

A Overview of an E-Utility query

Search query

Task: Search
What: Viruses
Where: Nucleotide

Fetch query

Task: Fetch
What:
UIDs: 123,234,...
Where: Nucleotide
Format: FASTA

>LC431552.1
GTTCCATACAGAGACC..

| Query | E-Utility | POST parameter |
|--------|--------------|--|
| Search | esearch.fcgi | db='nucleotide'&term='viruses[ORGN]' |
| Fetch | efetch.fcgi | db='nucleotide'&rettype=fasta&id='123,234,...' |

B Overview of an E-Utility query using the Entrez History server

Search query

Task: Search
What: Viruses
Where: Nucleotide

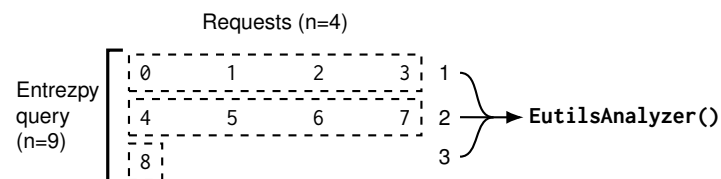
Fetch query

Task: Fetch
What:
WebEnv: 2743NCID
query_key: 1
Where: Nucleotide
Format: FASTA

>LC431552.1
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| Query | E-Utility | POST parameter |
|--------|--------------|---|
| Search | esearch.fcgi | db='nucleotide'&term='viruses[ORGN]&usehistory=y' |
| Fetch | efetch.fcgi | WebEnv='2743NCID'&query_key=1&rettype=fasta' |

C Entrezpy query and requests



D Entrez Direct command for the example query

```
esearch -db nucleotide -query "viruses[organism]" | efetch -format fasta
```

E Implementing the example query with Wally

```
1 import entrezpy.wally
2
3 w = entrezpy.wally.Wally('email') # Create new Wally instance
4 fetch_ppl = w.new_pipeline()      # Create new and empty Wally pipeline
5 # Add search query to the pipeline and store its id
6 sid = fetch_ppl.add_search({'db': 'nucleotide',
7                             'term': 'viruses[organism]',
8                             'rettype': 'count'})
9 # Add fetch query: request sequences in FASTA based on search result
10 fetch_ppl.add_fetch({'retmode': 'text', 'rettype': 'fasta'}, dependency=sid)
11 w.run(fetch_ppl)
```