DNATool

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eda-lvl5-dnatool

- Fecha de entrega: 19/05/2022
- Grupo: 7
  - DALZOTTO, Rafael
  - HEIR, Alejandro Nahuel

22.08 - Algoritmos y Estructuras de Datos - Ingeniería Electrónica - ITBA

Chapter 2

Class Index

2.1 Class List

Here are the classes, structs, unions and interfaces with brief descriptions:

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Chapter 3

File Index

3.1 File List

Here is a list of all files with brief descriptions:

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Chapter 4

Class Documentation

4.1 Cell Struct Reference

```
#include <DirectionMat.h>
```

Public Attributes

- uint8_t c0: 2
- uint8_t c1: 2
- uint8_t c2: 2
- uint8_t c3: 2

4.1.1 Member Data Documentation

4.1.1.1 c0

```
uint8_t Cell::c0
```

4.1.1.2 c1

```
uint8_t Cell::c1
```

4.1.1.3 c2

```
uint8_t Cell::c2
```

4.1.1.4 c3

```
uint8_t Cell::c3
```

The documentation for this struct was generated from the following file:

- DirectionMat.h

4.2 DirectionMat Class Reference

```
#include <DirectionMat.h>
```

Public Member Functions

- DirectionMat (size_t rows, size_t cols)
- ~DirectionMat ()
- uint8_t at (size_t row, size_t col)

  Reads a given DirectionMap cell.
- void set (uint8_t val, size_t row, size_t col)

  Writes a given DirecitonMat cell.
- size_t getRows ()

  Returns the DirectionMat row size.
- size_t getCols ()

  Returns the DirectionMat column size.

4.2.1 Constructor & Destructor Documentation

4.2.1.1 DirectionMat()

```
DirectionMat::DirectionMat (
            size_t rows,
            size_t cols )
```

4.2.1.2 ~DirectionMat()

```
DirectionMat::~DirectionMat ( )
```

4.2.2 Member Function Documentation

4.2.2.1 at()

```
uint8_t DirectionMat::at (
            size_t row,
            size_t col )
```

Reads a given DirectionMap cell.

Parameters

row	
col	

Returns

uint8_t

4.2.2.2 getCols()

```
size_t DirectionMat::getCols ( )
```

Returns the DirectionMat column size.

Returns

size_t

4.2.2.3 getRows()

```
size_t DirectionMat::getRows ( )
```

Returns the DirectionMat row size.

Returns

size_t

4.2.2.4 set()

```
void DirectionMat::set (
             uint8_t val,
             size_t row,
             size_t col )
```

Writes a given DirecitonMat cell.

Parameters

val	Data to store
row	
col	

The documentation for this class was generated from the following files:

- DirectionMat.h
- DirectionMat.cpp

Chapter 5

File Documentation

5.1 Aligner.cpp File Reference

Genetic sequence aligner, based on Needleman-Wunsch algorithm.

```
#include "Aligner.h"
#include <iostream>
#include <cstring>
#include <algorithm>
#include <cstdio>
```

Enumerations

- enum Direction { VERTICAL , DIAGONAL , HORIZONTAL }

Functions

- void printMat (DirectionMat ∗mat)

  Prints the given DirectionMat.
- DirectionMat ∗ initMat (const size_t rows, const size_t cols)

  Initializes a DirectionMat for storing Needleman-Wunsch directions.
- int32_t fillMat (DirectionMat ∗mat, const string &seq1, const string &seq2)

  Completes a DirectionMat based on two given genetic sequences.
- void buildAligment (DirectionMat ∗mat, const string &seq1, const string &seq2, array< string, 3 > &output)

  Builds the optimal alignment for two genetic sequences and an already filled DirectionMat.
- int32_t getGlobalAlignment (const string &seq1, const string &seq2, array< string, 3 > &alignment)

  Runs aligner for two acgt-like strings.

5.1.1 Detailed Description

Genetic sequence aligner, based on Needleman-Wunsch algorithm.

Authors

DALZOTTO, Rafael; HEIR, Alejandro - Grupo 7

Version

0.1

Date

2022-05-08

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5.1.2 Enumeration Type Documentation

5.1.2.1 Direction

```
enum Direction
```

Enumerator

VERTICAL	
DIAGONAL	
HORIZONTAL	

5.1.3 Function Documentation

5.1.3.1 buildAligment()

```
void buildAligment (
             DirectionMat * mat,
             const string & seq1,
             const string & seq2,
             array< string, 3 > & output )
```

Builds the optimal alignment for two genetic sequences and an already filled DirectionMat.

Parameters

mat	
seq1	String with one acgt-like genetic sequence.
seq2	String with one acgt-like genetic sequence.
output	3-string array to store the optimal alignment.

5.1.3.2 fillMat()

```
int32_t fillMat (
            DirectionMat * mat,
            const string & seq1,
            const string & seq2 )
```

Completes a DirectionMat based on two given genetic sequences.

Parameters

mat	
seq1	String with one acgt-like genetic sequence.
seq2	String with one acgt-like genetic sequence.

Returns

int32_t Optimal score

5.1.3.3 getGlobalAlignment()

```
int32_t getGlobalAlignment (
            const string & seq1,
            const string & seq2,
            array< string, 3 > & alignment )
```

Runs aligner for two acgt-like strings.

Parameters

seq1	String with one acgt-like genetic sequence.
seq2	String with one acgt-like genetic sequence.
alignment	3-string array to store the optimal alignment.

Returns

int32_t Optimal score

5.1.3.4 initMat()

```
DirectionMat * initMat (
            const size_t rows,
            const size_t cols )
```

Initializes a DirectionMat for storing Needleman-Wunsch directions.

Parameters

rows	
cols	

Returns

DirectionMat∗

5.1.3.5 printMat()

```
void printMat (
            DirectionMat * mat )
```

Prints the given DirectionMat.

Parameters

mat	

5.2 Aligner.h File Reference

Genetic sequence aligner, based on Needleman-Wunsch algorithm.

```
#include <string>
#include <array>
#include "DirectionMat.h"
```

Functions

- DirectionMat ∗ initMat (const size_t rows, const size_t cols)

  Initializes a DirectionMat for storing Needleman-Wunsch directions.
- int32_t fillMat (DirectionMat ∗mat, const std::string &seq1, const std::string &seq2)
- void buildAligment (DirectionMat ∗mat, const std::string &seq1, const std::string &seq2, std::array< std::string, 3 > &output)
- int32_t getGlobalAlignment (const std::string &seq1, const std::string &seq2, std::array< std::string, 3 > &alignment)

5.2.1 Detailed Description

Genetic sequence aligner, based on Needleman-Wunsch algorithm.

Authors

DALZOTTO, Rafael; HEIR, Alejandro - Grupo 7

Version

0.1

Date

2022-05-08

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5.2.2 Function Documentation

5.2.2.1 buildAligment()

```
void buildAligment (
             DirectionMat * mat,
             const std::string & seq1,
             const std::string & seq2,
             std::array< std::string, 3 > & output )
```

5.2.2.2 fillMat()

```
int32_t fillMat (
             DirectionMat * mat,
             const std::string & seq1,
             const std::string & seq2 )
```

5.2.2.3 getGlobalAlignment()

```
int32_t getGlobalAlignment (
             const std::string & seq1,
             const std::string & seq2,
             std::array< std::string, 3 > & alignment )
```

5.2.2.4 initMat()

```
DirectionMat * initMat (
             const size_t rows,
             const size_t cols )
```

Initializes a DirectionMat for storing Needleman-Wunsch directions.

Parameters

rows	
cols	

Returns

DirectionMat∗

5.3 Aligner.h

Go to the documentation of this file.

```

#ifndef NEEDLEMACHINE_H
#define NEEDLEMACHINE_H

#include <string>
#include <array>

#include "DirectionMat.h"

DirectionMat *initMat(const size_t rows, const size_t cols);

int32_t fillMat(DirectionMat *mat, const std::string &seq1, const std::string &seq2);

void buildAligment(DirectionMat *mat, const std::string &seq1, const std::string &seq2,
              std::array<std::string, 3> &output);

int32_t getGlobalAlignment(const std::string &seq1, const std::string &seq2,
                           std::array<std::string, 3> &alignment);

#endif
```

5.4 DirectionMat.cpp File Reference

Implements 2 bit-size matrix cells.

```
#include "DirectionMat.h"
```

5.4.1 Detailed Description

Implements 2 bit-size matrix cells.

Authors

DALZOTTO, Rafael; HEIR, Alejandro - Grupo 7

Version

0.1

Date

2022-05-08

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5.5 DirectionMat.h File Reference

Implements 2 bit-size matrix cells.

```
#include <iostream>
#include <stdint.h>
#include <vector>
#include <chrono>
#include <random>
#include <algorithm>
```

Classes

- struct Cell
- class DirectionMat

5.5.1 Detailed Description

Implements 2 bit-size matrix cells.

Authors

DALZOTTO, Rafael; HEIR, Alejandro - Grupo 7

Version

0.1

Date

2022-05-08

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5.6 DirectionMat.h

Go to the documentation of this file.

```

#ifndef CELL_H
#define CELL_H

#include <iostream> // size_t
#include <stdint.h>

#include <vector>
#include <chrono>
#include <iostream>
#include <random>
#include <algorithm>

typedef struct
```

```
{
    uint8_t c0 : 2;
    uint8_t c1 : 2;
    uint8_t c2 : 2;
    uint8_t c3 : 2;
} Cell;

class DirectionMat
{
public:
    DirectionMat(size_t rows, size_t cols);
    ~DirectionMat();

    uint8_t at(size_t row, size_t col);
    void set(uint8_t val, size_t row, size_t col);

    size_t getRows();
    size_t getCols();

private:
    Cell *data;

    size_t compactCols;
    size_t rows;
    size_t cols;
};

#endif
```

5.7 GBReader.cpp File Reference

Sequence extractor for GenBank-like files.

```
#include "GBReader.h"
#include <algorithm>
```

Functions

- bool notIsACGT (char c)

  Checks if a given character is not 'a', 'c', 'g' or 't'.
- bool getSequence (string &output, istream &file)

  Extracts an acgt-like string from a GenBank file.

5.7.1 Detailed Description

Sequence extractor for GenBank-like files.

Authors

DALZOTTO, Rafael; HEIR, Alejandro - Grupo 7

Version

0.1

Date

2022-05-08

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5.7.2 Function Documentation

5.7.2.1 getSequence()

```
bool getSequence (
             string & output,
             istream & file )
```

Extracts an acgt-like string from a GenBank file.

Parameters

output	String to store the acgt sequence
file	ifstream file handler.

Returns

true Success

false Failure

5.7.2.2 notIsACGT()

```
bool notIsACGT (
             char c )
```

Checks if a given character is not 'a', 'c', 'g' or 't'.

Parameters

c	

Returns

true It's not

false It is

5.8 GBReader.h File Reference

Sequence extractor for GenBank-like files.

```
#include <iostream>
```

Functions

- bool getSequence (std::string &output, std::istream &file)

5.8.1 Detailed Description

Sequence extractor for GenBank-like files.

Authors

DALZOTTO, Rafael; HEIR, Alejandro - Grupo 7

Version

0.1

Date

2022-05-08

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5.8.2 Function Documentation

5.8.2.1 getSequence()

```
bool getSequence (
            std::string & output,
            std::istream & file )
```

5.9 GBReader.h

Go to the documentation of this file.

```

#ifndef GBREADER_H
#define GBREADER_H

#include <iostream>

bool getSequence(std::string &output, std::istream &file);

#endif
```

5.10 main.cpp File Reference

Runs the genetic sequence aligner.

```
#include <iostream>
#include <fstream>
#include <sstream>
#include <chrono>
#include "GBReader.h"
#include "Aligner.h"
```

Functions

- int main (int argc, char **argv)

5.10.1 Detailed Description

Runs the genetic sequence aligner.

Authors

DALZOTTO, Rafael; HEIR, Alejandro - Grupo 7

Version

0.1

Date

2022-05-08

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5.10.2 Function Documentation

5.10.2.1 main()

```
int main (
            int argc,
            char ** argv )
```

5.11 main_test.cpp File Reference

Tests for the genetic sequence aligner.

```
#include <iostream>
#include <string>
#include <array>
#include <fstream>
#include <sstream>
#include "GBReader.h"
#include "Aligner.h"
```

Functions

- bool testMatInit (DirectionMat ∗&mat, const string &s1, const string &s2, DirectionMat &expectedMat)
- bool testFillMat (DirectionMat ∗mat, const string &s1, const string &s2, int32_t expectedScore, DirectionMat &expectedMat)
- bool testAlignment (DirectionMat ∗mat, const string &s1, const string &s2, array< string, 3 > &expected↩ Alignment)
- int main ()

5.11.1 Detailed Description

Tests for the genetic sequence aligner.

Authors

DALZOTTO, Rafael; HEIR, Alejandro - Grupo 7

Version

0.1

Date

2022-05-08

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5.11.2 Function Documentation

5.11.2.1 main()

```
int main ( )
```

5.11.2.2 testAlignment()

```
bool testAlignment (
            DirectionMat * mat,
            const string & s1,
            const string & s2,
            array< string, 3 > & expectedAlignment )
```

5.11.2.3 testFillMat()

```
bool testFillMat (
            DirectionMat * mat,
            const string & s1,
            const string & s2,
            int32_t expectedScore,
            DirectionMat & expectedMat )
```

5.11.2.4 testMatInit()

```
bool testMatInit (
            DirectionMat *& mat,
            const string & s1,
            const string & s2,
            DirectionMat & expectedMat )
```

5.12 README.md File Reference

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