MDR-PDT changes

Version	Date	Issue	Solution
1.1	11/20/06	Compiling / execution issues on solaris.	Removed Blitz library
1.1.2	12/15/06	0% Affected/Unaffected & 100% missing data were reported in final reports.	The mask associated with missing data had been flipped.
		P-Test scores were always being reported as best achievable score considering the number of tests run if they were larger than the worst test in the distribution.	Sorting for distribution had been ordered differently and the evaluation hadn't been updated to reflect the correct order
		Data files containing uneven numbers were being reported using a cryptic warning and execution continued with only completed genotypes.	Application was altered to abort under this condition with a more understandable error message.
		Changes were made in the distribution output to reflect changes in the trunk application required for parallel processing	Removed dependency on the presence of a valid model object to report the details of the model (such as the ID).
1.1.3	1/08/07	Application Segfaulted when encountering single affected individual pedigrees	Added a check for empty genotypes to GenotypeData::CountGenotypesPresent()
	1/09/07	Abort when data has no affected individuals (due to non-default status assignment)	Added an error message indicating that the data has no meaningful information and suggest that the status in the configuration file might need to be adjusted.
1.1.4	1/09/07	Abort when encountering carriage returns from MS-DOS style returns	Updated tokenizer to consider /r as whitespace
		There was some inconsistency with the implementation with random seeds	Updated application to use a macro to determine which srand to use based on compiler definitions.
	1/25/07	Classification Error was incorrectly labelled as Prediction Error.	Corrected the labels.