## **Running Schema from the Sequence View**

Prepare a query schema and save it to a file.

Open a nucleotide sequence that you want to analyze with this query schema. You can see the sequence displayed in the Sequence view.

To learn more about the Sequence view read the main UGENE User Manual.

Select the Analyze Find query designer pattern item in the Actions main menu or in the context menu:

| S          | *             | D           | K                | N               | K      | I       | I        | L            | N                                    | E                                   | E              | *           | Y      | N    | Ъ       | S | Г | F           | I      | Q        |
|------------|---------------|-------------|------------------|-----------------|--------|---------|----------|--------------|--------------------------------------|-------------------------------------|----------------|-------------|--------|------|---------|---|---|-------------|--------|----------|
| V<br>L     | ۵             | Go t        | o posi           | tion            |        |         |          | Ctr          | I+G                                  | ACG                                 | K S<br>Find pa | N<br>attern |        | I    | Y       | H | S | S<br>Ctrl+F | F      | K        |
| .GTT<br>75 | ш<br><b>Љ</b> | Sele<br>New | ct seq<br>/ anno | uence<br>tation | region | <b></b> |          | Ctrl<br>Ctrl | I+A<br>I+N                           | sw                                  | Find pa        | attern (    | Smith- | Wate | rman].  |   |   | Ctrl+SI     | hift+F | AA       |
| 'CAA<br>*  |               | Rename item |                  |                 |        |         |          |              |                                      | Find ORFs<br>Find annotated regions |                |             |        |      | TT<br>F |   |   |             |        |          |
| N          |               | Сор         | Сору             |                 |        |         |          |              | Annotate plasmid and custom features |                                     |                |             |        |      | F       |   |   |             |        |          |
| T          |               | Sele        | ct               |                 |        |         |          |              | •                                    |                                     | Build d        | lotplot     |        |      |         |   |   |             |        |          |
|            |               | Add         |                  |                 |        |         | +        |              | Find re                              | peats                               | •              |             |        |      |         |   |   |             |        |          |
|            |               | Ana         | lyze             |                 |        |         |          |              | •                                    | <u> </u>                            | Find ta        | ndems       | 5      |      |         |   |   |             |        | <b>_</b> |
|            |               | Align       |                  |                 |        |         | +        |              | 1                                    | Analyze with query schema           |                |             |        |      |         |   |   |             |        |          |
|            | Cloning       |             |                  |                 | S.     | Find re | strictio | on sites     |                                      |                                     |                |             |        |      |         |   |   |             |        |          |

The Analyze with query schema dialog appears:

| 🗞 Analyze with                             | Query Schema                                |  |               | ? <mark>x</mark> |
|--|---|--|---------------|------------------|
| File with query                            |   |  |               |                  |
| Hint:<br>Queries can be<br>To launch the Q | created using the Q<br>uery Designer select | uery Designer tool.<br>t the <i>"Tools &gt; Query Designer</i> " item. |               |                  |
| Region Selected                            | d region 🔻                                  | 77889  | •             | 134409           |
| ▼ Save appotat                             | ion(s) to                                   |  |               |                  |
| Save annotat     Save annotat              | able  | O NC 014267 features INC 014267 1                                      | ab]           | <b>_ </b>        |
| <ul> <li>Create ne</li> </ul>              | ew table                                    |  |               |                  |
| 🔘 Use auto-                                | annotations table                           |  |               |                  |
| <ul> <li>Annotation pa</li> </ul>          | arameters                                   |  |               |                  |
| Group name                                 | <auto></auto>                               |  |               | *                |
| Description                                |   |  |               |                  |
|  |   |  |               |                  |
|  |   |  |               |                  |
|  |   |  | Search Cancel | Help             |

Browse for the file with a query schema. The selected schema preview appears in the dialog, for example:

| 🗞 Analyze with Query Schema                    |  | S ×   |  |  |  |  |  |
|--|--|---|--|--|--|--|--|
| File with query C:/work/ugene/dat              | a/query_samples/SimpleGene.uql   |   |  |  |  |  |  |
| TATA-box ("tata-box")<br>Order: 2<br>TATA      | TFBS ("tfbs") Order:         3         Searches transcription factor binding sites (TFBS) with profile provided by unset. Recognize sites with         0150 bp | ORF ("ORF") Order: 1<br>Finds ORFs in <u>direct strand</u> using the <u>1. The</u><br><u>Standard Genetic Code</u> .<br>Detects only ORFs <u>not shorter than 1000 bps</u> , <u>not</u><br><u>longer than 10000 bps</u> . |  |  |  |  |  |
| Region Selected region ▼                       | 778  | 39 - 134409   |  |  |  |  |  |
| <ul> <li>Existing table</li> </ul>             | OP NC_014267 features [NC_014267.1.gb]   |   |  |  |  |  |  |
| Create new table                               |  |   |  |  |  |  |  |
| <ul> <li>Use auto-annotations table</li> </ul> |  |   |  |  |  |  |  |
| <ul> <li>Annotation parameters</li> </ul>      |  |   |  |  |  |  |  |
| Group name <auto></auto>                       |  | *   |  |  |  |  |  |
| Description                                    |  |   |  |  |  |  |  |
|  |  | Search Cancel Help  |  |  |  |  |  |

You can also adjust other parameters:

Region — the sequence range to analyze with the query schema, you can select:

- Whole sequence to analyze the whole sequence.
  Selected range to analyze the currently selected sequence region. This item is disabled if there is no region selected.
  Custom range to specify manually a range to analyze.

In the Save annotation(s) to group you can set up a file to store annotations. It could be either an existing annotation table object, a new annotation table or auto-annotations table (if it is available).

In the Annotation parameters group you can specify the name of the group. If the group name is set to <auto> UGENE will use the group name as the name for the group. Also you can add a description in the corresponding text field.