

## 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

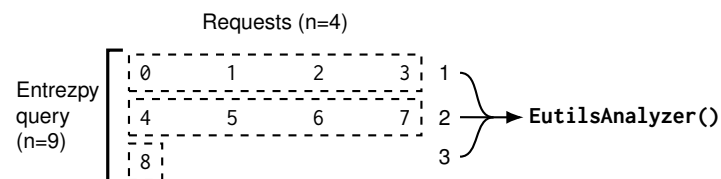
### Fetch query

Task: Fetch  
What:  
WebEnv: 2743NCID  
query\_key: 1  
Where: Nucleotide  
Format: FASTA

>LC431552.1  
GTTCCATACAGAGACC..

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 Conduit

```
1 import entrezpy.conduit
2
3 c = entrezpy.conduit.Conduit('email') # Create new Conduit instance
4 fetch_ppl = c.new_pipeline()           # Create empty Conduit 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 c.run(fetch_ppl)
```