

An Effective Analysis of Electroencephalographic Nano Wave Patterns

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Abstract

Presently days, the utilizations of Information and Communications Technology (ICT) are not restricted to information transmission, cloud arrangements, web based life, web servers and portable applications. From a decade ago, Information Technology is contacting each zone of social and corporate world including wellbeing and therapeutic sciences. The majority of the therapeutic determination research facilities are presently furnished with the development electronic machines to precisely analyze and bring the parameters of human body including Magnetic Resonance Imaging (MRI), Computed tomography (CT), Electroencephalography (EEG), Electrocardiography (ECG), Ultrasound, Mammography, Laparoscopy, Blood Examination, X-Ray and numerous others. These frameworks give higher level of precision in the examination of human body which helps the therapeutic specialist or specialist to foresee the

ailment. By this procedure, the therapeutic specialists can prescribe the reasonable treatment to the patients.

Keywords: Electroencephalographic Evaluation, Nano Particles, Deep Learning

Introduction

In addition to the enormous diagnosis machines in medical sciences, the software tools and libraries are also used. These software tools and applications evaluate the biological data which are fetched from the computerized diagnosis machines. Here, the concept of Bioinformatics comes to the scenario in which the software tools and applications are used to understand the biological and medical data. These software suites make use of high performance programming languages at the back-end to process and evaluate the biological dataset with the objectives to find out the human body parameters for effective treatment.

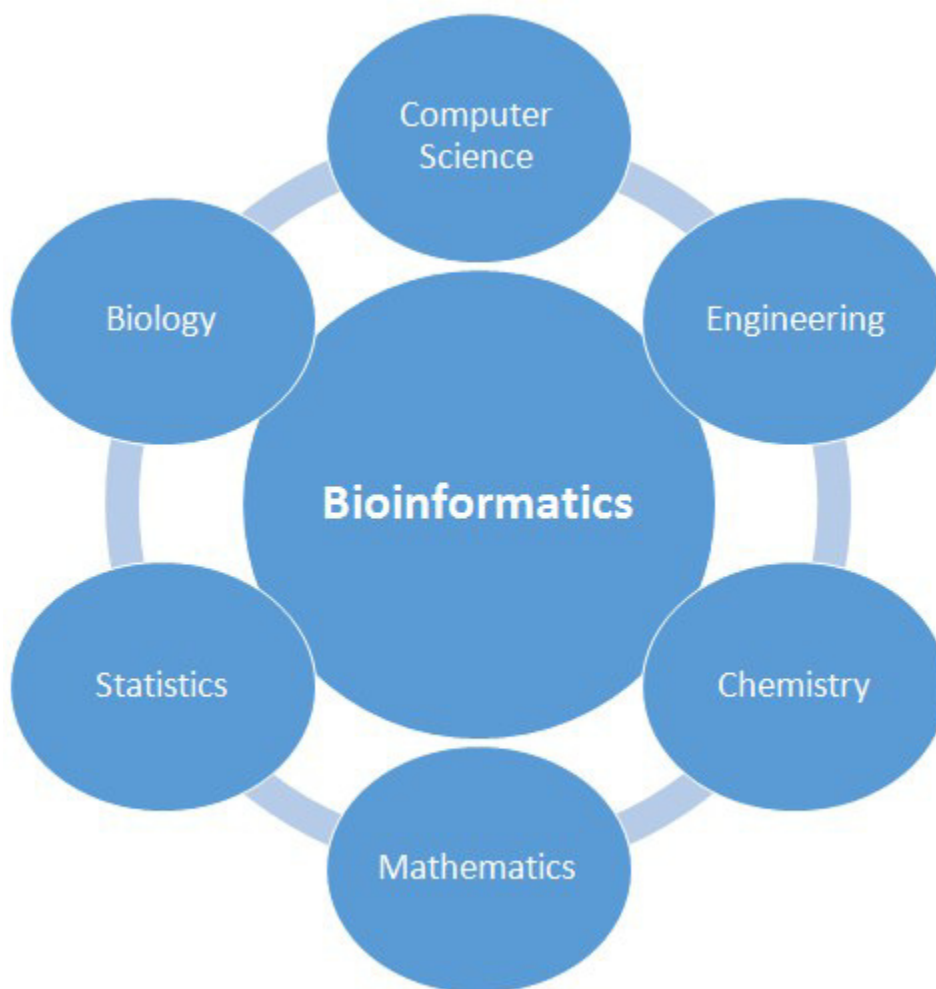


Figure 1: Elements and Constituents of Bioinformatics

Bioinformatics is the interdisciplinary area which integrates biology, computer science, mathematics, engineering, chemistry and statistics for advanced predictions and analytics. The field of molecular biology is also closely associated with Bioinformatics for accurate analysis of biological structures. Molecular biology deals with the deep analysis of the bimolecular movements in the cell of body along with the details of Proteins, DNA, RNA and biosynthesis.

Datasets for Research in Medical and Biological Areas

With the deployments of computerized machines, the researchers in diagnosis and medical sciences are taking assistance from software professionals in their field so that the programming modules can be processed by the software developers. Even, the computer scientists are now taking the interdisciplinary field of bioinformatics for their research so that their programming knowledge can be utilized for health sciences.

There are enormous medical datasets available for researches which are released by the diagnosis laboratories so that the overall architecture and structure of medical-biological data can be analyzed by the software experts. The programmers working in bioinformatics can download these medical datasets and they can perform the analysis using their effective algorithms.

Following are few links from where the medical data on EEG, ECG, MRI and X-Ray can be fetched for analysis using programming languages and tools

Dataset Library	Link
UCI Machine Learning Repository	https://archive.ics.uci.edu/ml/datasets.html
Health Data	https://www.healthdata.gov
Physionet	https://www.physionet.org/pn6/chbmit/
BrainSignals	http://www.brainsignals.de/
EEG Dataset	http://www.bsp.brain.riken.jp/~qibin/homepage/Datasets.html

OpenfMRI	https://openfmri.org/dataset/
Alyward	http://www.aylward.org/notes/open-access-medical-image-repositories
ECG Dataset	https://www.physionet.org/physiobank/database/ptbdb/
ECG Library	https://ecglibrary.com/ecghome.php
Ultrasound	http://splab.cz/en/download/databaze/ultrasound

Besides the abovementioned links, there are many resources available from where the medical and microbiological data can be downloaded for research and predictions.

Free and Open Source Tools for analysis of Medical Data

Following are the software tools which can be used for the analysis and evaluation of medical data for specific type of dataset

OpenEEG (URL : <http://openeeg.sourceforge.net/doc/>)

OpenEEG is free and open source software which can be used for EEG Signal analysis with enormous libraries as add-on including Neuroserver, BioEra, BrainBay, Brainathlon, BrainWave Viewer and EEGMIR.

EEGNET (URL : <https://sites.google.com/site/eegnetworks/>)

It is Free and Open Source Tool for the analysis and visualization of EEG Brain Signals. It is having features to visualize the brain network.

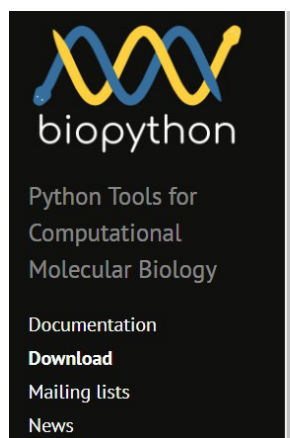
BioSig (URL : <http://biosig.sourceforge.net/>)

BioSig is a software library under free and open source distribution with the enormous features of biomedical signal processing. This library is having excellent features to process the biosignals including electrocorticogram (ECoG), electromyogram (EMG), electrocardiogram (ECG), electrooculogram (EOG), electroencephalogram (EEG), respiration and many others. In addition, the interfacing toolboxes and drivers for Octave, MATLAB, Python, PHP, Perl, Ruby, Tcl, C and C++ are also available. The key areas of brain-computer interfaces, psychology, Neuroinformatics, Cardiovascular Systems, Neurophysiology and sleep research are effectively processed in BioSig.

GenomeTools (URL : <http://genometools.org/>)

GenomeTools is the open source software for the analysis of genome and biological parameters. It is having a free library of tools for bioinformatics. The APIs in C are available with the detailed manual of usage. In addition, the deep analysis of biological structures are integrated in GenomeTools.

Working with BioPython for Molecular Biology (URL : <http://biopython.org/>)



Download

Current Release - 1.70 - 10 July 2017

See also [What's new.](#)

Files

Biopython 1.70

- [biopython-1.70.tar.gz](#) 15Mb – Source Tarball
- [biopython-1.70.zip](#) 16Mb – Source Zip File
- [Pre-compiled wheel files on PyPI](#)

Figure 2: Biopython Library for Molecular Biology

Biopython provides the set of tools and libraries for the analysis and computations of biological structures. Biopython is available in free and open source distribution and member of Open

Bioinformatics Foundation (OBF). Biopython can parse the files of bioinformatics into the data structures which can be processed by Python code.

Following international formats are supported in Biopython

- UniGene
- PubMed
- GenBank
- Medline
- GenBank
- FASTA
- Clustalw
- Blast

Installation of Biopython on Ubuntu

```
$ sudo apt-get install python-biopython
```

Installation of Biopython with Documentation

```
$ sudo apt-get install python-biopython-doc
```

BioSQL (<http://biosql.org>) can be used with Biopython to store the biological database. To integrate BioSQL, following instruction is executed

```
$ sudo apt-get install python-biopython-sql
```

Sequence is the key object in bioinformatics. The sequences can be processed in Biopython with following instructions

```
>>> from Bio.Seq import Seq  
>>> my_seq = Seq("MyDefinedSequence")
```

```
>>> my_seq
Seq(' MyDefinedSequence ', Alphabet())
>>> print(my_seq)
MyDefinedSequence
>>> my_seq.alphabet
Alphabet()
```

Transcription Functions on DNA and RNA

If you have a DNA sequence, you may want to turn it into RNA. In bioinformatics we normally assume the DNA is the coding strand (not the template strand) so this is a simple matter of replacing all the thymines with uracil:

Complement and reverse complement

These are very simple - the methods return a new Seq object with the appropriate sequence and the same alphabet:

```
>>> from Bio.Seq import Seq
>>> from Bio.Alphabet import generic_dna

>>> my_values_dna = Seq("MY_VALUES_DNA", generic_dna)
>>> my_values_dna
Seq('MY_VALUES_DNA', DNAAlphabet())

>>> my_values_dna.complement()
Seq('ATCATGTGACCA', DNAAlphabet())

>>> my_values_dna.reverse_complement()
```



```
Seq('ACCAGTGTACTA', DNAAlphabet())
```

If you have a DNA sequence, you may want to turn it into RNA. In bioinformatics we normally assume the DNA is the coding strand (not the template strand) so this is a simple matter of replacing all the thymines with uracil:

```
>>> my_values_dna
Seq('MY_VALUES_DNA', DNAAlphabet())
```

```
>>> my_values_dna.transcribe()
Seq('AGUACACUGGU', RNAAlphabet())
```

With the specification of RNA, the associated DNA can be fetched

```
>>> my_values_rna = my_values_dna.transcribe()
```

```
>>> my_values_rna
Seq('AGUACACUGGU', RNAAlphabet())
```

```
>>> my_values_rna.back_transcribe()
Seq('MY_VALUES_DNA', DNAAlphabet())
```

```
>>> my_values_rna
Seq('AGUACACUGGU', RNAAlphabet())
```

```
>>> my_values_rna.back_transcribe().reverse_complement()
Seq('ACCAGTGTACT', DNAAlphabet())
```

Conclusion

Presently days, Bioinformatics and Biomedical Predictive Analytics is one of the key spaces of research for arranged applications. The extraction, handling and prescient mining from cerebrum, heart and other human body created signals are assessed with the utilization of data innovation. The datasets from Physionet, UCSD, FPMS and others can be utilized for the exploration work in bioinformatics with the reconciliation of information mining and machine learning devices.

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