Using 3DNA: A Mini-Tutorial

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1 Installation

To install 3DNA you first need to register in the x3dna forum and then login as a registered user and head to:
`http://forum.x3dna.org/downloads/3dna-download/`
Where you will be able to download compiled versions of 3DNA for the Linux, Mac-OS, and Windows operating systems. The compiled versions also contain the source code in ansi-C. If you download the Linux 64-bit version yourfile will be named something like: **x3dna-v2.3-linux-64bit.tar.gz**

You will need to uncompress this file by issuing the following command in the terminal:

```
tar -xvzf x3dna-v2.3-linux-64bit.tar.gz
```

This will create a new folder named **x3dna-v2.3** which you will have to include in your environment variables by changing your shell environment configuration file named ".bashrc" in bash, and ".chsrc" in csh and tcsh.
If you are using .bashrc the following lines will need to be added:

```
export X3DNA=/home/yourusername/x3dna-v2.3
export PATH=$PATH:$X3DNA/bin
```

A detailed explanation of how to configure X3DNA can be found in the pdf file **x3dna_v1.5.pdf** found in the x3dna-v2.3/doc folder. If you're stuck in the installation process feel free to drop me a line at `mauricio.esguerra@gmail.com`

2 fiber

The fiber program included in the 3DNA package allows you to easily generate protein data bank (pdb) files of fiber models corresponding to common nucleic acid conformations, for example A-DNA, B-DNA, and Z-DNA. To get a list of all possible fiber models which you can reconstruct using fiber, type:

```
fiber -l
```

If you type fiber alone in the terminal you will get a usage message.
Stop and read the usage message carefully.

Now, you know that the crystal structures of A-RNA and B-DNA must have a total of 11 and 10 residues per turn respectively, so, go ahead and use fiber to make an A-RNA with 12 residues and a B-DNA with 11 residues. Using a molecular visualization program such as pymol, vmd, or chimera check the generated structure to corroborate that you have the correct number of residues per turn.

3 find_pair

The find_pair program of 3DNA allows you to find pairs in a given pdb file. To read the usage message open a terminal and type:

```
find_pair
```

Now go to the protein data bank website at `http://www.pdb.org` and download the structure with PDB_ID: 1ehz. This is the structure for yeast phenylalanine tRNA. Run it through find_pair:

```
find_pair 1ehz.pdb 1ehz.inp
```

The ouput will be a file named *1ehz.inp*. Go ahead and open the resulting file in a text editor and you will see that the find_pair program has found the canonical Watson-Crick base-pairs G·C and A·U, as well as non-canonical base-pairs such as G·U and A·G.

4 analyze

The analyze program of the 3DNA software package allows you to compute the base-pair, and base-pair step parameters associated with a given nucleic acid structure. Analyze provides additional analysis features such as computing the overlap areas between stacked nucleic acid bases, sugar conformations, and sugar-phosphate backbone torsion angles.
A requirement of the analyze program is that you have to run the find_pair program beforehand.
Go ahead and read the usage message of the analyze program by typing:

```
analyze --help
```

in your terminal.

Now run the analyze program on the previously produced file using the find_pair program:

```
analyze 1ehz.inp
```

Notice that you can run the find_pair and analyze programs in one line by issuing the command:

```
find_pair 1ehz.pdb stdout | analyze
```

This command will produce a wealth of files with derived structural information, but the main one will just have the name of the input file followed by the .out extension. That is, you should now have a *1ehz.out* file in your folder. Go ahead and take a look at the *1ehz.out* file in your favorite text editor.

5 rebuild

The very useful 3DNA program called rebuild can do just that, rebuild nucleic acid structures. It uses as input either a set of base step, or base-pair step parameters, or a set of helical parameters to create a pdb file. To test the rebuild program first run find_pair and analyze on the A-RNA structure you previously created:

```
find_pair A-RNA.pdb stdout | analyze
```

Issuing the previous command must have created a file called *bp_step.par*. Open this file in a text editor and change the Twist values from 31.5 degrees to a smaller value, say 25.0 degrees, and save the new file with the name *undertwisted.par*.
Rebuild the undertwisted RNA by typing the following command in your good-ole terminal:

```
rebuild -atomic undertwisted.par undertwisted.pdb
```

This will generate a pdb structure with no sugar-phosphate backbone. To add a sugar-phosphate backbone you will need to issue the cp_std command before you perform the rebuild command, in the following way:

```
cp_std RNA
rebuild -atomic undertwisted.par undertwisted.pdb
```

Now rebuild a pdb file using the unmmodified base-pair step parameters, that is, using the original *bp_step.par* file. Open both structures in a molecular visualization program and confirm that one helix is undertwisted with respect to the original.

6 blocview

Blocview is a perl script which calls various 3DNA functionalities as well as raster3D, molscript, and pymol to generate an automated picture. Since blocview is just a script it can be easily modified, for example, following row 83 which invokes get_part -c (an undocumented command that creates a molscript header) one can add a line to change the inner color of protein ribbons:

```
# change inner color of ribbons from default 0.8
system("sed 's/grey 0.8/grey 0.5/g' temp2a > temp2");
```

7 Exercises

1. Run find_pair and analyze on your A-RNA structure and modify the resulting *bp_step.par* file so that the sequence is AAAGGGUUUCCC instead of AAAAAAAAAAAA.
   Use rebuild to generate a pdb file with the AAAGGGUUUCCC sequence.

2. Download the file with PBD_ID: 1aoi, that is, chromatin's nucleosome core particle, from the protein data bank website. Run it through find_pair and analyze.

3. Produce a "publication quality" plot of Slide vs. base-pair step number for the chromatin parameters you've computed in the previous exercise. Ask around (e.g. drop me a line) for which solutions are good for such a task.
   I recommend xmgrace, the matplotlib library of python, and igor-pro.

4. Repeat the recipe for Twist vs. base-pair step number (bpsn), and Roll vs. bpsn.

5. Compare your graphs to Figure 2 of the journal article "DNA Sequence-Directed Organization of Chromatin: Structure-Based Computational Analysis of Nucleosome-Binding Sequences" *Biophysical Journal*, **2009**, 96, 2245-2260.
   What regularities do you see?
   How would you describe the DNA wrapping around the nucleosome in terms of Sliding, Twisting, and Rolling?

6. Go to the website: `http://w3dna.rutgers.edu` and analyze the structure of your choice, for example the large subunit of the ribosome.

8 Config

In the config folder one can find most of the files for configuration of 3DNA internals. The following are descriptions of what they do.

8.1 col_chain.dat

This file specifies color defaults for the molscript files which 3DNA produces. I don't like to have purple proteins, so the first thing I do i this file is to change the default protein color from purple to blue. I also dislike having a wide tube to represent the nucleic acid backbone so I change the value from 0.8 (default) to 0.5

8.2 my_header_hres.r3d

The header file for the raster3d objects.

8.3 my_raster3d.par

The name is self-explanatory.

9 Interaction with gromacs

Gromacs will read pdb files in PDB v3 format, so, for a pdb created with 3DNA to work with gromacs one has to do:

```
pdb_get 355d
get_part -pdbv3 355d.pdb 355d-only-dna.pdb
pdb2gmx -f 355d-only-dna.pdb -o dna.gro -ff amber03 -water tip3p -p dna.top -i posre.itp
editconf -f dna.gro -o dna.gro -d 0.85
genbox -cp dna.gro -cs -o dna_b4em.gro -p dna.top

Here a miracle occurs KABUM! to create the steep.mdp that is!

grompp -f steep.mdp -c dna_b4em.gro -p dna -o dna.em
mdrun -nice 4 -s dna.em.tpr -o dna.em.tpr -c dna_b4em.gro -v
trjconv -f dna.em.tpr.trr -s dna.em.tpr -o dnatraj.pdb
```