```
1 import esearch.esearcher
2
3 p = {'db':'nucleotide',
4      'term':'biomol_trna',
5      'field':'prop'}
6 es = esearch.esearcher.Esearcher('esearcher', email)
7 print(es.inquire(parameter=p).result.uids)
```

(a) Example of searching the Entrez databases using entrezpy esearcher. The nucleotide Entrez database is queried for UIDs with the term 'biomo trna' in their property field. The found UIDs are printed to the standard output using the default EsearcherAnalyzer.

```
1 esearch -db gene  \
2        -query "tp53[preferred_symbol]_AND_human[orgn]"\|
3 elink -target protein  | esummary  \ |
4 xtract -pattern DocumentSummary -element Caption SourceDb
5
```

(b) Entrez Direct example to fetch the 'caption' and 'source database' information for sequences in the protein database linked from results in the gene database

```
1 import wally.wally
2
3 p = {'db' : 'gene', 'term' : 'tp53[preferred_symbol]_AND_human[organism]'}
4
5 w = wally.wally.Wally(email)
6 px = w.new_pipeline()
7 qid = px.add_search(parameter=p)
8 qid = px.add_link(parameter={'db' : 'protein'}, dependency=qid)
9 qid = px.add_summary(dependency=qid)
10 analyzer = w.run(px)
11 for i in analyzer.result.summaries:
12   print(analyzer.result.summaries[i].get('caption'),
13          analyzer.result.summaries[i].get('sourcedb')))
14
```

(c) entrezpy Wally example reproducing Figure 1b

Figure 1: entrezpy usage examples. Figure 1a shows the usage for a single E-Utility function, here ESearch. Figure 1b depicts a query using the Entrez Direct tool while 1c the same same query using the Wally class from entrezpy.