

```
In [1]: %matplotlib inline
import pylipid
from pylipid.api import LipidInteraction
```

```
In [34]: trajfile_list = ["../skipallbt1.1.xtc", "../skipallbt1.2.xtc"]
topfile_list = ["../bt1.1.gro", "../bt1.2.gro"]
lipid = "HBHT"
cutoffs = [0.55, 0.7]
nprot = 1
timeunit = 'us' # micro-second

# initialize
li = LipidInteraction(trajfile_list, topfile_list, cutoffs=cutoffs, lipi
```

```
In [35]: li.collect_residue_contacts(write_log=True, print_log=False)

# print_log=True will print out the residues with the highest interaction
# occupancy and lipid count from each trajectory.

# write_log=True will write such information in a log file.
```

```
COLLECT INTERACTIONS FROM TRAJECTORIES: 0%|          | 0/2 [00:00<?,
?it/s]
```

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AttributeError                                Traceback (most recent call
last)
<ipython-input-35-ac80fc5d634b> in <module>
----> 1 li.collect_residue_contacts(write_log=True, print_log=False)
      2
      3 # print_log=True will print out the residues with the highest
      4 # occupancy and lipid count from each trajectory.
      5

~/anaconda3/lib/python3.7/site-packages/pylipid/api/api.py in collect_
residue_contacts(self, write_log, print_log, fn_log)
    257         contact_high, _, _ = cal_contact_residues(
dist_matrix, self._cutoffs[1])
    258         self.contact_residues_high[residue_id].app
end(contact_high)
--> 259         self.r[residue_id].append(contact_low)
    260         self.durations[residue_id].append(
    261             Duration(contact_low, contact_high, ti
mestep).cal_durations())

AttributeError: 'LipidInteraction' object has no attribute 'r'
```

```
In [ ]:
```