

How to use FlexMap(ASPE) or (OLA) space

1. Install Perl with all of the default settings
<http://downloads.activestate.com/ActivePerl/Windows/5.8/ActivePerl-5.8.4.810-MSWin32-x86.msi>
2. Create a file named “TEMP” on the C drive (C:\TEMP)
3. Install Crypt-SSLeay & Install Bioperl
 - a. Go to Start->Run and type “ppm”
 - b. Type “rep add theoryx5 <http://theoryx5.uwinnipeg.ca/ppms/>”
 - c. Type “install Crypt-SSLeay” (case sensitive)
 - d. After installation you will be asked whether or not to fetch a file named “libeay32.dll”. Type y or yes.
 - e. You will then be asked where to save the file. Simply press enter to save the file to the default location.
 - f. Repeat steps 5 and 6 for a file named “ssleay32.dll”
 - g. Type “repository add bioperl <http://bioperl.org/DIST>”
 - h. Then type “install Bioperl-1.4” (case sensitive)
 - i. Type “quit” to exit PPM
4. Download Genome to use as local BLAST database
 - a. ftp://ftp.ncbi.nih.gov/genbank/genomes/H_sapiens/ OR
 - b. Go to Start->Run and type “cmd”
 - c. Type “ftp ftp.ncbi.nih.gov”
 - d. Username is "anonymous" and password is your email address.
 - e. Type “cd genbank”
 - f. Type “cd genomes”
 - g. Type “cd H_sapiens” (Case sensitive)(this is for Human Genome)
 - h. Type “get hs_phase3.fna.gz”
5. Import “FlexMap(ASPE) or (OLA).space” into DNASpace
 - a. Launch DNASpace
 - b. Click the “Import” button on the first dialog box that opens
 - c. Navigate to where the .space file is saved and click OK
6. Configure the Space for use
 - a. Open the FlexMap(ASPE)or(OLA) Space
 - b. Launch Sequence Database Manager under Database drop down menu
 - Click New
 - Select In-House tab
 - Rename “Untitled” to “FlexMap”
 - Click “Blank(Nucleotides)”
 - Click Ok
 - Click “New” again
 - Select In-House tab
 - Rename as “Human Genome”
 - Click “fasta file(Nucleotides)”

- Navigate to the genome file downloaded in Step 4 (change view to all file types)
 - Click Ok
- c. Open Blast DB Manger from Database drop down Menu
- Click New
 - Select the Human Genome database
 - Click Make
 - Select the Human Genome Database in the Blast Database Manager window and click “Update”
 - Close the Blast Database Manager
- d. Double Click the “Sequence DB Updater- fasta” node
- Make Sure “In-house fasta” is selected for Source Data
 - Check all 3 boxes in the upper right hand corner
 - Select the FlexMap database and click OK
- e. Double click each “Smith-Waterman Search” node in the workflow and perform the following
- Click “Setting”
 - Click “OK”
 - Click on the box next to FlexMap
 - Click “OK” again
- f. Double click on the 2 “Blast search against the Human Genome” nodes in the workflow and perform the following
- Click “Setting”
 - Click “OK”
 - Click on the box next to “Human Genome”
 - Click “OK” again

The space is now ready to use. Please be aware that the input sequences must be in a .csv file in the following format:

#	Name	Sequence*	Position**	Type***
1	R506Q	CAAAAAAAAAA	178	C,T
2	20210	TCTTTATCCAG	77	C,T
3	677	ACCCCGAAGCA	64	C,T
4	1298	CCAGCATCACT	76	G,T

*Contains the entire sequence in plain text

**Position refers to the bp position of the SNP of interest

***Type represents the different bases that may be present.