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# **pyxona Documentation**

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Pyxona has no documentation yet.

```
>>> import pyxona
>>> import os
>>> import numpy as np
>>> current_dir = os.path.dirname(".")
>>> test_data_dir = os.path.join(current_dir, "..", "pyxona", "tests", "test_data")
>>> axona_file_path = os.path.join(current_dir, "..", "pyxona", "tests", "axona_raw_
↳data/DVH_2013103103.set")
>>> def _check_array_equal(a, b):
...     if a.dtype == "<U1" and b.dtype == "<U1":
...         return (a == b).all()
...     else:
...         return ((a == b) | (np.isnan(a) & np.isnan(b))).all()
>>> axona_file = pyxona.File(axona_file_path)
>>> for i, cut in enumerate(axona_file.cuts):
...     indices = np.load(os.path.join(test_data_dir, "cut_indices"+str(i)+".npy"))
...     assert _check_array_equal(indices, cut.indices)
```



## REFERENCES

- `genindex`
- `search`