Querying Sequence Strands

As the **Example1** above shows, both sequence strands are queried by default.

To modify this behavior select the *Actions Query Sequence Mode* item in the main menu or *Query Sequence Mode* toolbar button. You can choose between the following values:

- *Direct strand* — the search is performed for the direct strand only.

  Note, that the results can still be found in the complement strand if you have set the *Any* or *Backward* direction for an element.
- *Reverse complementary strand* — the search is performed for the reverse complementary strand.
- *Both strands* — the search is performed for the both strands.

Example2:

Create the following schema:

1. The Smith-Waterman *algorithm element* with *AAG* patern and the *Forward* direction.
2. The Smith-Waterman element with *CGG* pattern and the *Forward* direction.
3. Add a *constraint* to these elements.
4. Set the *Query Sequence Mode* to *Direct strand*.
5. Run the schema for a sequence.

Only the following results will be found: