BeadStudio Merlin Input Report Plug-in v1.0.1

1. Introduction

The Illumina BeadStudio Merlin Input Report Plug-in is a software plug-in that works with Illumina's BeadStudio Genotyping module v3.2 and above. This plug-in allows you to create input files for the Merlin application developed by the [Abecasis](#) group at the University of Michigan.

2. Installing the Merlin Input Report Plug-in

Perform the following steps to install the Merlin Input Report plug-in on your computer:

1. Download the Merlin Input Report Plug-in setup program (*.msi) from the illumina•connect website, http://www.illumina.com/illuminaconnect, or from the BeadStudio Portal.

2. Run the Merlin Input Report Plug-in setup program.

   The Merlin Input Report Plug-in is installed in the appropriate directory on your workstation.

   Note: The setup program also includes a file named *Genetic_Distances_Build_36.tsv*. This file includes genetic distances derived from data obtained from the [UCSC Genome Browser web site](#). The data are used to estimate genetic positions for each genotyping probe.

3. Using the Merlin Input Report Plug-in

Perform the following steps to use the newly-installed plug-in to create a Merlin Input Report from data loaded into BeadStudio:

1. In BeadStudio, open an existing genotyping project, or create a new genotyping project.

2. In the BeadStudio genotyping project, select **Analysis** | **Reports** | **Report Wizard**.

   The Report Wizard appears.

3. From the Custom Report dropdown list, choose **Merlin Input Report**.

4. If desired, browse to your config file and adjust the algorithm input parameters.

   The Configuration Parameters table on the next page of this document includes descriptions of the input parameters.

5. Click **OK** to create the report.

   A progress bar shows the report creation status. When the report has finished processing, a dialog box asking "**Would you like to view this report?**" appears.

6. Click **Yes** to display a text file showing the location of the output file.

   Note: If the file is too large to open in your default Windows text viewer (e.g., NotePad), you can open it using WordPad.

   Three files are created:

   > *<projectname>.ped*, the LINKAGE format input file
   >
   > *<projectname>.map*, the map file
   >
   > *<projectname>.dat*, the dat file

4. Configuring the Merlin Input Report Plug-in

The Merlin Input Report format can be changed via an editable configuration file. When you install the Merlin Input Report Plug-in, the config file is installed on your computer in this location:

C:\Program Files\Illumina\BeadStudio 2.0\Modules\BSGT\ReportPlugins\MerlinInputReport\

Note: When you modify and save the default config file, changes are preserved for future sessions.

The following tables contain configuration settings for and descriptions of Merlin Input Reports.

Configuration Parameters

Parameter Name	Description	Default Value
PedigreeFile	The path to the pedigree file	
TraitDataFile	[Optional] The path to the trait data file. You can create this report manually, or by using the GX Custom Output Report.	

Pedigree File Format (Tab-Delimited)

Column Name	Description	Mandatory?
Sample ID	Sample ID used in the genotyping project	Yes
Individual ID	Numeric ID representing the sample ID	Yes
Pedigree	Numeric ID representing the family ID	Yes
Father ID	Sample ID for the father; 0 for no father sample available	Yes
Mother ID	Sample ID for the mother; 0 for no mother sample available	Yes
Affected Status	0 = Unknown 1 = Affected 2 = Non-affected	Yes
Additional Columns	Ignored	No

Trait Data File Format (Tab-Delimited)

The trait data file includes the quantitative trait data with probe IDs in row 1 and sample IDs in column 1.

5. Technical Support

Direct questions about the BeadStudio Genotyping Module Merlin Input Report Plug-in to Illumina Technical Support at techsupport@illumina.com or +1.800.809.4566.