

Q-K Analysis Workflow

There are two ways to run a QK analysis in JMP Genomics. One example uses the **Q-K Mixed Model** process (See *QK Association Analysis Step-Guide*), which is a general tool that has a great deal of flexibility, but requires you to construct the input dataset yourself. A simpler option is the **Genetics Q-K Analysis Workflow**, which performs all the steps for the **Q-K** analysis and merges the data automatically. It is, however, less flexible than the **Q-K Mixed Model** process: The workflow only allows a Q matrix computed from PCA, and a K matrix from IBD calculations from the **Relationship Matrix** process.

Let's briefly work through a **Q-K** analysis using the workflow. The marker data file is output from the *Recode Genotypes Step-Guide*: **rice_genos_recgeno.sas7bdat**, and the corresponding annotation file **rice_anno_recgeno.sas7bdat**.

1. From the **Genomics Starter** menu, choose **Genetics > Workflows > Genetics Q-K Analysis Workflow**.
2. On the **General** tab, select **rice_genos_recgeno.sas7bdat** as the Input.
3. Select **FL, PH, PW, GW** as Trait Variables.
4. Enter "recgeno:" in the box under List-Style Specification of SNP Variables.
5. Choose an Output Folder.
6. On the **Annotation** tab, Choose **rice_anno_recgeno.sas7bdat** as the **Annotation SAS Data Set**.
7. Fill out the **Annotation** tab with **RS** as the **Annotation Label**, **chrom** as the **Annotation Group Variable** and **pos** as the **Annotation Location Variable**.
8. Leave the default selections on the **PCA Options** and **K Matrix Options** tabs.
9. On the **Model Variables** tab, select the **Continuous** for **Type of Trait**.
10. On the **Options** tab, specify **Numeric Genotypes** for the **Format of Marker Variables**.
11. Also on the **Options** tab, deselect **Genotype** from the **Association Tests** menu.
12. Click **Run** to launch the analysis.
 - When the workflow analysis is complete, a results journal will be displayed.

