**Function Pre-requisites:**

Please download and install the "GenomicLayers" package.

Extract the Prototype Zip file and place the XML files in the work area.

ImportDB and ExportDB files contain the script and comments to implement the functions.

**Database Specification and Pre-requisites:**

Table 1 lists the datapoints present in the database along with its metadata. The data type of all the datapoints are listed as character since they are all passed on to the function as characters. The core requirement of the datapoints as metadata and as function parameters is also listed.

**Table 1** – Database Specification

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Name** | **Label** | **Type** | **Format** | **Notes** | **Core** |
| Binding\_Factor | Binding Factor | Char |  | Name of the binding factor | Required |
| Species | Species | Char |  | Name of the species | Optional |
| Description | Description | Char |  | A short description about the binding factor | Optional |
| Author | Author | Char |  | Name of the author | Required |
| Date\_of\_Creation | Date of Creation | Char | DD-MM-YYYY |  | Required |
| Version | Version | Char |  | Version number | Required |
| Reference | Reference | Char | Hyperlink | Reference URL | Optional |
| Pattern\_String | Pattern String | Char |  | DNA Motif string or Regex pattern | Required |
| Pattern\_Length | Pattern Length | Char |  | Length of the pattern to be matched | Optional |
| Profile\_Layers | Profile Layers | Char |  | An array of layers to match | Optional |
| Profile\_Marks | Profile Marks | Char |  | An array of 0,1 to match with the profile layers | Optional |
| Mod\_Layers | Modification Layers | Char |  | An array of layers to modify on match | Required |
| Mod\_Marks | Modification Marks | Char |  | An array of 0,1 to match with the modification layers | Required |
| stateWidth | State Width | Char |  | Width of the pattern to recognize | Optional |
| MinMismatch | Minimum Permissible Mismatches | Char |  | The minimum number of permissible mismatches while marking the pattern string | Optional |
| MaxMismatch | Maximum Permissible Mismatches | Char |  | The maximum number of permissible mismatches while marking the pattern string | Optional |

**Database Prerequisites:**

* + - 1. The name of the binding factor has to be unique.
      2. The datapoints are to be present in the same order seen in Table 1 for readability and ease of implementation.
      3. The references are to be provided in the form of Digital Object Identifiers (DOI) or URLs.
      4. The Binding factor information are conditionally optional. For example, the presence of Pattern Length does not mandate the presence of Pattern String and vice versa.
      5. Version number is to be provided by the user and the default number is 1.0. The user may increment it wholly or decimally for a major and a minor change respectively. Major changes include but are not restricted to, changes to more than one binding factor information. Minor changes include but are not restricted to, changes to meta data information and or a change to at most one binding factor information data point.