Querying Genomic Databases

by

Alexandra Baehr, Ray Hagstrom, David Joerg, and Ross Overbeek

September 1991

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**MATHEMATICS AND
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Mathematics and Computer Science Division

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Abstract

A natural-language interface has been developed that retrieves genomic information by using a simple subset of English. The interface spares the biologist from the task of learning database-specific query languages and computer programming. Currently, the interface deals with the *E. coli* genome. It can, however, be readily extended and shows promise as a means of easy access to other sequenced genomic databases as well.

1 Introduction

Molecular biologists investigating the genomes of various species have long been frustrated by the difficulty of accessing the genomic information once it has been entered into databases. To spare biologists the task of learning either database-specific query languages or computer programming, we have built a prototype interface that retrieves genomic information using a simple subset of a familiar natural language – English. Though this natural language interface deals specifically with the *E. coli* genome, it may be readily extended, and shows promise as a means of easy access to other sequenced genomic databases as well.

Here we present our natural language interface not as a set of formal rules, but as a set of illustrative queries which will suggest many other queries of biological interest. Our rather ambitious future goal is to design a set of semantic primitives flexible enough to express almost any *E. coli* query a biologist might care to frame. In the meantime, however, our “pidgin” English can retrieve from the integrated *E. coli* database much useful information that had previously required hours of work, including the reconciliation of diverse notational schemes, to acquire.

Biologists may use this system as it stands, and we plan to add enhancements whenever they find themselves unable to formulate a query into the restricted dialect we support. We also welcome suggestions for other ways of improving the natural language interface. Thus we expect the linguistic model to grow – initially, at least – by accretion. Our hope is that the final linguistic model will be valuable in itself as a framework to support researchers desiring access to wider classes of genomic data.

2 Locating Reference Points

2.1 Origin of Replication

2.1.1 Print the point oriC

query: print the point oriC

3953061/3953061

1

(point)

2.1.2 Print the point terA

query: print the point terA

```
1348264/1348264      1                      (point)
```

2.2 Establishing Partitions of the Genome

2.2.1 Print 4 equal partitions of the genome

query: print 4 equal partitions of the genome

```
----- 4 found -----
0/1168149      1168150                      (region)
1168150/2336299 1168150                      (region)
2336300/3504449 1168150                      (region)
3504450/4672599 1168150                      (region)
```

2.2.2 Print 4 equal partitions of the genome starting at oriC

query: print 4 equal partitions of the genome starting at oriC

```
----- 4 found -----
448611/1616760 1168150                      (region)
1616761/2784910 1168150                      (region)
2784911/3953060 1168150                      (region)
---      composite: length 1168150      ---
3953061/4672599 719539                      (region)
0/448610      448611                      (region)
---      end composite      ---
```

2.2.3 Print 8 equal partitions of the genome starting at 9802

query: print 8 equal partitions of the genome starting at 9802

```
----- 8 found -----
9802/593876      584075                      (region)
593877/1177951  584075                      (region)
1177952/1762026 584075                      (region)
1762027/2346101 584075                      (region)
2346102/2930176 584075                      (region)
2930177/3514251 584075                      (region)
3514252/4098326 584075                      (region)
---      composite: length 584075      ---
4098327/4672599 574273                      (region)
0/9801      9802                      (region)
.
.
.
```

3 Retrieving Information on Kohara Clones

3.1 Locate All Kohara Clones

3.1.1 Print all kohara clones in the genome

query: print all kohara clones in the genome

```
----- 479 found -----
0/400          401    [676]15A5(part 2)    (Kohara clone)
383/17253      16871   [101]9E4      (Kohara clone)
9400/24157     14758   [102]6H3      (Kohara clone)
20930/38500    17571   [103]22B12    (Kohara clone)
35700/53352    17653   [104]2F7      (Kohara clone)
39400/55700    16301   [105]4A3      (Kohara clone)
51970/65027    13058   [106]8D2      (Kohara clone)
63866/80200    16335   [107]5R5      (Kohara clone)
68512/83300    14789   [108]8H11     (Kohara clone)
79200/96783    17584   [109]6C1      (Kohara clone)
96404/118500   22097   [111]15B8     (Kohara clone)
.
.
.
```

3.2 Locate Kohara Clones by Region or Landmark

3.2.1 Print the kohara clones in the region from 400 kb to 800 kb

query: print the kohara clones in the region from 400 kb to 800 kb

```
----- 36 found -----
409727/425481  15755   [143]6A12     (Kohara clone)
416700/433300  16601   [144]9G9      (Kohara clone)
429100/442800  13701   [145]4F3      (Kohara clone)
434622/452100  17479   [146]19F6     (Kohara clone)
446000/462911  16912   [147]2H5      (Kohara clone)
459067/475300  16234   [148]3B6      (Kohara clone)
468713/484200  15488   [149]7E2      (Kohara clone)
472500/492900  20401   [150]19B7     (Kohara clone)
484200/502105  17906   [151]8C4      (Kohara clone)
497700/509300  11601   [152]12H5     (Kohara clone)
.
.
.
```

3.2.2 Print the kohara clones in the region from the start of gene thrC - 5000 to the start of gene thrC

query: print the kohara clones in the region
from the start of gene thrC - 5000 to the start of gene thrC

0/400 401 [676]15A5(part 2) (Kohara clone)

3.3 Locate Clones Containing Particular Nucleotide Patterns

3.3.1 Print all kohara clones that contain the pattern GATC

query: print all kohara clones that contain the pattern GATC

```
----- 371 found -----
383/17253            16871            [101]9E4            (Kohara clone)
9400/24157           14758            [102]6H3            (Kohara clone)
20930/38500           17571            [103]22B12           (Kohara clone)
35700/53352           17653            [104]2F7            (Kohara clone)
39400/55700           16301            [105]4A3            (Kohara clone)
51970/65027           13058            [106]8D2            (Kohara clone)
63866/80200           16335            [107]5H5            (Kohara clone)
68512/83300           14789            [108]8H11            (Kohara clone)
79200/96783           17584            [109]6C1            (Kohara clone)
96404/118500           22097            [111]15B8            (Kohara clone)
.
.
.
```

3.3.2 Print all (kohara clones in the region from 400 kb to 800 kb) that contain the pattern GATC

query: print all (kohara clones in the region from 400 kb to 800 kb)
that contain the pattern GATC

```
----- 31 found -----
409727/425481           15755            [143]6A12            (Kohara clone)
416700/433300           16601            [144]9G9            (Kohara clone)
429100/442800           13701            [145]4F3            (Kohara clone)
434622/452100           17479            [146]19F6            (Kohara clone)
446000/462911           16912            [147]2H5            (Kohara clone)
459067/475300           16234            [148]3B6            (Kohara clone)
468713/484200           15488            [149]7E2            (Kohara clone)
484200/502105           17906            [151]8C4            (Kohara clone)
497700/509300           11601            [152]12H5            (Kohara clone)
504333/521000           16668            [153]4B10            (Kohara clone)
.
.
.
```

3.3.3 Let SpecialGenes be translated counterclockwise genes that contain the pattern GATCGATC

query: let SpecialGenes be translated counterclockwise genes
that contain the pattern GATCGATC

----- 11 found -----

3.3.4 For each member of SpecialGenes Gene, {print Gene; print all kohara clones that contain Gene}

query: for each member of SpecialGenes Gene,
{print Gene; print all kohara clones that contain Gene}

677007/678908	1902	mrda	(gene)	counterclockwise
674353/693900	19548	[169]15D7	(Kohara clone)	
762290/763573	1284	gltA	(gene)	counterclockwise
760100/775500	15401	[176]7E10	(Kohara clone)	
1696993/1698639	1647	fumA	(gene)	counterclockwise
----- 2 found -----				
1687191/1702300	15110	[313]6A3	(Kohara clone)	
1696926/1714800	17875	[314]6A5	(Kohara clone)	
2367471/2368829	1359	glpT	(gene)	counterclockwise
----- 2 found -----				
2355835/2374200	18366	[377]20E7	(Kohara clone)	
	.			
	.			
	.			

4 Retrieving Information on Genes

4.1 Locate Genes by Id

4.1.1 Print gene entA

query: print gene entA

636874/637620	747	entA	(gene)	clockwise
---------------	-----	------	--------	-----------

4.2 Locate Clockwise or Counterclockwise Genes

4.2.1 Print all clockwise genes in the genome

query: print all clockwise genes in the genome

```

----- 618 found -----
207/2669      2463      thrA      (gene)      clockwise
2671/3600      930      thrB      (gene)      clockwise
3601/4887      1287      thrC      (gene)      clockwise
12280/14196    1917      dnaK      (gene)      clockwise
14285/15415    1131      dnaJ      (gene)      clockwise
15562/16836    1275      orf       (gene)      clockwise
17571/18659    1089      ant       (gene)      clockwise
18719/19507    789      orf       (gene)      clockwise
21425/22363    939      orf       (gene)      clockwise
22406/23929    1524     ileS      (gene)      clockwise

```

.
.
.

4.2.2 Print all clockwise genes in the region from 5 minutes to 10 minutes

query: print all counterclockwise genes in the region from 5 minutes to 10 minutes

```

----- 13 found -----
243936/244012    77      aspV      (gene)      counterclockwise
244175/244906    732     dnaQ      (gene)      counterclockwise
262253/263710    1458    pepD      (gene)      counterclockwise
266265/267320    1056    phoE      (gene)      counterclockwise
332849/334882    2034    betT      (gene)      counterclockwise
367935/368546    612     lacA      (gene)      counterclockwise
368610/369863    1254    lacY      (gene)      counterclockwise
369915/372989    3075    lacZ      (gene)      counterclockwise
373112/374194    1083    lacI      (gene)      counterclockwise

```

.
.
.

4.3 Locate Genes Contained in Other Objects on the Chromosome

4.3.1 Print all genes that are contained in kohara clone [101]9E4

query: print all genes that are contained in kohara clone [101]9E4

```

----- 7 found -----
2671/3600      930      thrB      (gene)      clockwise
3601/4887      1287      thrC      (gene)      clockwise
5550/5932      383      orf       (gene)      counterclockwise
12280/14196    1917      dnaK      (gene)      clockwise
14285/15415    1131      dnaJ      (gene)      clockwise
15562/16836    1275      orf       (gene)      clockwise
16867/17019    153      gef       (gene)      counterclockwise

```

4.4 Locate Genes by Region or Landmark

4.4.1 Print the gene containing the region from 2396 to 2496

query: print the gene containing the region from 2396 to 2496

207/2669	2463	thrA	(gene)	clockwise
----------	------	------	--------	-----------

4.4.2 Print the gene which contains point 20901

query: print the gene which contains point 20901

20833/21096	264	rpsT	(gene)	counterclockwise
-------------	-----	------	--------	------------------

4.5 Locate Genes Satisfying Multiple Criteria

4.5.1 Print all clockwise genes in the region from 2 kb to 210 kb

query: print all clockwise genes in the region from 2 kb to 210 kb

```
----- 61 found -----
2671/3600      930      thrB      (gene)      clockwise
3601/4887      1287     thrC      (gene)      clockwise
12280/14196    1917     dnaK      (gene)      clockwise
14285/15415    1131     dnaJ      (gene)      clockwise
15562/16836    1275     orf       (gene)      clockwise
17571/18659    1089     ant       (gene)      clockwise
18719/19507    789      orf       (gene)      clockwise
21425/22363    939      orf       (gene)      clockwise
22406/23929    1524     ileS      (gene)      clockwise
25142/25636    495      lspA      (gene)      clockwise
.
.
.
```

4.5.2 Print all translated clockwise genes in the region from oriC to oriC + 8 kb

query: print all translated clockwise genes in the region
from oriC to oriC + 8 kb

```
----- 2 found -----
3954493/3955485  993      asnA      (gene)      clockwise
3960633/3961052  420      rbsD      (gene)      clockwise
```

4.6 Locate Genes Containing Specific Nucleotide Patterns

4.6.1 Let GATCGATC_Genes be all genes that contain the pattern GATCGATC

query: let GATCGATC_Genes be all genes that contain the pattern GATCGATC

----- 20 found -----

4.6.2 Print the lengths of GATCGATC_Genes

query: print the lengths of GATCGATC_Genes

----- 20 found -----

---	1041	---
---	1245	---
---	1902	---
---	1284	---
---	2358	---
---	1011	---
---	2676	---
---	1647	---
---	723	---
---	1359	---

.
.
.

4.7 Display K-mer Usage of Genes

4.7.1 Print the 1-mer decomposition of GATCGATC_Genes

query: print the 1-mer decomposition of GATCGATC_Genes

----- 5 found -----

---	0	---
---	8368	---
---	9375	---
---	9059	---
---	8262	---

4.7.2 Print the 1-mer decomposition of GATCGATC_Genes as 1-mer usage

query: print the 1-mer decomposition of GATCGATC_Genes as 1-mer usage

----- 5 found -----

invalid 1-mers: 0 0.00%

A: 8368	0.24%
C: 9375	0.27%
G: 9059	0.26%
T: 8262	0.24%

4.7.3 Print the 2-mer decomposition of GATCGATC_Genes as 2-mer usage

query: print the 2-mer decomposition of GATCGATC_Genes as 2-mer usage

```

----- 17 found -----
invalid 2mers: 0      0.00%
AA: 2313              0.07%
AC: 1983              0.06%
AG: 1882              0.05%
AT: 2183              0.06%
CA: 2607              0.07%
CC: 2130              0.06%
CG: 2967              0.08%
CT: 1671              0.05%
GA: 2032              0.06%
.
.
.

```

4.8 Investigate the Codon Usage of Genes

4.8.1 Display Codon Usage of Genes

4.8.1.1 Print the codon usage of gene entA

query: print the codon usage of gene entA

```

----- 65 found -----
--- 0 ---
--- 8 ---
--- 4 ---
--- 0 ---
--- 3 ---
--- 1 ---
--- 7 ---
--- 6 ---
--- 3 ---
--- 0 ---
.
.
.

```

4.8.1.2 Print the codon usage of gene entA as codon info

query: print the codon usage of gene entA as codon info

```
----- 65 found -----
alanine
  GCA: 3
  GCC: 8
  GCG: 21
  GCT: 3

arginine
  AGA: 0
  AGG: 0
  CGA: 2
  .
  .
  .
```

4.8.1.3 Print the codon usage of gene entA as codon usage

query: print the codon usage of gene entA as codon usage

```
----- 65 found -----
number valid codons = 249
number invalid codons = 0

alanine: 35          14.06%
  GCA: 3            1.20%
  GCC: 8            3.21%
  GCG: 21           8.43%
  GCT: 3            1.20%

arginine: 12         4.82%
  .
  .
  .
```

4.8.2 Assess Distribution of Codons

4.8.2.1 Let entA_Codons be the codon usage of gene entA

query: let entA_Codons be the codon usage of gene entA

```
----- 65 found -----
```

4.8.2.2 Let entA_Frac be entA_Codons / sum of entA_Codons

```
query: let entA_Frac be entA_Codons / sum of entA_Codons
```

----- 65 found -----

4.8.2.3 Print entA_Frac

```
query: print entA_Frac
```

----- 65 found -----

```
---      0.0      ---
--- 0.0321285    ---
--- 0.0160643    ---
---      0.0      ---
--- 0.0120482    ---
--- 0.00401606   ---
--- 0.0281124    ---
--- 0.0240964    ---
--- 0.0120482    ---
---      0.0      ---
```

.
.
.

4.8.2.4 Let AllCodons be codon usage of all translated genes

```
query: let AllCodons be codon usage of all translated genes
```

----- 65 found -----

4.8.2.5 Let AllFrac be AllCodons / sum of AllCodons

```
query: let AllFrac be AllCodons / sum of AllCodons
```

----- 65 found -----

4.8.2.6 Print AllFrac as codon info

query: Print AllFrac as codon info

----- 65 found -----

alanine

GCA: 0.0201498

GCC: 0.0242952

GCG: 0.035903

GCT: 0.0165187

arginine

AGA: 0.00114233

AGG: 8.4399e-04

CGA: 0.00279891

.

.

.

4.8.2.7 Plot AllFrac

query: plot AllFrac

Enter file name (EX to exit)

enter x-axis column:

enter y-axis column:

EXPAND PLOTTO

1 XLOW 0. 2 XUPP 0. 5 LOGX 0 7 XHIS 0
3 YLOW 0. 4 YUPP 0. 6 LOGY 0 8 YHIS 0
9 NBNS 0 10 ACCUM HISTs 0 11 LIST X,Y 12 SETLIMITS 0

13 ENTER TITLE:tmp_plot

14 ENTER LABEL:GGPlot -1 RETURN <CR> PLOT

EXPAND PLOTTO

1 XLOW 7.851E-06 2 XUPP 5.763E-02 5 LOGX 0 7 XHIS 1
 3 YLOW 7.851E-06 4 YUPP 5.763E-02 6 LOGY 0 8 YHIS 0
 9 NBNS 0 10 ACCUM HISTS 0 11 LIST X,Y 12 SETLIMITS 0

13 ENTER TITLE:tmp_plot

14 ENTER LABEL:GGPlot -1 RETURN <CR> PLOT

-1

Welcome back to the database interface.

5 Retrieving Information on Sequence Fragments

5.1 Print the sequence fragment that contains point oriC

query: print the sequence fragment which contains point oriC

3929220/3956394	27175	bglBecoM	(DNA fragment)
-----------------	-------	----------	----------------

5.2 Print all sequence fragments that are in the region from 700 kb to 760 kb

query: print all sequence fragments that are in the region
from 700 kb to 760 kb

----- 3 found -----			
707654/719805	12152	glnVecoM	(DNA fragment)
732241/740153	7913	kdpEecoM	(DNA fragment)
748624/750662	2039	ECOPHRORF	(DNA fragment)

5.3 Print all restriction fragments for enzyme EcoR5 that are in ampDecoM

query: print all restriction fragments for enzyme EcoR5 that are in ampDecoM

----- 8 found -----			
118912/119502	591	[EcoR5,EcoR5]	(computed rest. frag.)
119503/120144	642	[EcoR5,EcoR5]	(computed rest. frag.)
120145/124639	4495	[EcoR5,EcoR5]	(computed rest. frag.)
124640/126354	1715	[EcoR5,EcoR5]	(computed rest. frag.)
126355/126657	303	[EcoR5,EcoR5]	(computed rest. frag.)
126658/127317	660	[EcoR5,EcoR5]	(computed rest. frag.)
127318/128481	1164	[EcoR5,EcoR5]	(computed rest. frag.)
128482/129174	693	[EcoR5,EcoR5]	(computed rest. frag.)

6 Retrieving Information on Restriction Fragments and Restriction Sites

6.1 Print all restriction fragments for enzymes {Pst1, EcoR1} in gene dnaK

query: print all restriction fragments for enzymes {Pst1, EcoR1} in gene dnaK

```

----- 3 found -----
13007/13143      137      [EcoR1,Pst1]      (computed rest. frag.)
13144/13253      110      [Pst1,Pst1]      (computed rest. frag.)
13254/13604      351      [Pst1,Pst1]      (computed rest. frag.)

```

6.2 Print all restriction fragments for enzymes {Pst1, EcoR1, EcoR5} in the region from the start of gene ileS - 5 kb to the start of gene ileS

query: print all restriction fragments for enzymes {Pst1, EcoR1, EcoR5}
in the region from the start of gene ileS - 5 kb
to the start of gene ileS

```

----- 2 found -----
19423/20405      983      [Pst1,Pst1]      (computed rest. frag.)
20406/21873      1468     [Pst1,EcoR5]     (computed rest. frag.)

```

6.3 Print all restriction sites for enzyme Aat2 in the genome

query: print all restriction sites for enzyme Aat2 in the genome

```

----- 207 found -----
20222/20227      6          Aat2          (seq. rest. site)
86869/86874      6          Aat2          (seq. rest. site)
88454/88459      6          Aat2          (seq. rest. site)
109301/109306    6          Aat2          (seq. rest. site)
122553/122558    6          Aat2          (seq. rest. site)
127555/127560    6          Aat2          (seq. rest. site)
170755/170760    6          Aat2          (seq. rest. site)
171543/171548    6          Aat2          (seq. rest. site)
181157/181162    6          Aat2          (seq. rest. site)
197165/197170    6          Aat2          (seq. rest. site)
.
.
.

```

7 Investigating Regions on the Chromosome

7.1 Locate Gaps between Objects

7.1.1 Print the gap between kohara clone [101]9E4 and gene aceE

query: print the gap between kohara clone [101]9E4 and gene aceE

17254/123343 106090 (gap)

7.1.2 Print the gap between point 7272 and kohara clone [122]6F5

query: print the gap between point 7272 and kohara clone [122]6F5

7273/210469 203197 (gap)

7.1.3 Let GATC_Gaps be the gaps between the occurrences of the pattern GATC

query: let GATC_Gaps be the gaps between the occurrences of the pattern GATC

----- 6370 found -----

7.2 Compute Gap Length Statistics

7.2.1 Let GATC_GapsLength be the length of GATC_Gaps

query: let GATC_GapsLength be the length of GATC_Gaps

----- 6370 found -----

7.2.2 Print the mean of GATC_GapsLength

query: print the mean of GATC_GapsLength

--- 763.286 ---

7.2.3 Print the max of GATC_GapsLength

query: print the max of GATC_GapsLength

--- 101907 ---

7.2.4 Let RealGaps be GATC_Gaps that are sequenced

query: let RealGaps be GATC_Gaps that are sequenced

----- 6094 found -----

7.2.5 Let RealGapsLength be the length of RealGaps

query: let RealGapsLength be the length of RealGaps

----- 6094 found -----

7.2.6 Print the mean of RealGapsLength

query: print the mean of RealGapsLength

--- 213.602 ---

7.3 Specify Regions In Terms of Minutes or Kilobases

7.3.1 Let SpecialRegion be the region from 34 minutes to 48 minutes

query: let SpecialRegion be the region from 34 minutes to 48 minutes

----- 1 found -----

7.4 Let SpecialRegion be the region from oriC to oriC + 600 kb

query: let SpecialRegion be the region from oriC to oriC + 600 kb

----- 1 found -----

7.5 Specify Contiguous Pieces of Genome in Terms of Percent Sequenced

7.5.1 Let TinyPieces be (2 kb pieces of the genome) that are 76 percent sequenced

query: let TinyPieces be (2 kb pieces of the genome)
that are 76 percent sequenced

----- 494 found -----

8 Displaying Sequences of Objects on the Genome

8.1 Display Sequence of a Sequenced Object on the Chromosome

8.1.1 Print the sequence of kohara clone [147]2H5

query: print the sequence of kohara clone [147]2H5

```
446000/462911:      sequence
                   446000 .....
                   446050 .....
                   446100 .....
                   446150 .....
                   446200 .....
                   446250 .....
                   446300 .....
                   446350 .....
                   446400 .....
                   446450 .....
                   .
                   .
                   .
```

8.1.2 Print the sequence of gene lspA

query: print the sequence of gene lspA

```
25142/25636:      sequence
                25142 ATGAGTCAATCGATCTGTTCAACAGGGCTACGCTGGCTGTGGCTGGTGGT
                25192 AGTCGTGCTGATTATCGATCTGGGCAGCAAATACCTGATCCTCCAGAACT
                25242 TTGCTCTGGGGGATACGGTCCCGCTGTTCCCGTCGCTTAATCTGCATTAT
                25292 GCGCGTAACTATGGCGCGGCGTTTAGTTTCCTTGCCGATAGCGGCGGCTG
                25342 GCAGCGTTGGTTCTTTGCCGGTATTGCGATTGGTATTAGCGTGATCCTGG
                25392 CAGTGATGATGTATCGCTCGAAGGCCACGCAGAAGCTAAACAATATCGCT
                25442 TACGCGCTGATTATTGGCGGCGCGCTGGGCAACCTGTTTCGACCGCCTGTG
                25492 GCACGGCTTCGTTGTCGATATGATCGACTTCTACGTCGGCGACTGGCACT
                25542 TCGCCACCTTCAACCTTGCCGATACTGCCATCTGTGTGGTGCGGCACTG
                25592 ATTGTGCTGGAAGGTTTTTTGCCTTCTAGAGCGAAAAACAATAA
                   .
                   .
                   .
```

8.1.3 Print the sequence of the region from 20 to 89

query: print the sequence of the region from 20 to 89

```
20/89:           sequence
                20    AGCGCACAGACAGATAAAAAATTACAGAGTACACAACATCCATGAAACGCA
                70    TTAGCACCACCATTACCACC
```

8.2 Display Common Sequences of Given Length

8.2.1 Print all sequences of length at least 7 common to {gene aceE, gene entA, gene dnaK}

query: print all sequences of length at least 7 common
to {gene aceE, gene entA, gene dnaK}

```
----- 30 found -----
12283/12289:      sequence
                  12283      GGTAAAA
124547/124553:   sequence
                  124547      GGTAAAA
636886/636892:   sequence
                  636886      GGTAAAA

12304/12310:      sequence
                  12304      CTGGGTA
13474/13480:      sequence
                  .
                  .
                  .
```

8.2.2 Print all sequences of length at least 8 common to {gene aceE, gene apaG}

query: print all sequences of length at least 8 common
to {gene aceE, gene apaG}

```
----- 9 found -----
51680/51688:      sequence
                  51680      GAACGGCGA
125242/125250:   sequence
                  125242      GAACGGCGA

51708/51716:      sequence
                  51708      GATGCTGAA
124855/124863:   sequence
                  124855      GATGCTGAA

                  .
                  .
```

8.2.3 Print all sequences of length at least 8 common to {gene aceE, gene apaG} using both strands

query: print all sequences of length at least 8 common
to {gene aceE, gene apaG} using both strands

----- 27 found -----

```
51680/51688:      sequence
                  51680      GAACGGCGA
125242/125250:    sequence
                  125242      GAACGGCGA

51693/51700:      sequence
                  51693      GAATACGG
123583/123590:    sequence
                  123583      CCGTATTC
```

.
.
.

8.2.4 Print all sequences of length at least 7 common to {gene entA, gene aceA} within 0.8 to 1.2 turns apart

query: print all sequences of length at least 7 common
to {gene entA, gene aceA} within 0.8 to 1.2 turns apart

```
637269/637275:    sequence
                  637269      CGCCGCG
637280/637286:    sequence
                  637280      CGCCGCG
4247654/4247660:  sequence
                  4247654      CGCCGCG
```

8.2.5 Print all sequences of length at least 7 common to {gene entA, gene aceA} within 0.8 to 1.2 turns apart using both strands

query: print all sequences of length at least 7 common
to {gene entA, gene aceA} within 0.8 to 1.2 turns apart using both strands

----- 2 found -----

```
637269/637275:    sequence
                  637269      CGCCGCG
637280/637286:    sequence
                  637280      CGCCGCG
4247654/4247660:  sequence
                  4247654      CGCCGCG
4247132/4247138:  sequence
                  4247132      CGCGGCG

637545/637551:    sequence
```

.
.
.

8.2.6 Print last_val sorted by length

query: print last_val sorted by length

```
----- 2 found -----
637545/637551:      sequence
                   637545  CCTCGCC
637557/637563:      sequence
                   637557  CCTCGCC
4247604/4247610:    sequence
                   4247604 GGCGAGG

637269/637275:      sequence
                   637269  CGCCGCG
637280/637286:      sequence
                   .
                   .
                   .
```

8.3 Display the Proportion Sequenced of a Given Object

8.3.1 Let ClockGenes be all clockwise genes

query: let ClockGenes be all clockwise genes

```
----- 707 found -----
```

8.3.2 For each clockwise gene ClockGenes, {print ClockGenes; print proportion sequenced of ClockGenes }

query: for each clockwise gene ClockGenes,
 {print ClockGenes; print proportion sequenced of ClockGenes }

```
207/2669           2463      thrA      (gene)      clockwise
--- 1.0           ---
2671/3600           930      thrB      (gene)      clockwise
--- 1.0           ---
3601/4887           1287     thrC      (gene)      clockwise
--- 1.0           ---
12280/14196         1917     dnaK      (gene)      clockwise
--- 1.0           ---
14285/15415         1131     dnaJ      (gene)      clockwise
--- 1.0           ---
                   .
                   .
                   .
```

8.4 Display Alignment of Sequenced Objects

8.4.1 Align (the region from 1548642 to 1548670, the region from 1799611 to 1799636)

query: align (the region from 1548642 to 1548670,
the region from 1799611 to 1799636)

```
1      GCATTATCCTGATCAATCAGCACAATGC-----
1      -----ATGCCATTCTGACGGAATGGGCA

51      -
51      T
```

8.4.2 Align (the region from 0 to 100, the region from 200 to 300)

query: align (the region from 0 to 100, the region from 200 to 300)

Sorry, I can only align completely sequenced objects.
sorry, unable to answer that query

9 Locating Occurrences of Nucleotide Patterns

9.1 Locate Occurrences of Standard Nucleotide Patterns

9.1.1 Display Explicit Patterns or Their Complements

9.1.1.1 Print the occurrences of pattern GCATC in gene aceE

query: print the occurrences of pattern GCATC in gene aceE

```
----- 2 found -----
124182/124186:      sequence
                  124182      GCATC
125738/125742:      sequence
                  125738      GCATC
```

9.1.1.2 Print the occurrences of pattern GCATC' in gene aceE

query: print the occurrences of pattern GCATC' in gene aceE

```

----- 5 found -----
123892/123896:      sequence
                   123892  GATGC
124631/124635:      sequence
                   124631  GATGC
124855/124859:      sequence
                   124855  GATGC
125873/125877:      sequence
                   125873  GATGC
125972/125976:      sequence
                   125972  GATGC
                   .
                   .
                   .

```

9.1.1.3 Print the occurrences of pattern CCYGG in gene thrC

query: print the occurrences of pattern CCYGG in gene thrC

```

----- 2 found -----
3813/3817:          sequence
                   3813   CCTGG
3846/3850:          sequence
                   3846   CCCGG

```

9.1.1.4 Print the occurrences of pattern RYRYRYRY in gene aceE

query: print the occurrences of pattern RYRYRYRY in gene aceE

```

----- 11 found -----
123628/123635:      sequence
                   123628  GCGTGCGT
123699/123706:      sequence
                   123699  ATGTGTGC
123723/123730:      sequence
                   123723  GTGCACGC
123783/123790:      sequence
                   123783  GCGTGTAC
123785/123792:      sequence
                   123785  GTGTACGC
                   .
                   .
                   .

```


9.1.1.5 Print the occurrences of pattern RYNNRY in gene aceE

query: print the occurrences of pattern RYNNRY in gene aceE

```
----- 165 found -----
123368/123373:      sequence
                   123368      GTGGAT
123383/123388:      sequence
                   123383      ACTCGC
123390/123395:      sequence
                   123390      ACTGGC
123409/123414:      sequence
                   123409      ATCGGT
123416/123421:      sequence
                   123416      ATCCGT
                   .
                   .
                   .
```

9.1.1.6 Print the occurrences of pattern RYNNRY in gene aceE sorted by sequence

query: print the occurrences of pattern RYNNRY in gene aceE sorted by sequence

```
----- 165 found -----
124009/124014:      sequence
                   124009      ACAAAC
125484/125489:      sequence
                   125484      ACAAAC
124866/124871:      sequence
                   124866      ACAAGT
123506/123511:      sequence
                   123506      ACAGGT
125433/125438:      sequence
                   125433      ACATGC
                   .
                   .
                   .
```

9.1.2 Display Hairpin Loops of Any Size

9.1.2.1 Print the occurrence of pattern TAG 3...6 TAGT' in the genome

query: print the occurrence of pattern TAG 3...6 TAGT' in the genome

```

----- 34 found -----
22023/22034:      sequence
                  22023      TAG GCGC ACTA
266698/266709:   sequence
                  266698      TAG GCCCC ACTA
338352/338362:   sequence
                  338352      TAG TCCA ACTA
631137/631149:   sequence
                  631137      TAG CCTGGA ACTA
957859/957869:   sequence
                  957859      TAG ATGC ACTA
1214319/1214330: sequence
                  .
                  .
                  .

```

9.1.2.2 Print the occurrences of pattern $p1 = \text{RYRY } 3 \dots 8 \sim p1$ in gene dnaK

query: print the occurrences of pattern $p1 = \text{RYRY } 3 \dots 8 \sim p1$ in gene dnaK

```

----- 2 found -----
12353/12368:      sequence
                  12353      GCGT GCTGGAGA ACGC
13433/13445:      sequence
                  13433      ACGT AAAAG ACGT

```

9.1.2.3 Print the occurrences of pattern $p1 = 7 \dots 7 \ 3 \dots 6 \sim p1$ in the gap between kohara clone [101]9E4 and gene aceE

query: print the occurrences of pattern $p1 = 7 \dots 7 \ 3 \dots 6 \sim p1$
in the gap between kohara clone [101]9E4 and gene aceE

```

----- 28 found -----
18675/18694:      sequence
                  18675      GGGAGCC ATAAAC GGCTCCC
20992/21010:      sequence
                  20992      TACTTTC TTGAT GAAAGTA
24955/24971:      sequence
                  24955      CTGCTGA TGC TCAGCAG
27191/27210:      sequence
                  27191      TGCCGGT CTTGTT ACCGGCA
50299/50318:      sequence
                  50299      GGCATGG AAAACG CCATGCC
                  .
                  .
                  .

```

9.1.2.4 Print occurrences of the pattern $p1=4...6\ 3...6\ \neg p1$ in the region from 3400 kb to 3600 kb

query: print occurrences of the pattern $p1=4...6\ 3...6\ \neg p1$
in the region from 3400 kb to 3600 kb

```
----- 2153 found -----
3400749/3400762:      sequence
                    3400749  CGTC ATCAAC GACG
3400764/3400777:      sequence
                    3400764  CGAT CAGATC ATCG
3400834/3400847:      sequence
                    3400834  ACCG ATCTGG CGGT
3400881/3400894:      sequence
                    3400881  CATT CCAATT AATG
3401080/3401090:      sequence
                    3401080  TCGC TGG GCGA
                    .
                    .
                    .
```

9.1.2.5 Print the occurrences of pattern RYRYRY $p1=4...4\ 6...10\ \neg p1[1,0,0]$ contained in all translated clockwise genes

query: print the occurrences of pattern RYRYRY $p1=4...4\ 6...10\ \neg p1[1,0,0]$
contained in all translated clockwise genes

```
----- 1508 found -----
260/281:              sequence
                    260      GCGTGT TGCC GATATTCT GGAA
1558/1581:             sequence
                    1558      GCGTGC GCGT TACTCATCAG ATGC
1688/1707:             sequence
                    1688      ACATAT CGAC TTACGT GTCT
2639/2662:             sequence
                    2639      ACGTAC CCTC TCATGGAAGT TAGG
3498/3520:             sequence
                    3498      GCGCGT TGCC GACTGGTTG GGTA
                    .
                    .
                    .
```

9.1.2.6 Print the occurrences of pattern RYRYRY p1=4...4 6...10 ~p1[1,1,1] contained in all clockwise genes in the region from 20 minutes to 40 minutes

query: print the occurrences of pattern RYRYRY p1=4...4 6...10 ~p1[1,1,1]
 contained in all clockwise genes
 in the region from 20 minutes to 40 minutes

```
----- 2858 found -----
947424/947444:      sequence
                   947424  GCACGC CGGG GCTTTAA GCTG
947424/947445:      sequence
                   947424  GCACGC CGGG GCTTTAAG CTGG
947556/947578:      sequence
                   947556  GCGCGC GGGG AAGATATCG AGCC
947556/947579:      sequence
                   947556  GCGCGC GGGG AAGATATCGA GCCT
947802/947825:      sequence
                   947802  ATGCAC TCTG GCCTCGACTT TGCA
                   .
                   .
                   .
```

9.1.2.7 {Let LargeHairpins be the occurrences of pattern p1=10...10 3...8 ~p1 in the region from 200 kb to 550 kb; print the second punit of LargeHairpins}

query: {let LargeHairpins be the occurrences of pattern p1=10...10 3...8 ~p1
 in the region from 200 kb to 550 kb;
 print the second punit of LargeHairpins}

```
----- 10 found -----
----- 10 found -----
244078/244083:      sequence
                   244078  CCCAAT
366950/366955:      sequence
                   366950  TGCTTA
366951/366954:      sequence
                   366951  GCTT
372783/372790:      sequence
                   372783  CGCTTCTG
372784/372789:      sequence
                   .
                   .
                   .
```

9.1.2.8 Print the occurrences of pattern `p1=RYYRRY 2...8 ~p1` in the region from 1500 kb to 2500 kb

query: print the occurrences of pattern `p1=RYYRRY 2...8 ~p1`
in the region from 1500 kb to 2500 kb

```
----- 12 found -----
1551760/1551779:      sequence
                     1551760  GTTGAC CGAGCAGG GTCAAC
1657772/1657787:      sequence
                     1657772  GTTAGT CATA ACTAAC
1659444/1659457:      sequence
                     1659444  GTTAAC TG GTTAAC
1807784/1807800:      sequence
                     1807784  ACCAGC GGCAA GCTGGT
1832255/1832272:      sequence
                     1832255  ACCGGC GCAATG GCCGGT
                     .
                     .
                     .
```

9.1.2.9 Print `last_val` sorted by sequence

query: print `last_val` sorted by sequence

```
----- 12 found -----
2205683/2205697:      sequence
                     2205683  ACCAAT TGA ATTGGT
1807784/1807800:      sequence
                     1807784  ACCAGC GGCAA GCTGGT
1832255/1832272:      sequence
                     1832255  ACCGGC GCAATG GCCGGT
2354632/2354651:      sequence
                     2354632  ATCAGC CCTTCAAT GCTGAT
1864547/1864562:      sequence
                     1864547  GCCAGT CAGG ACTGGC
                     .
                     .
                     .
```

9.1.2.10 Print `last_val` sorted by length

query: print `last_val` sorted by length

```

----- 12 found -----
1659444/1659457:      sequence
                      1659444  GTTAAC TG GTTAAC
2205683/2205697:      sequence
                      2205683  ACCAAT TGA ATTGGT
2000570/2000584:      sequence
                      2000570  GCCGAT GAT ATCGGC
1864547/1864562:      sequence
                      1864547  GCCAGT CAGG ACTGGC
2331164/2331179:      sequence
                      2331164  GTCAGT CCA  ACTGAC
                      .
                      .
                      .

```

9.1.2.11 Print the 1st punit of last_val sorted by sequence

query: print the 1st punit of last_val sorted by sequence

```

----- 12 found -----
2205683/2205688:      sequence
                      2205683  ACCAAT
1807784/1807789:      sequence
                      1807784  ACCAGC
1832255/1832260:      sequence
                      1832255  ACCGGC
2354632/2354637:      sequence
                      2354632  ATCAGC
1864547/1864552:      sequence
                      1864547  GCCAGT
                      .
                      .
                      .

```

9.1.2.12 Print the occurrences of pattern p1=RYYRRY 2...8 ~p1 in the region from 1500 kb to 2500 kb

query: print the occurrences of pattern p1=RYYRRY 2...8 ~p1
in the region from 1500 kb to 2500 kb

```

----- 12 found -----
1551760/1551779:      sequence
                      1551760  GTTGAC CGAGCAGG GTCAAC
1657772/1657787:      sequence

```

```

          1657772  GTTAGT CATA ACTAAC
1659444/1659457:  sequence
          1659444  GTTAAC TG GTTAAC
1807784/1807800:  sequence
          1807784  ACCAGC GGCAA GCTGGT
1832255/1832272:  sequence
          1832255  ACCGGC GCAATG GCCGGT
          .
          .
          .

```

9.1.2.13 Print the 3rd punit of last_val sorted by length

query: print the 3rd punit of last_val sorted by length

```

----- 12 found -----
1657782/1657786:  sequence
          1657782  ACTAA
2331174/2331178:  sequence
          2331174  ACTGA
1864557/1864561:  sequence
          1864557  ACTGG
2000579/2000583:  sequence
          2000579  ATCGG
2205692/2205696:  sequence
          2205692  ATTGG
          .
          .
          .

```

9.1.2.14 Print the occurrences of pattern p1=RYYRRY 2...8 ~p1 in the region from 1500 kb to 2500 kb sorted by length

query: print the occurrences of pattern p1=RYYRRY 2...8 ~p1
in the region from 1500 kb to 2500 kb sorted by length

```

----- 12 found -----
1659444/1659457:  sequence
          1659444  GTTAAC TG GTTAAC
2205683/2205697:  sequence
          2205683  ACCAAT TGA ATTGGT
2000570/2000584:  sequence
          2000570  GCCGAT GAT ATCGGC
1864547/1864562:  sequence
          1864547  GCCAGT CAGG ACTGGC
2331164/2331179:  sequence

```

2331164 GTCAGT CCCA ACTGAC

.
. .
.

9.1.2.15 Print the occurrences of pattern $p1=RYYRRY\ 2\dots 8$ $\sim p1$ in the region from 1500 kb to 2500 kb sorted by length

query: print the occurrences of pattern $p1=RYYRRY\ 2\dots 8$ $\sim p1$ in the region from 1500 kb to 2500 kb sorted by length

----- 12 found -----
1659444/1659457: sequence
1659444 GTTAAC TG GTTAAC
2205683/2205697: sequence
2205683 ACCAAT TGA ATTGGT
2000570/2000584: sequence
2000570 GCCGAT GAT ATCGGC
1864547/1864562: sequence
1864547 GCCAGT CAGG ACTGGC
2331164/2331179: sequence
2331164 GTCAGT CCCA ACTGAC
. . .

9.1.3 Display Embedded Hairpin Loops

9.1.3.1 Print the occurrences of pattern $p1=RYRYY\ 2\dots 4$ $p2=4\dots 6\ 3\dots 4$ $\sim p2\ 2\dots 3$ $\sim p1$ in all sequence fragments

query: print the occurrences of pattern $p1=RYRYY\ 2\dots 4$ $p2=4\dots 6\ 3\dots 4$ $\sim p2\ 2\dots 3$ $\sim p1$ in all sequence fragments

----- 16 found -----
203790/203816: sequence
203790 ATGTT TGG CAAA TTG TTTG GTA AACAT
683941/683965: sequence
683941 GCGCT TT CTGA TTT TCAG TC AGCGC
1548642/1548670: sequence
1548642 GCATT TATC CTGA TCAA TCAG CAC AATGC
1799611/1799636: sequence
1799611 ATGCC CA TTCC TGAC GGAA TG GGCAT
2368955/2368982: sequence
2368955 ACATT AT TAAAT AAG ATTTA CAA AATGT
. . .

9.1.3.2 Print the occurrences of pattern p1=RYRYY 2...4 p2=4...6 3...4 ~p2 2...3 ~p1 in the region from 30 minutes to 40 minutes

query: print the occurrences of pattern p1=RYRYY 2...4 p2=4...6 3...4 ~p2 2...3 ~p1 in the region from 30 minutes to 40 minutes

```
----- 2 found -----
1548642/1548670:      sequence
                   1548642  GCATT TATC CTGA TCAA TCAG CAC AATGC
1799611/1799636:      sequence
                   1799611  ATGCC CA TTCC TGAC GGAA TG GGCAT
```

9.1.3.3 Print the occurrences of pattern p1=RYRYY 2...4 p2=4...6 3...4 ~p2 2...3 ~p1 in the region from 1500 kb to 2500 kb sorted by length

query: print the occurrences of pattern p1=RYRYY 2...4 p2=4...6 3...4 ~p2 2...3 ~p1 in the region from 1500 kb to 2500 kb sorted by length

```
----- 3 found -----
1799611/1799636:      sequence
                   1799611  ATGCC CA TTCC TGAC GGAA TG GGCAT
2368955/2368982:      sequence
                   2368955  ACATT AT TAAAT AAG ATTTA CAA AATGT
1548642/1548670:      sequence
                   1548642  GCATT TATC CTGA TCAA TCAG CAC AATGC
```

9.1.3.4 Print last_val sorted by sequence

query: print last_val sorted by sequence

```
----- 3 found -----
2368955/2368982:      sequence
                   2368955  ACATT AT TAAAT AAG ATTTA CAA AATGT
1799611/1799636:      sequence
                   1799611  ATGCC CA TTCC TGAC GGAA TG GGCAT
1548642/1548670:      sequence
                   1548642  GCATT TATC CTGA TCAA TCAG CAC AATGC
```

9.1.3.5 Print the 1st punit of last_val sorted by sequence

query: print the 1st punit of last_val sorted by sequence

```
----- 3 found -----
2368955/2368959:      sequence
                   2368955  ACATT
1799611/1799615:      sequence
                   1799611  ATGCC
1548642/1548646:      sequence
                   1548642  GCATT
```

9.1.3.6 Print the occurrences of pattern p1=RYRYY 2...4 p2=4...6 3...4 ~p2 2...3 ~p1 in the region from 1500 kb to 2500 kb sorted by length

query: print the occurrences of pattern p1=RYRYY 2...4 p2=4...6 3...4 ~p2 2...3 ~p1 in the region from 1500 kb to 2500 kb sorted by length

```
----- 3 found -----
1799611/1799636:      sequence
                   1799611  ATGCC CA TTCC TGAC GGAA TG GGCAT
2368955/2368982:      sequence
                   2368955  ACATT AT TAAAT AAG ATTTA CAA AATGT
1548642/1548670:      sequence
                   1548642  GCATT TATC CTGA TCAA TCAG CAC AATGC
```

9.1.3.7 Print the 3rd punit of last_val sorted by sequence

query: print the 3rd punit of last_val sorted by sequence

```
----- 3 found -----
1548651/1548654:      sequence
                   1548651  CTGA
2368962/2368966:      sequence
                   2368962  TAAAT
1799618/1799621:      sequence
                   1799618  TTCC
```

9.2 Display Overlapping Patterns

9.2.1 Print all occurrences of pattern $p1=2...2 \ 2...2 \ \sim p1$ that overlap with occurrences of pattern ATTGTTA in the region from 4500 kb to 4700 kb

query: print all occurrences of pattern $p1=2...2 \ 2...2 \ \sim p1$
that overlap with occurrences of pattern ATTGTTA
in the region from 4500 kb to 4700 kb

```
----- 5 found -----
4544446/4544451:      sequence
                     4544446  AA AG TT
4572386/4572391:      sequence
                     4572386  AT CT AT
4608785/4608790:      sequence
                     4608785  AA GA TT
4617703/4617708:      sequence
                     4617703  AT TA AT
4698573/4698578:      sequence
                     4698573  TT AG AA
                     .
                     .
                     .
```

9.3 Display Occurrences of Nucleotide Patterns in Multiple Objects

9.3.1 For each clockwise gene Gene, {print Gene; print the occurrences of pattern GATC in Gene}

query: for each clockwise gene Gene,
{print Gene; print the occurrences of pattern GATC in Gene}

```
207/2669      2463      thrA      (gene)      clockwise
----- 13 found -----
489/492:      sequence
               489      GATC
596/599:      sequence
               596      GATC
651/654:      sequence
               651      GATC
750/753:      sequence
               750      GATC
1037/1040:    sequence
               .
               .
               .
```

9.3.2 For (each translated counterclockwise gene in the region from 2400 kb to 2500 kb) Gene, {print Gene; print the occurrences of pattern $p1=6...6 \ 10...16 \ \sim p1[1,0,0]$ in Gene}

query: for (each translated counterclockwise gene

```

    in the region from 2400 kb to 2500 kb) Gene,
    {print Gene;
    print the occurrences of pattern p1=6...6 10...16 ~p1[1,0,0] in Gene}

```

```

2448124/2448693      570      ubiX      (gene)      counterclockwise
----- 20 found -----
2448210/2448237:      sequence
      2448210      CATCAT CAAGGGATTGCGGGCG ATGATA
2448211/2448236:      sequence
      2448211      ATCATC AAGGGATTGCGGGC GATGAT
2448212/2448235:      sequence
      2448212      TCATCA AGGGATTGCGGG CGATGA
2448212/2448238:      sequence
      2448212      TCATCA AGGGATTGCGGGCGA TGATAA
2448223/2448248:      sequence
      .
      .
      .

```

9.3.3 For (each translated counterclockwise gene in the region from 2400 kb to 2500 kb) Gene, collect the occurrences of pattern $p1=6...6\ 10...16\ \sim p1[1,0,0]$ in Gene into SpecialLoops

```

query: for (each translated counterclockwise gene
      in the region from 2400 kb to 2500 kb) Gene,
      collect the occurrences of pattern p1=6...6 10...16 ~p1[1,0,0]
      in Gene into SpecialLoops

```

```

----- 424 found -----

```

9.3.4 For each (gene that contains a member of last_val) Gene, {Print Gene; print the members of last_val contained in Gene}

```

query: for each (gene that contains a member of last_val) Gene,
      {print Gene; print the members of last_val contained in Gene}

```

```

2452799/2453458      660      dedA      (gene)      counterclockwise
2452799/2453458      660      dedA      (gene)      counterclockwise

```

9.3.5 let GATCGATC_Occs be the occurrences of pattern GATCGATC

```

query: let GATCGATC_Occs be the occurrences of pattern GATCGATC

```

```

----- 21 found -----

```

9.3.6 for each (gene that contains a member of GATCGATC_Occs) Gene, {print Gene;
print the members of GATCGATC_Occs contained in Gene}

query: for each (gene that contains a member of GATCGATC_Occs) Gene,
{print Gene; print the members of GATCGATC_Occs contained in Gene}

90050/91090	1041	orf	(gene)	clockwise
90307/90314:		sequence		
	90307	GATCGATC		
98459/99703	1245	ftsW	(gene)	clockwise
98872/98879:		sequence		
	98872	GATCGATC		
677007/678908	1902	mrda	(gene)	counterclockwise
677702/677709:		sequence		
	677702	GATCGATC		
762290/763573	1284	gltA	(gene)	counterclockwise
763348/763355:		sequence		

.
.
.

9.3.7 {let GATCGATC_Occs be the occurrences of pattern GATCGATC; for each
(gene that contains a member of GATCGATC_Occs) Gene, {print Gene; print
the members of GATCGATC_Occs contained in Gene}}

query: {let GATCGATC_Occs be the occurrences of pattern GATCGATC;
for each (gene that contains a member of GATCGATC_Occs) Gene,
{print Gene; print the members of GATCGATC_Occs contained in Gene}}

----- 21 found -----

90050/91090	1041	orf	(gene)	clockwise
90307/90314:		sequence		
	90307	GATCGATC		
98459/99703	1245	ftsW	(gene)	clockwise
98872/98879:		sequence		
	98872	GATCGATC		
677007/678908	1902	mrda	(gene)	counterclockwise
677702/677709:		sequence		
	677702	GATCGATC		
762290/763573	1284	gltA	(gene)	counterclockwise

.
.
.

10 Locating Closest Occurrences of One Nucleotide Pattern to Another

10.1 Let DAM_Occs be the occurrences of pattern GATC in SpecialRegion

query: let DAM_Occs be the occurrences of pattern GATC in SpecialRegion

----- 1074 found -----

10.2 Print all DAM_Occs

query: print all DAM_Occs

----- 1074 found -----

3953061/3953064:	sequence
3953061	GATC
3953082/3953085:	sequence
3953082	GATC
3953098/3953101:	sequence
3953098	GATC
3953113/3953116:	sequence
3953113	GATC
3953126/3953129:	sequence
3953126	GATC
.	
.	
.	

10.3 Let SelectedGenes be translated clockwise genes

query: let SelectedGenes be translated clockwise genes

----- 372 found -----

10.4 Print closest occurrences of pattern GATC in SelectedGenes to occurrences of pattern TAG in SelectedGenes

query: print closest occurrences of pattern GATC in SelectedGenes
to occurrences of pattern TAG in SelectedGenes

----- 1706 found -----

489/492:	sequence
489	GATC

```

596/599:          sequence
                596      GATC
651/654:          sequence
                651      GATC
750/753:          sequence
                750      GATC
1037/1040:        sequence
                1037     GATC
                .
                .
                .

```

10.5 Print pairs of occurrences of pattern GATC in SelectedGenes and their closest neighboring occurrences of pattern TAG in SelectedGenes

query: print pairs of occurrences of pattern GATC in SelectedGenes
and their closest neighboring occurrences of pattern TAG in SelectedGenes

```

----- 1706 found -----
--- pair: distance 41 ---
489/492:          sequence
                489      GATC
530/532:          sequence
                530      TAG

--- pair: distance 23 ---
596/599:          sequence
                596      GATC
619/621:          sequence
                .
                .
                .

```

10.6 Let TATA_Boxes be occurrences of pattern TATAA

query: let TATA_Boxes be occurrences of pattern TATAA

```

----- 794 found -----

```

10.7 Print the pairs of TATA_Boxes and their closest neighboring genes

query: print the pairs of TATA_Boxes and their closest neighboring genes

```

----- 392 found -----
--- pair: distance 82 ---

```

```

14203/14207:          sequence
                  14203      TATAA
14285/15415          1131          dnaJ          (gene)          clockwise

---          pair: distance 354          ---
14285/15415          1131          dnaJ          (gene)          clockwise
14639/14643:          sequence
                  14639      TATAA

.
.
.

```

10.8 Print the pairs of TATA_Boxes and their closest neighboring counterclockwise translated genes

query: print the pairs of TATA_Boxes
and their closest neighboring counterclockwise translated genes

```

----- 154 found -----
---          pair: distance 96          ---
51947/51951:          sequence
                  51947      TATAA
52043/52864          822          ksgA          (gene)          counterclockwise

---          pair: distance 1068          ---
65121/65125:          sequence
                  65121      TATAA
66189/66884          696          araD          (gene)          counterclockwise

.
.
.

```

10.9 Print the pairs of TATA_Boxes and their closest neighboring counterclockwise translated genes sorted by distance

query: print the pairs of TATA_Boxes
and their closest neighboring counterclockwise translated genes
sorted by distance

```

----- 154 found -----
---          pair: distance 11          ---
1322911/1322915:          sequence
                  1322911      TATAA
1322922/1323428          507          orf          (gene)          counterclockwise

---          pair: distance 12          ---
711799/711803:          sequence
                  711799      TATAA

```


711811/713031 1221 nagC (gene) counterclockwise

.
.
.

11 Locating Amino Acid Patterns In Translated Genes

11.1 Standard Patterns or Prefixes

11.1.1 Print occurrences of amino acid pattern C (??? | ???) C in translated genes

query: print occurrences of amino acid pattern C (??? | ???) C
in translated genes

```
----- 106 found -----
2069825/2069842      18      amn      (expressed) clockwise
                     C YIGH C
1998522/1998539      18      araH      (expressed) counterclockwise
                     C GMLF C
3538241/3538258      18      aroB      (expressed) counterclockwise
                     C IRR C
3538244/3538258      15      aroB      (expressed) counterclockwise
                     C IRR C
1799404/1799418      15      aroH      (expressed) clockwise
                     C EDI C
```

.
.
.

11.2 Zinc Fingers

11.2.1 Print occurrences of amino acid pattern C (??? | ???)

C ????????? (? | (?? | (??? | ???)))

H (??? | ???) H in translated genes

query: print occurrences of amino acid pattern
C (??? | ???)
C ????????? (? | (?? | (??? | ???)))
H (??? | ???) H
in translated genes

----- 0 found -----

12 Assessing the Distribution of Objects

12.1 Count the Occurrences of Objects on the Chromosome

12.1.1 Count the occurrences of pattern TGGATGGA in 20-minute pieces of the genome

query: count the occurrences of pattern TGGATGGA
in 20 minute pieces of the genome

0/934519	934520	6	(count)
934520/1869039	934520	1	(count)
1869040/2803559	934520	2	(count)
2803560/3738079	934520	5	(count)
3738080/4672599	934520	3	(count)

12.1.2 Count the occurrences of pattern GATC in 10-minute pieces of the genome starting at oriC

query: count the occurrences of pattern GATC
in 10 minute pieces of the genome starting at oriC

214981/682240	467260	471	(count)
682241/1149500	467260	549	(count)
1149501/1616760	467260	343	(count)
1616761/2084020	467260	396	(count)
2084021/2551280	467260	363	(count)
2551281/3018540	467260	443	(count)
3018541/3485800	467260	601	(count)
3485801/3953060	467260	711	(count)
3953061/4420320	467260	968	(count)
4420321/214980	467260	697	(count)

.
.
.

12.1.3 Count all restriction fragments for enzymes {Aat2, EcoR1} in 10 equal partitions of the genome

query: count all restriction fragments for enzymes {Aat2, EcoR1}
in 10 equal partitions of the genome

0/467259	467260	65	(count)
467260/934519	467260	36	(count)
934520/1401779	467260	39	(count)
1401780/1869039	467260	21	(count)

1869040/2336299	467260	23	(count)
2336300/2803559	467260	40	(count)
2803560/3270819	467260	31	(count)
3270820/3738079	467260	57	(count)
3738080/4205339	467260	77	(count)
4205340/4672599	467260	66	(count)

.

.

.

12.1.4 Count the translated counterclockwise genes in (10 equal partitions of the genome starting at oriC)

query: count the translated counterclockwise genes in
(10 equal partitions of the genome starting at oriC)

214981/682240	467260	19	(count)
682241/1149500	467260	21	(count)
1149501/1616760	467260	19	(count)
1616761/2084020	467260	34	(count)
2084021/2551280	467260	18	(count)
2551281/3018540	467260	23	(count)
3018541/3485800	467260	50	(count)
3485801/3953060	467260	76	(count)
3953061/4420320	467260	31	(count)
4420321/214980	467260	28	(count)

12.1.5 Count the genes in 10 equal partitions of the genome

query: count the genes in 10 equal partitions of the genome

0/467259	467260	137	(count)
467260/934519	467260	103	(count)
934520/1401779	467260	89	(count)
1401780/1869039	467260	47	(count)
1869040/2336299	467260	64	(count)
2336300/2803559	467260	73	(count)
2803560/3270819	467260	91	(count)
3270820/3738079	467260	119	(count)
3738080/4205339	467260	161	(count)
4205340/4672599	467260	122	(count)

12.1.6 Count the translated genes in 100 kb pieces of the genome

query: count the translated genes in 100 kb pieces of the genome

0/999999	100000	37	(count)
100000/199999	100000	27	(count)
200000/299999	100000	14	(count)
300000/399999	100000	7	(count)
400000/499999	100000	19	(count)
500000/599999	100000	16	(count)
600000/699999	100000	14	(count)
700000/799999	100000	32	(count)
800000/899999	100000	8	(count)
900000/999999	100000	14	(count)
1000000/1099999	100000	13	(count)

.
.
.

12.1.7 Count the clockwise translated genes in 10 equal partitions of the genome
 query: count the clockwise translated genes in 10 equal partitions of the genome

0/467259	467260	83	(count)
467260/934519	467260	47	(count)
934520/1401779	467260	41	(count)
1401780/1869039	467260	15	(count)
1869040/2336299	467260	21	(count)
2336300/2803559	467260	12	(count)
2803560/3270819	467260	31	(count)
3270820/3738079	467260	19	(count)
3738080/4205339	467260	54	(count)
4205340/4672599	467260	47	(count)

.
.
.

12.2 Compute the Adjusted Counts of Objects

12.2.1 Print the adjusted counts of genes in 10 equal partitions of the genome
 query: print the adjusted counts of genes in 10 equal partitions of the genome

```
----- 10 found -----
--- 358.891 ---
--- 403.344 ---
--- 371.146 ---
--- 349.228 ---
--- 417.943 ---
--- 363.871 ---
--- 349.815 ---
--- 380.601 ---
--- 383.082 ---
--- 357.739 ---
```

.
.
.

12.2.2 Print the adjusted counts of translated counterclockwise genes in (10 equal partitions of the genome starting at oriC)

query: print the adjusted counts of translated counterclockwise genes in
(10 equal partitions of the genome starting at oriC)

```
----- 10 found -----  
--- 76.9559 ---  
--- 81.998 ---  
--- 113.418 ---  
--- 170.588 ---  
--- 109.91 ---  
--- 96.4954 ---  
--- 188.821 ---  
--- 229.787 ---  
--- 64.6265 ---  
--- 79.509 ---  
.  
.  
.
```

12.2.3 Print the adjusted counts of occurrences of pattern CCYGG in 4 equal partitions of the genome starting at oriC

query: print the adjusted counts of occurrences of pattern CCYGG in
4 equal partitions of the genome starting at oriC

```
----- 4 found -----  
--- 2633.41 ---  
--- 2815.19 ---  
--- 2577.84 ---  
--- 2875.09 ---
```

13 Defining New Concepts

13.1 Defining a Region of Interest

13.1.1 "Define Interesting to be the region from 87 minutes to 88 minutes"

query: define macro Interesting the region from 87 minutes to 88 minutes

Macro Interesting defined.

13.1.2 "Verify the location of region Interesting"

query: print Interesting

4058461/4112819 54359 (region)

13.1.3 "Find out about genes in region Interesting"

query: tell me about genes in Interesting

```
----- 20 found -----
4059464/4061404      1941      pepQ      (gene)      clockwise
4060929/Bach.(87.1)      chlB      (gene)      unknown
nitrate reductase;biosynthesis of molybdopterin
4061502/4062707      1206      orf      (gene)      clockwise
4062693/Bach.(87.1)      hemG      (gene)      unknown
Protoporphyrinogen oxidase activity
4063828/4065369      1542      rrsA      (gene)      clockwise
16S rRNA gene of rrnA operon
4064456/Bach.(87.2)      fcsA      (gene)      unknown
Cell division;septation
4064527/Bach.(87.2)      rrnA      (gene)      unknown
rRNA operon
4065438/4065514      77      ileT      (gene)      clockwise
isoleucine tRNA 1; in rrnA operon
.
.
.
```

13.2 Defining a Name for a Pattern

13.2.1 "Define HairpinLoop to be the name of a particular type of hairpin loop"

query: define macro HairpinLoop p1=6...8 3...20 ~p1

Macro HairpinLoop defined.

13.2.2 "Locate all occurrences of hairpin loops of desired type in region Interesting, ordered by location"

query: print all occurrences of pattern HairpinLoop in Interesting

```
----- 218 found -----
4058491/4058517:      sequence
4058491      CCGCAG CTTCAATGGTTTTTA CTGCGG
4058556/4058575:      sequence
4058556      ACCATC CCTTTAGC GATGGT
4058575/4058594:      sequence
4058575      TGAAGC TCATGGTG GCTTCA
4058943/4058961:      sequence
```

```

4058943 CCATTG ACGGCAG CAATGG
4059026/4059049: sequence
4059026 CTGTTC TTCAGGAACGAG GAACAG
4059060/4059078: sequence
4059060 TCGGTG ATATCAG CACCGA
4059086/4059114: sequence
4059086 GGCTGC TTGTTCGAACGCAGCA GCAGCC
4059086/4059114: sequence
4059086 GGCTGCT TTGTTCGAACGCAGC AGCAGCC
4059087/4059110: sequence
4059087 GCTGCT TTGTTCGAACGC AGCAGC
4059087/4059113: sequence
4059087 GCTGCT TTGTTCGAACGCAGC AGCAGC
4059300/4059316: sequence
4059300 ATCTGG TCGTA CCAGAT
4059300/4059316: sequence
4059300 ATCTGGT CGT ACCAGAT
.
.
.

```

13.3 Defining a New Concept in Terms of an Existing Object

13.3.1 "Define Upstream to be the region 100 base pairs upstream of an existing object"

```

query: define macro Upstream(G) the region from the start of G - 100
      to the start of G - 1

```

Macro Upstream defined.

13.3.2 "Define Initial to be the first 80 base pairs in an existing object"

```

query: define macro Initial(G) the region from the start of G
      to the start of G + 80

```

Macro Initial defined.

13.3.3 "Use the new concepts Upstream and Initial to investigate each clockwise gene X in region Interesting"

```

query: for each clockwise gene in Interesting X, {print X;
      print all sequences of length at least 5 common to {Upstream(X),
      Upstream(X), Initial(X)} using both strands}

```

```

4059464/4061404      1941      pepQ      (gene)      clockwise

```

```

----- 3 found -----

```

```

4059380/4059384:      sequence
4059380      ATCAC
4059396/4059400:      sequence
4059396      ATCAC
4059469/4059473:      sequence

```

4059469	ATCAC			
4059384/4059388:	sequence			
4059384	CGCTC			
4059400/4059404:	sequence			
4059400	CGCTC			
4059480/4059484:	sequence			
4059480	CGCTC			
4059443/4059447:	sequence			
4059443	AAAAA			
4059444/4059448:	sequence			
4059444	AAAAA			
4059445/4059449:	sequence			
4059445	AAAAA			
4059459/4059463:	sequence			
4059459	AAAAA			
4059488/4059492:	sequence			
4059488	AAAAA			
4061502/4062707	1206	orf	(gene)	clockwise
4061440/4061444:	sequence			
4061440	AGATG			
4061483/4061487:	sequence			
4061483	CATCT			
4061528/4061532:	sequence			
4061528	CATCT			
	.			
	.			
	.			

END

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