

## ENTREZ DIRECT - XML DATA EXTRACTION

The Entrez Direct (EDirect) xtract function uses command-line arguments to direct the selective conversion of XML data into a tab-delimited table. The -pattern argument divides the results into rows, while placement of data into columns is controlled by -element.

Additional arguments limit exploration to specified XML regions (-group, -block, and -subset), filter by data content (-match and -avoid) or elements (-present and -absent), and customize the report presentation. Individual fields can be grouped with commas and given specific prefix, suffix, and separator characters.

Inspection of the XML with -outline helps determine the appropriate arguments to employ. Tabular data can be piped to standard UNIX utilities or custom scripts for further processing. A query by specific PubMed unique identifiers:

```
efetch -db pubmed -id 781293,2678811,6301692,8332518 -format xml | \
xtract -pattern PubmedArticle -element "MedlineCitation/PMID" \
  -block AuthorList -sep "|" -element LastName "#Author" \
  -block PubDate -sep " " -element Year,Month MedlineDate \
  -block DateCreated -sep "-" -element Year,Month,Day | \
sort -t $'\t' -k 3,3n | column -s $'\t' -t
```

produces a table that allows easy parsing of author names, counts the number of authors present, and prints the date each record was published and the date it was entered into PubMed, sorting the results by the computed author count:

781293	Casadaban	1	1976 Jul	1976-10-02
6301692	Krasnow Cozzarelli	2	1983 Apr	1983-06-17
8332518	Benson Lipman Ostell	3	1993 Jul	1993-08-17
2678811	Mortimer Schild Contopoulou Kans	4	1989 Sep-Oct	1989-11-22

(The PubDate object can exist either in structured or string form, but would not contain a mixture of both types, so "-element Year,Month MedlineDate" will only contribute a single column to the output.)

Sequence records can be retrieved in an XML version of the GenBank or GenPept flatfile. Feature and qualifier names are data values, not XML tags, and require -match to select the desired object. A query for snail venom mature peptides:

```
esearch -db protein -query "conotoxin AND mat_peptide [FKEY]" | \
efetch -format gpc -mode xml | \
xtract -pattern INSDSeq -ACCN INSDSeq_accession-version \
  -group INSDFeature -match ">mat_peptide<" \
  -avoid "<INSDFeature_partial" -pfx "\n" -element "&ACCN" \
  -block INSDQualifier -match ">peptide<" -element "%INSDQualifier_value" \
  -block INSDQualifier -match ">product<" -element INSDQualifier_value \
  -block INSDQualifier -match ">peptide<" -element INSDQualifier_value | \
grep conotoxin | sort -t $'\t' -u -k 3,4 | \
sort -t $'\t' -k 2,2n | column -s $'\t' -t
```

calculates the length of each mature peptide, and prints the product name and peptide sequence, removing redundant entries and sorting by peptide length:

ADB43130.1	15	conotoxin Cal 1a	KCKKRHHGCHPCGRK
ADB43131.1	15	conotoxin Cal 1b	LCCKRHHGCHPCGRT
AA033169.1	16	alpha-conotoxin GIC	GCCSHPACAGNNQHIC
ADB43127.1	16	conotoxin Cal 5.1	DPAPCCQHPIETCCRR
AAD31913.1	18	alpha A conotoxin Tx2	PECCSHPACNVDHPEICR
...			

(The sequence accession is captured in a variable for use with each mat\_peptide in the record. Prefix substitution ensures that every peptide is shown on a separate line. This also works for multi-product precursor proteins such as proinsulin.)

(Incorporating fragments of the surrounding XML tags in -match arguments prevents coincidental matches to free text in note qualifiers.)

Multiple -avoid or -match conditions are specified with -and and -or commands:

```
-group INSDFeature -avoid ">proprotein<" -and ">sig_peptide<" \
  -block INSDQualifier -match ">calculated_mol_wt<" -or ">peptide<" \
```

Setting a variable default value, by placing text in parentheses, can be used to prevent columns from shifting when data fields are missing:

```
-MLWT "(-)"
```

The normal column-oriented output can be extensively modified to produce a custom report. A query on a gene that undergoes messenger RNA splicing:

```
efetch -db nuccore -id "GQ370762.1" -format gbc -mode xml | \
xtract -pattern INSDSeq -pfx ">Feature " -sfx "\n" -tab "" -first INSDSeqid \
  -group INSDFeature -avoid "INSDFeature_key>source<" -FKEY INSDFeature_key \
  -block INSDInterval -element INSDInterval_from INSDInterval_to \
    INSDInterval_point INSDInterval_point "&FKEY" -FKEY "" -tab "" -lbl "\n" \
  -block INSDQualifier -avoid ">translation<" -and ">peptide<" -pfx "\t\t\t\t" \
    -sfx "\n" -tab "" -element INSDQualifier_name,INSDQualifier_value
```

clears the feature key variable after its first use to generate the 5-column feature table format used for GenBank submissions:

```
>Feature gb|GQ370762.1|
51      1474      gene
                                gene      HBB
                                allele     GZ

51      142      mRNA
273     495
1346    1474
                                gene      HBB
                                allele     GZ
                                product    beta-globin

51      142      CDS
273     495
1346    1474
                                gene      HBB
                                allele     GZ
                                codon_start 1
                                transl_table 1
                                product    beta-globin
                                protein_id  ACU56984.1
                                db_xref     GI:256028940

310     310      variation
                                gene      HBB
                                note       K43E
                                replace    g
```

(A location interval will have either an INSDInterval\_from and INSDInterval\_to pair or a single INSDInterval\_point. Additional work would be required to support the 5' and 3' partial flags for features with incomplete locations.)