

Absolute Risk Reduction

Author: Autumn Laughbaum, Golden Helix, Inc.

Overview

This script calculates the reduced risk for each genotype given binary disease status and treatment status columns. The script requires a spreadsheet that contains at least two binary columns and several genotypic columns.

The Absolute Risk Reduction (ARR) is calculated as

$$\text{ARR}(\text{geno}, \text{marker}) = n1/d1 - n2/d2$$

for each genotype in every marker, where

- N1 = Count of samples that had the given genotype at the given marker and did not receive treatment (treatment==0) and did not contract the disease (disease==0).
- D1 = Count of samples that had the given genotype at the given marker and did not receive treatment.
- N2 = Count of samples that had the given genotype at the given marker and received treatment and did not contract the disease.
- D2 = Count of samples that had the given genotype at the given marker and received treatment.

If the treatment was effective, you would expect a larger proportion of disease free samples in the treatment group, resulting in a negative ARR value.

Recommended Directory Location

Save the script to the following directory:

*..\Application Data\Golden Helix SVS\UserScripts\Spreadsheet\Genotype

Note: The **Application Data** folder is a hidden folder on Windows operating systems and its location varies between XP and Vista. The easiest way to locate this directory on your computer is to open SVS and select **Tools > Open Folder > User Scripts Folder**. If saved to the proper folder, this script will be accessible from the spreadsheet **Genotype** menu.

Using the Script

1. From an appropriate spreadsheet, choose **Genotype > Absolute Risk Reduction**.
2. Choose the columns that contain the disease status and treatment status. Both of these columns must be binary. Click **OK**.

The resulting spreadsheet contains ARR values for each genotype found in the spreadsheet as well as 95% upper and lower bounds.