

DNA Motifs and Genomic Colocation

Identify a specific DNA motif and collocate this motif with genes:

For this exercise use <http://microsporidiadb.org>

- a. Find all *Bam*HI restriction sites in all microsporidia genomic sequences available in MicrosporidiaDB. The DNA motif search can be used to find simple DNA motifs or complex motifs like transcription factor binding sites using regular expressions. A DNA restriction site can be defined by a DNA motif. For example the *Bam*H1 restriction site is GGATCC.

The screenshot shows the MicrosporidiaDB search interface. On the left, a sidebar titled "Identify Other Data Types:" contains a list of data types: Isolates, Genomic Sequences, Genomic Segments (DNA Motif), DNA Motif Pattern, and Genomic Location. A red arrow points from the "Genomic Segments (DNA Motif)" option to the main search area. The main search area is titled "Identify Genomic Segments based on DNA Motif Pattern". It features an "Organism" section with a list of organisms and checkboxes: Anncalia, Edhazardia, Encephalitozoon, Enterocytozoon, Hamiltosporidium, Mitosporidium, Nematocida, Nosema, Ordozpora, Spraguea, Trachipleistophora, Vavraia, and Vittiforma. Below the organism list is a "Pattern" input field containing "GGATCC". At the bottom, there is an "Advanced Parameters" section and a "Get Answer" button.

- How many times does the *Bam*HI site occur in the genomes you searched? Take a look at your results. Notice the Genomic location and the Motif columns.

- b. Find genes that have one of these *Bam*HI sites within 500 nucleotides upstream of their start.

In 4a you found *Bam*HI sites anywhere in the genome. Now you are looking for genes that have one of these sites located within 500 nucleotides upstream of their start.

Hint: You can achieve this by running a genomic collocation search that defines the genomic relationship between the *Bam*HI sites and genes. Add a "Genes by Organism" step to the motif search and select the "1 relative to 2, using genomic locations" option.

DNA Motif
30994 Segments

Add Step

1

Step 1

Run a new Search for
Add contents of Basket
Add existing Strategy
Filter by Weight

Genes
Genomic Segments
ORFs

Text, IDs, Organism
Genomic Position
Gene Attributes
Protein Attributes
Protein Features
Similarity/Pattern
Transcript Expression
Cellular Location

Product name, notes, etc.)
Gene ID(s)
Organism
User Comments

2

Add Step 2 : Organism

Organism

- Anncalia
- Edhazardia
- Encephalitozoon
- Enterocytozoon
- Mitosporidium
- Nematocida
- Nosema
- Ordospora
- Spraguea
- Trachipleistophora
- Vavraia
- Vittiforma

Advanced Parameters

Combine Genomic Segments in Step 1 with Genes in Step 2:

1 Intersect 2 1 Minus 2
 1 Union 2 2 Minus 1
 1 Relative to 2, using genomic colocation

3

4

Add Step

Genomic Colocation ?

Combine Step 1 and Step 2 using relative locations in the genome

You had **30994 Genomic Segments** in your Strategy (Step 1). Your new **Genes** search (Step 2) returned **67093 Genes**.

"Return each Gene from Step 2 whose **upstream region** overlaps the **exact region** of a Genomic Segment in Step 1 and is on either strand"

(67093 Genes in Step)

Region
Gene

Exact
 Upstream: 500 bp
 Downstream: 1000 bp

Custom:
 begin at: start - 500 bp
 end at: start - 1 bp

(30994 Genomic Segments in Step)

Region
Genomic Segment

Exact
 Upstream: 1000 bp
 Downstream: 1000 bp

Custom:
 begin at: start + 0 bp
 end at: stop + 0 bp

- How did you modify the location relative to genes? How many genes did you get?

"Return each Gene from Step 2 whose upstream region overlaps"

(67093 Genes in Step)

Region

Gene

Upstream: 500 bp

Downstream: 1000 bp

Custom:

begin at: start - 500 bp

end at: start - 1 bp

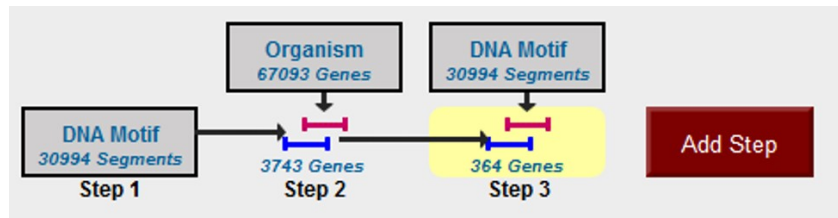
Organism 67093 Genes

DNA Motif 30994 Segments Step 1

3743 Genes Step 2

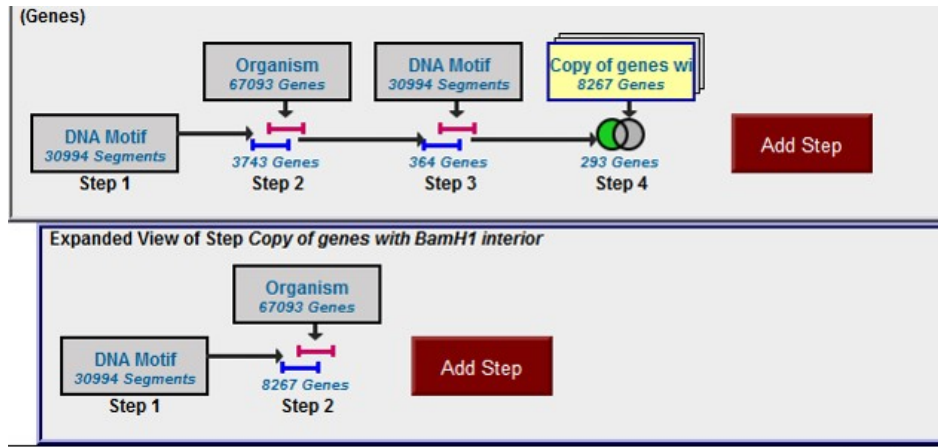
Add Step

- c. Using a similar sequence of steps as in 4b, define which of these genes also have a *Bam*HI site in their 500 nucleotide downstream region.
Hint: add a search for the BamHI site and collocate that with the genes that have a BamHI site upstream of their start sites.



Step 1 = BamHI anywhere in genome
 Step 2 = all genes
 2 (1+2) = genes with BamHI 1000bp upstream
 Step 3 = BamHI anywhere in genome
 3 (2+3) = genes from 2 with BamHI 1000bp downstream

- d. Taking this a step further, define which of these genes do NOT contain a *Bam*HI site within them. You will have to use a nested strategy.



- Look at your results. Do they make sense? Confirm your results by looking at one of the genes in Gbrowse and showing *Bam*HI restriction sites.

Note: you can add a column to any result table that allows you to go directly to GBrowse at the genomic coordinates of any ID in your result list. Click on the Add Columns button.

The screenshot shows a bioinformatics tool interface. At the top, it says '263 Genes from Step 4' and 'Strategy: DNA Motif'. Below this is a table with columns for 'All Results', 'Ortholog Groups', and various species like 'Anncaliia', 'A.algerae (nr Genes: 10)', 'Edhazardia', 'E.aedis', and 'E.cuniculi (nr Genes: 37)'. The 'All Results' column shows 263 genes. Below the table are 'Gene Results' and 'Genome View' tabs. A 'Select Columns' dialog box is open, showing a list of columns to be added to the table. The 'Genomic Location' and 'GBrowse' options are checked. The 'Add Columns' button is circled in red. The 'GBrowse' option is also highlighted with a red arrow.

All Results	Ortholog Groups	Anncaliia	A.algerae (nr Genes: 10)	Edhazardia	E.aedis	E.cuniculi (nr Genes: 37)
263	160	5	5	0	35	32

Note: you can display restriction sites by clicking on the configure button in GBrowse and selecting the restriction sites you would like to display. To view restriction sites, the “Restriction Sites” data track must be turned on. Go to the “Select Tracks” page and click “Restriction Sites” under the “Analysis” section.

Browser | [Select Tracks](#) | [Snapshots](#) | [Custom Tracks](#) | [Preferences](#)

Search
 Landmark or Region: NC_003229:162.593..182.592 Annotate Restriction Sites

Data Source: MicrosporidiaDB GBrowse v2.48
 Scroll/Zoom: << < - Show 20 kbp + > >> Flip

Overview
 NC_003229
 0k 10k 20k 30k 40k 50k 60k 70k 80k 90k 100k 110k 120k 130k 140k 150k 160k 170k 180k 190k

Region
 0k 10k 20k 30k 40k 50k 60k 70k 80k 90k 100k 110k 120k 130k 140k 150k 160k 170k 180k 190k

Details
 NC_003229: 20 kbp
 5 kbp
 163k 164k 165k 166k 167k 168k 169k 170k 171k 172k 173k 174k

Annotated Genes (with UTRs in gray when available)
 ECU02_1360 ECU02_1380 ECU02_1400 ECU02_1420 ECU02_1440
 ECU02_1370 ECU02_1390 ECU02_1410 ECU02_1430

The restriction site plugin generates a restriction map on the current view.
 This plugin was written Elizabeth Nickerson & Lincoln Stein.

Select Restriction Sites To Annotate

Restriction Site Display off on

<input type="checkbox"/> AatII	<input type="checkbox"/> BspDI	<input type="checkbox"/> HpaII	<input type="checkbox"/> PspGI
<input type="checkbox"/> Acc65I	<input type="checkbox"/> BspEI	<input type="checkbox"/> Hpy188I	<input type="checkbox"/> PspOMI
<input type="checkbox"/> AccI	<input type="checkbox"/> BspHI	<input type="checkbox"/> Hpy188III	<input type="checkbox"/> PstI
<input type="checkbox"/> AclI	<input type="checkbox"/> BsrFI	<input type="checkbox"/> Hpy99I	<input type="checkbox"/> PvuI
<input type="checkbox"/> AfeI	<input type="checkbox"/> BsrGI	<input type="checkbox"/> HpyCH4III	<input checked="" type="checkbox"/> PvuII
<input type="checkbox"/> AflI	<input type="checkbox"/> BssHII	<input type="checkbox"/> HpyCH4IV	<input type="checkbox"/> RsaI
<input type="checkbox"/> AflIII	<input type="checkbox"/> BssKI	<input type="checkbox"/> HpyCH4V	<input type="checkbox"/> RsrII
<input type="checkbox"/> AgeI	<input type="checkbox"/> BstAPI	<input type="checkbox"/> KasI	<input type="checkbox"/> SacI
<input type="checkbox"/> AhdI	<input type="checkbox"/> BstBI	<input type="checkbox"/> KpnI	<input type="checkbox"/> SacII
<input type="checkbox"/> AluI	<input type="checkbox"/> BstEII	<input type="checkbox"/> MboI	<input type="checkbox"/> SalI
<input type="checkbox"/> AlwNI	<input type="checkbox"/> BstNI	<input type="checkbox"/> MfeI	<input type="checkbox"/> Sau3AI
<input type="checkbox"/> ApaI	<input type="checkbox"/> BstUI	<input type="checkbox"/> MluI	<input type="checkbox"/> Sau96I
<input type="checkbox"/> ApaLI	<input type="checkbox"/> BstXI	<input type="checkbox"/> MscI	<input type="checkbox"/> SbfI
<input type="checkbox"/> ApoI	<input type="checkbox"/> BstYI	<input type="checkbox"/> MseI	<input type="checkbox"/> Scal
<input type="checkbox"/> AscI	<input type="checkbox"/> BstZ17I	<input type="checkbox"/> MslI	<input type="checkbox"/> ScrFI
<input type="checkbox"/> AseI	<input type="checkbox"/> Bsu36I	<input type="checkbox"/> MspA1I	<input type="checkbox"/> SexAI

Overview
 AL590442
 0k 10k 20k 30k 40k 50k 60k 70k 80k 90k 100k 110k 120k 130k 140k 150k 160k 170k 180k 190k

Region
 0k 10k 20k 30k 40k 50k 60k 70k 80k 90k 100k 110k 120k 130k 140k 150k 160k 170k 180k 190k

Details
 AL590442: 30.81 kbp
 10 kbp
 160k 170k 180k

Restriction Sites
 BamHI restriction site
 BamHI BamHI BamHI BamHI

Annotated Genes (with UTRs in gray when available)
 ECU02_1310 ECU02_1340 ECU02_1370 ECU02_1390 ECU02_1410 ECU02_1440 ECU02_1460 ECU02_1480 ECU02_1500 ECU02_1530
 ECU02_1320 ECU02_1350 ECU02_1380 ECU02_1400 ECU02_1420 ECU02_1450 ECU02_1470 ECU02_1510
 ECU02_1330 ECU02_1360 ECU02_1430 ECU02_1490 ECU02_1520