

XWAS v3.0 Release Notes

XWAS 3.0 is fully backwards compatible and supports all functionality from previous versions. New features in the version include:

- X-wide genomic control for correcting unexpected inflation of test statistics.
- A new visualization suite for the output of association tests, including auto-generated X-wide Manhattan plots, QQ-plots, and QQ-plots following genomic control correction.
- A new tool for visualizing genotype array intensity information along with genotype calls, while highlighting differences between males and females; can help identify erroneous X-linked calls, such as false positives due to differential plate sex ratios.
- An option to test all X variants concurrently with male genotype 0/1 coding (1 being equivalent to a female heterozygote) and 0/2 coding (i.e. a male genotype equivalent to either female homozygote).
- Output of summary statistics of different association tests that include odds ratio or effect size with standard errors and confidence intervals.
- Options to run fixed- and random-effects meta-analyses based on the above output from different XWAS runs.
- Improved gene-gene interaction testing that considers all SNP-pairs between the genes of interest.
- An option to run genotype calling in parallel, providing a crucial speed-up when very large samples are involved.
- Finally, various bug fixes and user interface improvements.