

NCBI PowerScripting

Lecture 4:
Coding Basic eUtil Pipelines

April 20-22, 2005

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Overview

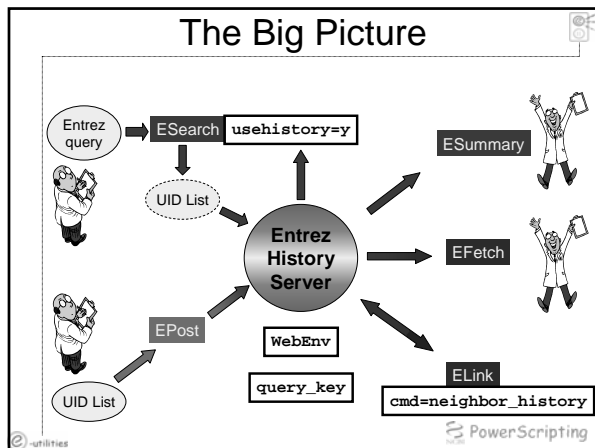
- General pipeline strategies
- Building pipelines using the Entrez History
- The Four Basic Pipelines
- UID List Operations

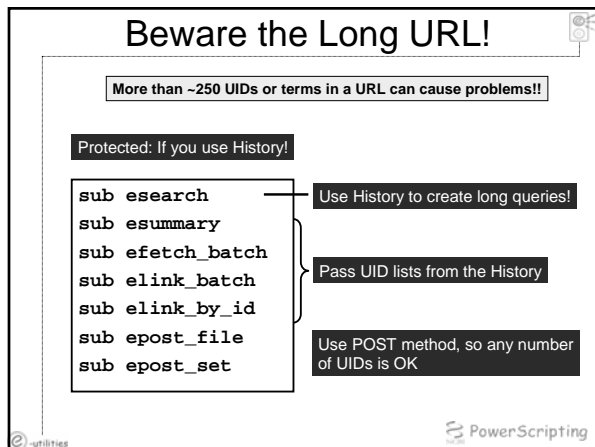
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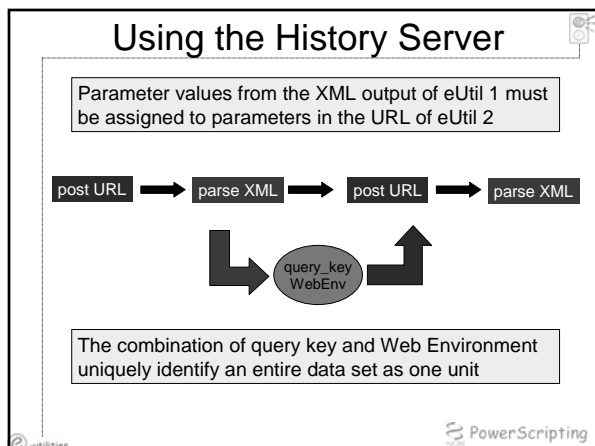
The General eUtil Pipeline

```
graph LR; EntrezQuery([Entrez query]) --> ESearch[ESearch]; ESearch --> Cloud((!$%*@$#!)); EPost[EPost] --> Cloud; UIDList([UID List]) --> Cloud; Cloud --> DocSums[DocSums]; Cloud --> ESummary[ESummary]; Cloud --> EFetch[EFetch]; Cloud --> FormattedData[Formatted Data];
```

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Using Sets Stored in History

Use &WebEnv and &query_key instead of &id

BASE/ **esummary.fcgi?** db=nucleotide&WebEnv=A1B2&query_key=3

BASE/ **efetch.fcgi?** db=nucleotide&WebEnv=A1B2&query_key=3

BASE/ **elink.fcgi?**
dbfrom=gene&db=nucleotide&WebEnv=A1B2&query_key=3

Use query_key in &term followed by %23 (#)

BASE/ **esearch.fcgi?** db=nucleotide&WebEnv=A1B2&term=%233
&usehistory=y

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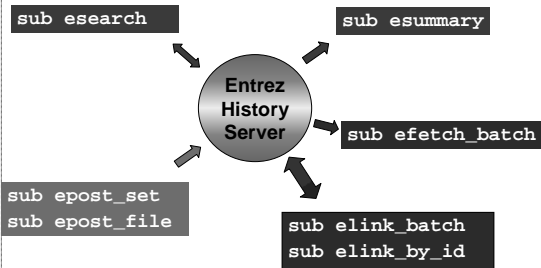
Building a Pipeline

1. Generate a UID list on the History using
 - ESearch (Entrez query)
 - EPost (UID list)
 - Optional exception: very small UID lists (< 5)
2. Operate on the UID list on the History by
 - Limiting the list using ESearch
 - Generating a linked UID list using ELink
3. Download the UID list from the History as
 - UIDs using ESearch
 - DocSums using ESummary
 - Formatted data using EFetch

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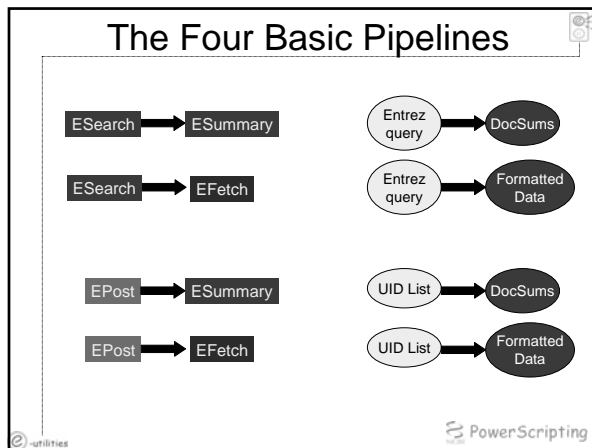
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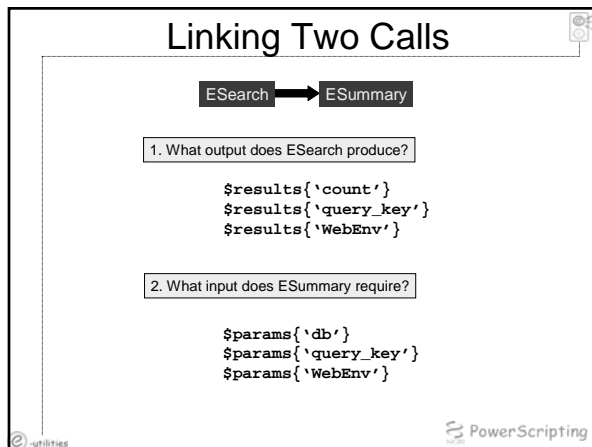
Summary of Routines

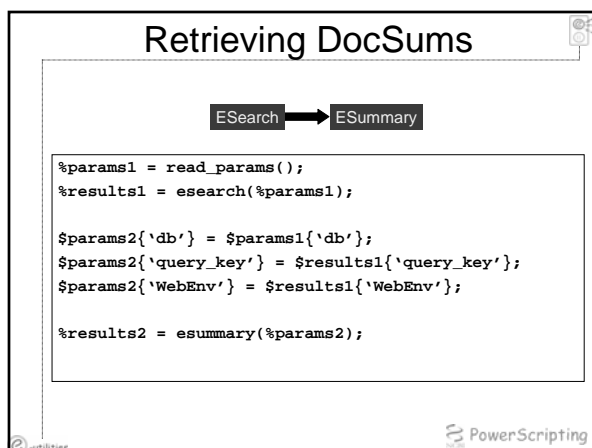


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Retrieving Data

ESearch → EFetch

```
%params1 = read_params();
%results1 = esearch(%params1);

$params2{'db'} = $params1{'db'};
$params2{'query_key'} = $results1{'query_key'};
$params2{'WebEnv'} = $results1{'WebEnv'};

efetch_batch(%params2);

for ($retstart = 0; $retstart < $count; $retstart += $retmax) {
    ...
    $params2{'retstart'} = $retstart;
    $raw = efetch(%params2);
}
```

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Problems

Plan pipelines that will...

1. Download all rat proteins in FASTA format
2. Download DocSums for all structures with resolutions less than 2 Angstroms
3. Download SNP DocSums for a file of mouse rs numbers

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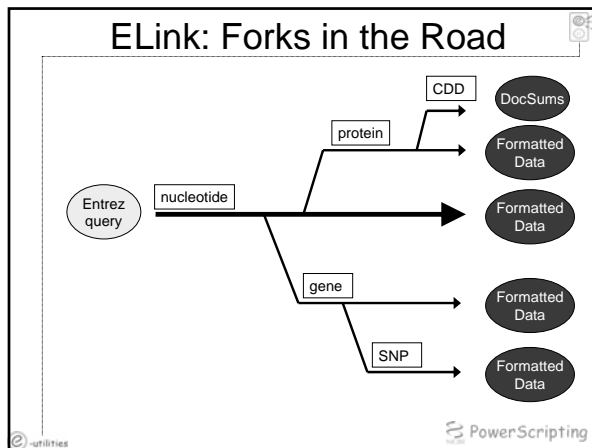
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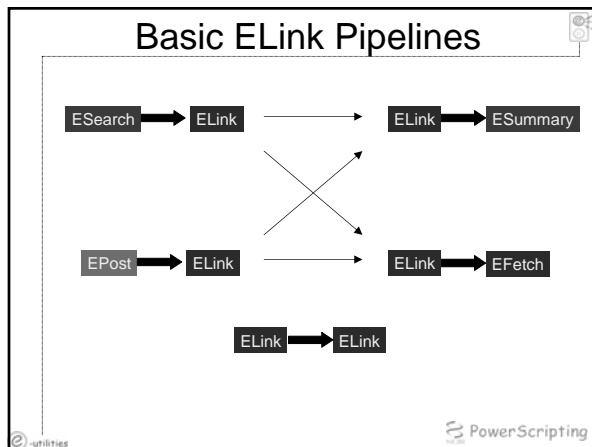
UID List Operations

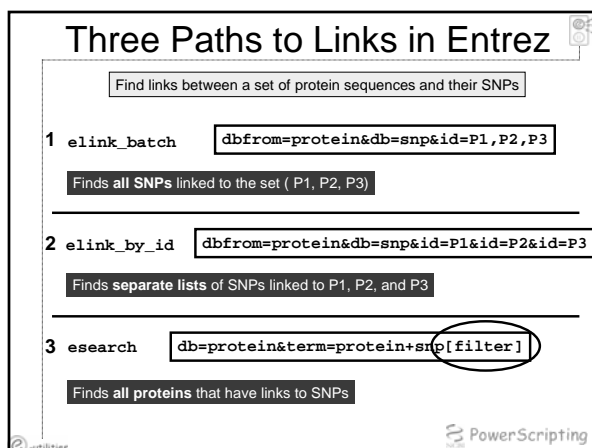
1. Links to another database (ELink)
2. Computational neighbors (ELink)
3. Limiting by an Entrez query (ESearch)
4. Combining multiple lists (ESearch)

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Problems

Plan pipelines that will...

1. Given a file of PubMed IDs, download a single set of linked nucleotide GLs
2. Download Gene XML records for all mouse genes that have SNPs
3. Given a file of zebrafish Unigene cluster IDs, download Genbank flat files for nucleotide records linked to each cluster

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Using History with ESearch

Use query keys as part of the ESearch &term!

#2 AND srcdb refseq[prop] → &term=%232+AND+srcdb+refseq[prop]

1. Limit a history set by an Entrez query

EPost → ESearch

ELink → ESearch

2. Combine multiple previous searches

ESearch → ESearch

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Limit a History Set by an Entrez query

EPost → ESearch

ELink → ESearch

&db=gene&term=%231+AND+1[chromosome]

```
%params1 = read_params();
%results1 = epost_file(%params1);

$params2{'db'} = $params1{'db'};
$params2{'term'} = "%23$results1{'query_key'}";
$params2{'term'} .= "+AND+1[chromosome]";
$params2{'WebEnv'} = $results1{'WebEnv'};
$params2{'usehistory'} = 'y';
%results2 = esearch(%params2);
```

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Problems

Plan pipelines that will...

- Given a set of Conserved Domain IDs (PSSM-IDs), find all RefSeq proteins that contain each domain
- Given two protein GIs, download DocSums for all proteins that are sequence-similar to both proteins
- Given a file of protein accessions, determine how many are from human

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A General Design Approach

- Know what you want before you begin
 - Do I need the full record? (EFetch)
 - Will a DocSum be sufficient? (ESummary)
- Know what Entrez database contains the data you want
 - If it's not in Entrez, the eUtils can't access it
- Try your pipeline in interactive web Entrez first
 - Some Entrez queries may surprise you
 - Some Entrez data may surprise you
 - Some Entrez links may surprise you
- Build your pipeline from the paired eUtil elements
- Keep track of the output and input
 - What output does call 1 produce?
 - What input does call 2 require?

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