT_NATIVE,GROUP_DESC,CHEMICAL_NAME,CAS_RN,FRACTION,ANALYTIC_METHOD,LEACHATE_METHOD,PREP_METHOD,RESULT_VALUE,LAB_QUALIFIERS,VALIDATOR_QUALIFIERS,INTERPRETED_QUALIFIERS,DETECT_FLAG,TARGET_UNIT,REPORTABLE_RESULT,VALIDATED_YN,VALIDATOR_REASON_CODE,BASIS,METHOD_DETECTION_LIMIT,REPORTING_DETECTION_LIMIT,DILUTION_FACTOR,LAB_NAME_CODE,LAB_SAMPLE_ID,ANL_SHORT_NAME,PARENT_LOC_CODE,DATA_RELEASE_STATUS,DATA_ANALYSIS_HIERARCHY,RESULT_VALUE_MDL,RISK_SCREEN_USABILITY,BASELINE_RA_USABILITY,CAS_RN_4PROUCL,CHEMICAL_NAME_4PROUCL,TREATMENT_FLAG_4PROUCL,CHEMICAL_NAME_4LABEL,USABILITY_HIERARCHY))

The error generated is

ValueError: Wrong number of items passed 283774, placement implies 1

The 283774 number is the number of rows in the structure and it seems that each tag in the dataframe has one row with 283774 elements.

Is there some layout adjustment that's needed to read a structure correctly in HDF5?

Eben
