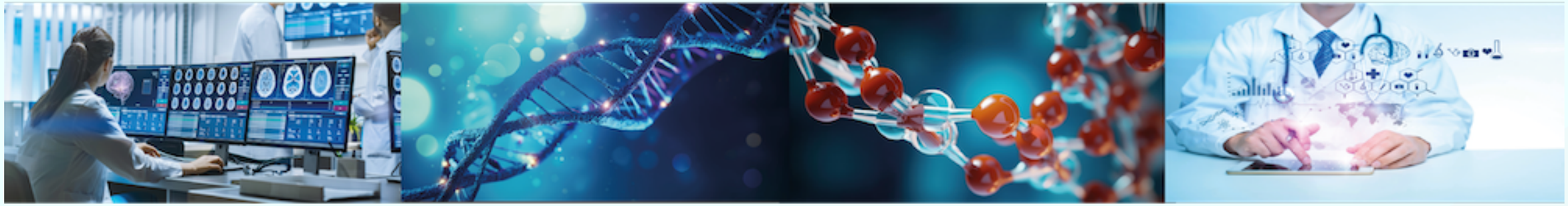

Programming for Biomedical Informatics

Lecture 6

“Data Integration & Summary Analysis”

https://github.com/tisimpson/pbi

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Coding

THE UNIVERSITY of EDINBURGH
informatics

BioPython

- BioPython - https://biopython.org/
- Available via pip, conda, or source download
  - pip install biopython
  - conda install conda-forge::biopython
  - http://biopython.org/DIST/biopython-1.84.tar.gz
- The Biopython package provides a library **Bio.Entrez** that can be used to access the eUtils
- This is the simplest way to begin working with the eUtils using Python
- Once you are comfortable with the way the system (APIs) operate you may choose to simply use urlib (or similar) to code more flexibly with
- Biopython has excellent "cookbooks" which are code recipes to achieve common tasks

Accessing NCBI's Entrez databases

Entrez (https://www.ncbi.nlm.nih.gov/Web/Search/entrezfs.html) is a data retrieval
provides users access to NCBI's databases such as PubMed, GenBank, GEO, and m
can access Entrez from a web browser to manually enter queries, or you can use Bi
`Bio.Entrez` module for programmatic access to Entrez. The latter allows you for ex
PubMed or download GenBank records from within a Python script.

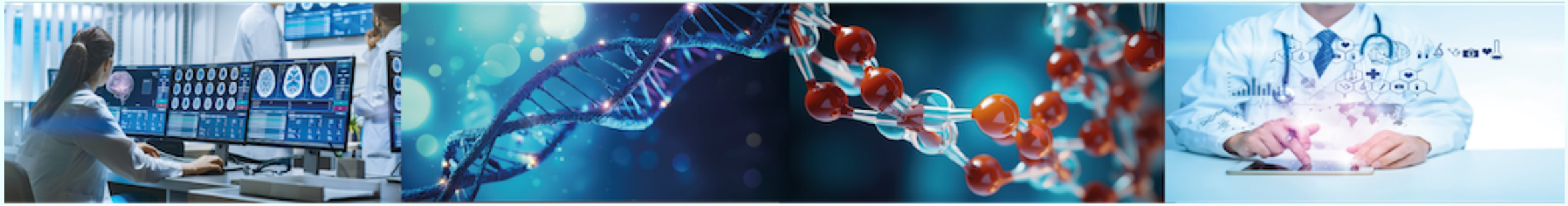
The `Bio.Entrez` module makes use of the Entrez Programming Utilities (also know
consisting of eight tools that are described in detail on NCBI's page at
https://www.ncbi.nlm.nih.gov/books/NBK25501/. Each of these tools corresponds
function in the `Bio.Entrez` module, as described in the sections below. This modu
that the correct URL is used for the queries, and that NCBI's guidelines for respons
are being followed.

The output returned by the Entrez Programming Utilities is typically in XML format
output, you have several options:

1. Use `Bio.Entrez`'s parser to parse the XML output into a Python object;
2. Use one of the XML parsers available in Python's standard library;
3. Read the XML output as raw text, and parse it by string searching and manipulation.

The NCBI-NLM eUtilities

- **EInfo (database statistics)** - eutils.ncbi.nlm.nih.gov/entrez/eutils/einfo.fcgi
  - Provides the number of records indexed in each field of a given database, the date of the last update of the database, and the available links from the database to other Entrez databases.
- **ESearch (text searches)** - eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi
  - Responds to a text query with the list of matching UIDs in a given database (for later use in ESummary, EFetch or ELink), along with the term translations of the query.
- **EPost (UID uploads)** - eutils.ncbi.nlm.nih.gov/entrez/eutils/epost.fcgi
  - Accepts a list of UIDs from a given database, stores the set on the History Server, and responds with a query key and web environment for the uploaded dataset.
- **ESummary (document summary downloads)** - eutils.ncbi.nlm.nih.gov/entrez/eutils/esummary.fcgi
  - Responds to a list of UIDs from a given database with the corresponding document summaries.
- **EFetch (data record downloads)** - eutils.ncbi.nlm.nih.gov/entrez/eutils/efetch.fcgi
  - Responds to a list of UIDs in a given database with the corresponding data records in a specified format.
- **ELink (Entrez links)** - eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi
  - Responds to a list of UIDs in a given database with either a list of related UIDs (and relevancy scores) in the same database or a list of linked UIDs in another Entrez database; checks for the existence of a specified link from a list of one or more UIDs; creates a hyperlink to the primary LinkOut provider for a specific UID and database, or lists LinkOut URLs and attributes for multiple UIDs.
- **EGQuery (global query)** - eutils.ncbi.nlm.nih.gov/entrez/eutils/egquery.fcgi
  - Responds to a text query with the number of records matching the query in each Entrez database.
- **ESpell (spelling suggestions)** - eutils.ncbi.nlm.nih.gov/entrez/eutils/espell.fcgi
  - Retrieves spelling suggestions for a text query in a given database.
- **ECitMatch (batch citation searching in PubMed)** - eutils.ncbi.nlm.nih.gov/entrez/eutils/ecitmatch.cgi
  - Retrieves PubMed IDs (PMIDs) corresponding to a set of input citation strings.



Programming for Biomedical Informatics

Next Lecture

“Biomedical Evidence”

Ask Questions on the EdStem Discussion Board

https://github.com/tisimpson/pbi

Background