


Wizard2011

Output	
<div><div>Information<div>Close</div></div><p>On this site you can describe an output of your functionality. In addition to the outputs name, short description and description you also have to define the representation and the handling. The representation is the type of your output data in bioinformatic terms (e.g. a certain type of FASTA). You can simplify the search for the right representation by using filters. The handling of your output defines how the output data comes out of the tool technically speaking (e.g. as a file). Per se it is also possible to insert an example for your output in the description. In most cases, however, this is not necessary because your tool will create example output if you define a valid example for your functionality (see there). On the right side of the screen you have an overview of existing outputs. You can edit and delete existing outputs and add new ones. Please note that if you use the "edit" or the "+" button your current output is not saved!</p></div>	
Name: *	<input type="text" value="Sequence Alignment"/>
Short Description: *	<div><div>This is a sequence alignment.</div></div>
Description: *	<div><div>Open Text-Editor</div></div>
Representation: *	<div><div>Filter: <input type="text" value="All"/></div><div>Filter: <input type="text" value="Fasta-Format"/></div><div>Filter: <input type="text" value="Alignment"/></div><div><input type="text" value="Fasta_DNA_Alignment"/></div></div>
Handling: *	<div><div><input type="text" value="File"/></div></div>
Option:	<div><div></div></div>
Example:	<div><div><div>Choose</div></div></div>
<div><div>Return</div><div>Save and return</div><div>Save</div></div>	

Outputs 

No output defined yet!