

# How to use LexMapr

For people who have  
**little to no experience with command line**

*and*

**For macOS and Linux users only**

*and*

**For IFSAC users only**

# Outline

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# Open up your terminal

## macOs:

*cmd + space* to open spotlight search

type terminal

hit *return*

## Linux:

*ctrl + alt + t*

# Terminal tutorial

The terminal opens in your Home (also known as ~) directory

Type the following command into your terminal:

```
ls
```

This will print out all the sub-directories and files in your home directory

# Terminal tutorial

You can change terminal directories with the `cd` command:

`cd Desktop`      Navigate to your Desktop subdirectory

`ls`      View the contents of your Desktop

`cd ..`      Navigate to the parent directory

`ls`      View the contents of your Home again

If you ever get lost, you can return Home with `cd ~`

# Do you have Conda?

In your terminal, type:

```
conda -V
```

**If you have Conda**, the terminal will tell you your Conda version number

**If you do not have Conda**, the terminal will tell you the `conda` command was not found

# Install Conda

Go to <https://docs.conda.io/en/latest/miniconda.html>

Install the appropriate **64-bit bash installer** for **Python 3.7**

In your terminal, navigate to the folder containing the installer

Assuming this was the Downloads folder:

```
cd ~
```

```
cd Downloads
```

# Install Conda

In this folder, we run the installer through a terminal command

**macOS:**

```
bash Miniconda3-latest-MacOSX-x86_64.sh
```

**Linux:**

```
bash Miniconda3-latest-Linux-x86_64.sh
```

Follow the prompts to completion



# Bioconda

Bioconda is a channel that allows users to easily install various bioinformatic packages, including LexMapr

Run the following terminal commands to set up Bioconda:

```
conda config --add channels default
```

```
conda config --add channels bioconda
```

```
conda config --add channels conda-forge
```

**RUN THESE COMMANDS IN ORDER**

# Install LexMapr into a Conda environment

Enter the following command from any directory:

```
conda create -n LexMapr python=3.6 lexmapr
```

Follow the prompts to completion

This creates a Conda environment called “LexMapr”, that contains a Bioconda installation of LexMapr

# Running LexMapr

Whenever you want to run LexMapr, all you have to do is:

Start the terminal

Activate your LexMapr Conda environment:

```
conda activate LexMapr
```

Run LexMapr commands

```
lexmapr {path_to_output_file} -p ifsac
```

# LexMapr input files

LexMapr takes input csv files with the following format:

SampleId,Sample

1,Chicken Breast

2,Baked Potato

3,Canned Corn

4,Frozen Yogurt

5,Apple Pie

# LexMapr input files

Open up Microsoft Excel, Apple Numbers or LibreOffice Calc  
Create a spreadsheet like so:

|   | A        | B              |
|---|----------|----------------|
| 1 | SampleId | Sample         |
| 2 | 1        | Chicken Breast |
| 3 | 2        | Baked Potato   |
| 4 | 3        | Canned Corn    |
| 5 | 4        | Frozen Yogurt  |
| 6 | 5        | Apple Pie      |

Save as “small\_simple.csv”

# Running LexMapr

In the terminal, `cd` to the folder containing `small_simple.csv`

**With the LexMapr Conda environment activated, try:**

```
lexmapr small_simple.csv -p ifsac
```

# Running LexMapr

**A new file called `ifsac_output.tsv` was just created in the same directory as `small_simple.csv`**

Open it up in Microsoft Excel, Apple Numbers or LibreOffice Calc:

|   | A             | B              | C              | D                                       | E                           |
|---|---------------|----------------|----------------|---|-----------------------------|
| 1 | Sample_Id     | Sample_Desc    | Cleaned_Sample | Matched_Components                      | Third Party Classification  |
| 2 | small_simple1 | Chicken Breast | chicken breast | [chicken breast:foodon_00002703]        | [chicken]                   |
| 3 | small_simple2 | Baked Potato   | baked potato   | [potato (whole, baked):foodon_03302196] | [root/underground (tubers)] |
| 4 | small_simple3 | Canned Corn    | canned corn    | [corn (canned):foodon_03302665]         | [seeded vegetables (other)] |
| 5 | small_simple4 | Frozen Yogurt  | frozen yogurt  | [frozen yogurt:foodon_03307445]         | [dairy]                     |
| 6 | small_simple5 | Apple Pie      | apple pie      | [apple pie:foodon_00002475]             | [pome fruit]                |

# Running LexMapr

You can specify your own output file name by running:

```
lexmapr {path_to_output_file} -p ifsac -o {path_to_output_file}
```

e.g.

```
lexmapr small_simple.csv -p ifsac -o small_simple_output.tsv
```

Now you results will be in `small_simple_output.tsv`, **not** `ifsac_output.tsv`



## Keep LexMapr up-to-date

Keep LexMapr up-to-date by running the following command from any directory:

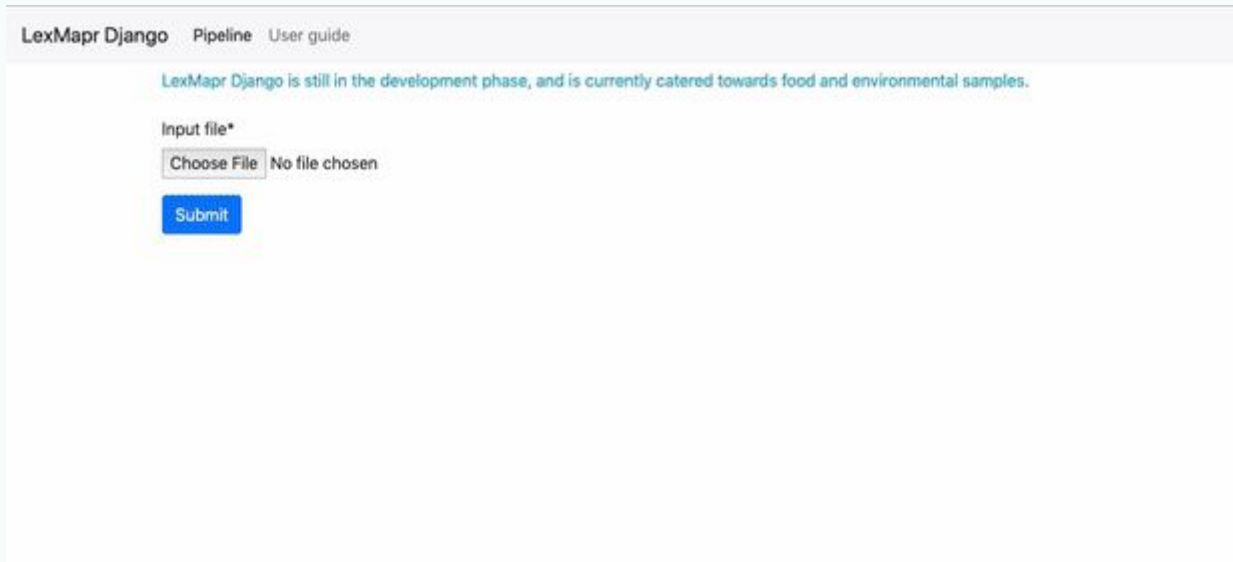
```
conda update lexmapr -n LexMapr
```

Follow the prompts to completion

This updates the lexmapr package installed inside your LexMapr conda environment

# LexMapr Django

<https://watson.bccdc.med.ubc.ca/lexmapr/>



The screenshot shows the LexMapr Django web interface. At the top, there are navigation links: "LexMapr Django", "Pipeline", and "User guide". Below these, a teal-colored message states: "LexMapr Django is still in the development phase, and is currently catered towards food and environmental samples." The main section is titled "Input file\*" and contains a "Choose File" button next to the text "No file chosen". Below this is a blue "Submit" button.

Django-powered web interface, that allows you to run LexMapr from your browser