Covar.cpp:611: LOGGER << "template: " << samples.size() << std::endl;

Covar.cpp:618: LOGGER << "X size: " << X.size() << std::endl;

Covar.cpp:622: LOGGER << X[i + j \* sample\_index.size()] << " ";

Covar.cpp:624: LOGGER << std::endl;

Covar.cpp:629: LOGGER << "X size: " << X.size() << std::endl;

Covar.cpp:633: LOGGER << X[i + j \* sample\_index.size()] << " ";

Covar.cpp:635: LOGGER << std::endl;

FastFAM.cpp:94: LOGGER << label << ": ";

FastFAM.cpp:96: LOGGER << v[i] << " ";

FastFAM.cpp:98: LOGGER << std::endl;

FastFAM.cpp:317: LOGGER << "Loading saved GLM model file prefixed with [" << options["model\_file"] << "]..." << std::endl;

FastFAM.cpp:318: LOGGER << "Note: phenotype, covariates, sparse GRM and association test methods are included in the model file, thus these flags will be ignored." << std::endl;

FastFAM.cpp:334: LOGGER << " " << num\_indi << " valid individuals to be included." << std::endl;

FastFAM.cpp:430: LOGGER << " loaded successfully." << std::endl;

FastFAM.cpp:435: LOGGER << "Loading saved model file prefixed with [" << options["model\_file"] << "]..." << std::endl;

FastFAM.cpp:436: LOGGER << "Note: phenotype, covariates, sparse GRM and association test methods are included in the model file, thus these flags will be ignored." << std::endl;

FastFAM.cpp:452: LOGGER << " " << num\_indi << " valid individuals to be included." << std::endl;

FastFAM.cpp:483: LOGGER << " loading phenotypes..." << std::endl;

FastFAM.cpp:504: LOGGER << " loading covariates..." << std::endl;

FastFAM.cpp:520: LOGGER << " loading " << head.covarVec\_cols << " covariates..." << std::endl;

FastFAM.cpp:536: LOGGER << " loading V matrix..." << std::endl;

FastFAM.cpp:572: LOGGER << " loaded successfully." << std::endl;

FastFAM.cpp:608: LOGGER << "Using random seed: " << seed << std::endl;

FastFAM.cpp:888: LOGGER << "fastGWA-REML runtime: ";

FastFAM.cpp:890: LOGGER << "HE regression runtime: ";

FastFAM.cpp:892: LOGGER << LOGGER.tp("HE") << " sec." << std::endl;

FastFAM.cpp:1011: LOGGER << "Saving fastGWA model information..." << std::endl;

FastFAM.cpp:1020: LOGGER << "Sample information has been saved to [" << id\_file << "]." << std::endl;

FastFAM.cpp:1090: LOGGER << "Model has been saved to [" << bin\_file << "]." << std::endl;

FastFAM.cpp:1243: LOGGER << "solve VinvY" << std::endl;

FastFAM.cpp:1256: LOGGER << "sum of betas" << std::endl;

FastFAM.cpp:1266: LOGGER << "Get the sum of betas" << std::endl;

FastFAM.cpp:1300: LOGGER << "Fitting MCREML, logdet: " << logdet1 << " h2: " << hsq1 << std::endl;

FastFAM.cpp:1310: LOGGER << "Fitting MCREML, logdet: " << logdet2 << " h2: " << hsq2 << std::endl;

FastFAM.cpp:1321: LOGGER << "Fitting MCREML, logdet: " << logdet << std::endl;

FastFAM.cpp:1330: LOGGER << " Vg = " << h2 << std::endl;

FastFAM.cpp:1371: LOGGER << "XtX:" << endl;

FastFAM.cpp:1372: LOGGER << XtX << endl;

FastFAM.cpp:1384: LOGGER << "beta:" << endl;

FastFAM.cpp:1385: LOGGER << betas.transpose() << endl;

FastFAM.cpp:1388: LOGGER << "SSE: " << sse << endl;

FastFAM.cpp:1391: LOGGER << "SD: " << SDs.transpose() << endl;

FastFAM.cpp:1400: LOGGER << "\nSource\tVariance\tSE" << std::endl;

FastFAM.cpp:1401: LOGGER << "Vg\t" << hsq << "\t" << sqrt(SD) << std::endl;

FastFAM.cpp:1402: LOGGER << "Ve\t" << Vpheno - hsq << std::endl;

FastFAM.cpp:1403: LOGGER << "Vp\t" << Vpheno << std::endl;

FastFAM.cpp:1405: LOGGER << "\nHeritability = " << hsq / Vpheno << " (Pval = " << p << ")" << std::endl;

FastFAM.cpp:1423: //LOGGER << "Non zeros V: " << V.nonZeros() << std::endl;

FastFAM.cpp:1577: LOGGER << "Iteration " << iter + 1 << ", step size: " << step << ", logL: " << max\_logL

FastFAM.cpp:1590: LOGGER << "\n" << "Upper boundary detail: " << std::endl;

FastFAM.cpp:1591: LOGGER << " " << "iter\tstep\tstart\tend\tendNAN" << std::endl;

FastFAM.cpp:1592: LOGGER << std::boolalpha;

FastFAM.cpp:1594: LOGGER << " " << iter << "\t" << steps[iter] << "\t" << starts[iter] << "\t" << ends[iter] << "\t" << bEndNAN[iter] << std::endl;

FastFAM.cpp:1596: LOGGER << std::endl;

FastFAM.cpp:1601: LOGGER << "Best guess Vg "

FastFAM.cpp:1610: LOGGER << "Best guess Vg "

FastFAM.cpp:1618: LOGGER << "fastGWA-REML converged." << std::endl;

FastFAM.cpp:1630: LOGGER << "logL: " << logL << std::endl;

FastFAM.cpp:1632: LOGGER <<"Sampling variance/covariance of the estimates of Vg and Ve:" << std::endl;

FastFAM.cpp:1633: LOGGER << Hinv << std::endl;

FastFAM.cpp:1635: LOGGER << "\nSource\tVariance\tSE" << std::endl;

FastFAM.cpp:1636: LOGGER << "Vg" << "\t" << varcomp[0] << "\t" << sqrt(Hinv(0, 0)) << std::endl;

FastFAM.cpp:1637: LOGGER << "Ve" << "\t" << varcomp[1] << "\t" << sqrt(Hinv(1, 1)) << std::endl;

FastFAM.cpp:1638: LOGGER << "Vp" << "\t" << Vp << std::endl;

FastFAM.cpp:1648: LOGGER << "\nHeritability = " << Vg / Vp << " (Pval = " << p << ")" << std::endl;

FastFAM.cpp:1834: //LOGGER << "TCG compute time: " << LOGGER.tp("TCG") << std::endl;

FastFAM.cpp:1839: //LOGGER << " time: " << LOGGER.tp("vi\_y") << std::endl;

FastFAM.cpp:1854: LOGGER << "Seed used: " << seed << std::endl;

FastFAM.cpp:1856: //LOGGER << "Setting seed to: " << seed << std::endl;

FastFAM.cpp:1895: LOGGER << " reading genotypes..." << std::endl;

FastFAM.cpp:1929: LOGGER << "Tuning of Gamma finished at the " << i << "th SNP." << std::endl;

FastFAM.cpp:1945: LOGGER << "Tuning of Gamma finished " << LOGGER.tp("tuning") << " seconds." << std::endl;

FastFAM.cpp:1967: LOGGER << "Saved GRAMMAR-Gamma residual to [" << options["out"] << ".fastGWA(.residual, .gamma)" << "]." << std::endl;

FastFAM.cpp:2285: LOGGER << "fastGWA results will be saved in text format to [" << sFileName << "]." << std::endl;

FastFAM.cpp:2300: LOGGER << "fastGWA results will be saved in binary format to [" << sFileName << "(.snpinfo, .bin)]" << std::endl;

FastFAM.cpp:2320: LOGGER << " Filtering out variants with MAF < 0.0001, or customise it with --maf flag." << std::endl;

FastFAM.cpp:2325: LOGGER << " Filtering out variants with imputation INFO score < 0.30, or customise it with --info flag." << std::endl;

FastFAM.cpp:2330: LOGGER << " Filtering out variants with missingness rate > 0.10, or customise it with --geno flag." << std::endl;

FastFAM.cpp:2366: LOGGER << "Saved " << numMarkerOutput << " SNPs." << std::endl;

FastFAM.cpp:2716: LOGGER << "Note: the sample IDs (FID IID) in the model file must also present in the genotype file for further association step." << std::endl;

FastFAM.cpp:2756: LOGGER << "fastGWA-BB results will be saved in text format to [" << sFileName << "]." << std::endl;

FastFAM.cpp:2775: LOGGER << "Processing " << numGeneBlock << " genes by " << options["regiontest"] << " test..." << std::endl;

FastFAM.cpp:2781: LOGGER << " Filtering out variants with missingness rate > 0.10, or customise it with --geno flag." << std::endl;

FastFAM.cpp:2997: LOGGER << "Performing GLM to get the starting values of beta for the covariates..." << std::endl;

FastFAM.cpp:3001: LOGGER << "GLM finished, fixed effects: " << est\_a.transpose() << std::endl;

FastFAM.cpp:3014: LOGGER << "Initial Var(Y): " << varVector(Y) << std::endl;

FastFAM.cpp:3046: LOGGER << "Initializing with tao: " << cur\_tao << ", Var(Y): " << varVector(Y) << cur\_tao << ", fixed effects: " << est\_a.transpose() << "." << std::endl;

FastFAM.cpp:3079: LOGGER << "------------------------------------" << std::endl;

FastFAM.cpp:3090: LOGGER << "Fine tuning within " << startTao << " ~ " << endTao << " with " << trails[0] << " steps." << std::endl;

FastFAM.cpp:3103: LOGGER << "Fine tuning within " << startTao << " ~ " << endTao << " with " << trails[0] << " steps." << std::endl;

FastFAM.cpp:3122: LOGGER << "Mean tao in first 3 iterations: " << meanTao << ". Fine tuning within " << startTao << " ~ " << endTao << " ." << std::endl;

FastFAM.cpp:3140: LOGGER << "Mean tao in past 3 iterations: " << meanTao << ". Fine tuning within " << startTao << " ~ " << endTao << " .\n" << std::endl;

FastFAM.cpp:3208: LOGGER << "Iteration " << iter + 1 << ", step size: " << step << ", logL: " << max\_logL

FastFAM.cpp:3212: LOGGER << "\n" << "Upper boundary detail: " << std::endl;

FastFAM.cpp:3213: LOGGER << " " << "iter\tstep\tstart\tend\tendNAN" << std::endl;

FastFAM.cpp:3214: LOGGER << std::boolalpha;

FastFAM.cpp:3216: LOGGER << " " << iter << "\t" << steps[iter] << "\t" << starts[iter] << "\t" << ends[iter] << "\t" << bEndNAN[iter] << std::endl;

FastFAM.cpp:3218: LOGGER << std::endl;

FastFAM.cpp:3253: //LOGGER << "Tao value: " << cur\_tao << ", Var(Y): " << varVector(Y) << std::endl;

FastFAM.cpp:3257: LOGGER << "Iter " << curIter << ", tao: " << cur\_tao << ", Var(Y): " << varVector(Y) << ", fixed effects: " << est\_a.transpose() << "." << std::endl;

FastFAM.cpp:3276: LOGGER << "fastGWA-BB-REML stopped at a very small tao value." << std::endl;

FastFAM.cpp:3281: LOGGER << "fastGWA-BB-REML converged." << std::endl;

FastFAM.cpp:3343: LOGGER << "fastGWA-BB-REML finished in " << LOGGER.tp("binREML") << " seconds." << std::endl;

FastFAM.cpp:3352: LOGGER << "Saving fastGWA-BB model information..." << std::endl;

FastFAM.cpp:3361: LOGGER << "Sample information have been saved to [" << id\_file << "]." << std::endl;

FastFAM.cpp:3386: LOGGER << "Data for model have been saved to [" << bin\_file << "]." << std::endl;

FastFAM.cpp:3466: LOGGER << " reading " << nModelSNP << " SNP..." << std::endl;

FastFAM.cpp:3491: LOGGER << "Not enough null SNPs." << std::endl;

FastFAM.cpp:3507: LOGGER << " GRAMMAR-Gamma value = " << c\_inf << ", CV = " << cv << ", rerun " << std::endl;

FastFAM.cpp:3519: LOGGER << "Tuning time: " << LOGGER.tp("tuning") << " seconds." << std::endl;

GRM.cpp:87: LOGGER << "Get " << keep\_lists.size() << " samples from list [" << options["keep\_file"] << "]." << std::endl;

GRM.cpp:93: LOGGER << "Get " << rm\_lists.size() << " samples from list [" << options["remove\_file"] << "]." << std::endl;

GRM.cpp:134: LOGGER << common\_id.size() << " samples have been read." << std::endl;

GRM.cpp:239: LOGGER << common\_id.size() << " samples have been read." << std::endl;

GRM.cpp:248: LOGGER << ids[i].size() << " samples have been read." << std::endl;

GRM.cpp:255: LOGGER << common\_id.size() << " common samples in GRMs" << std::endl;

GRM.cpp:260: LOGGER << keep\_id.size() << " samples have been read." << std::endl;

GRM.cpp:267: LOGGER << common\_id.size() << " common samples after merging." << std::endl;

GRM.cpp:272: LOGGER << remove\_id.size() << " samples have been read." << std::endl;

GRM.cpp:283: LOGGER << common\_id.size() << " common samples after merging." << std::endl;

GRM.cpp:1996: LOGGER << "Computing GRM..." << std::endl;

GRM.cpp:1998: LOGGER << " Used " << numValidMarkers << " valid SNPs."<< std::endl;

GRM.cpp:2034: LOGGER << "Computing GRM..." << std::endl;

GRM.cpp:2036: LOGGER << numValidMarkers << " valid SNPs are included."<< std::endl;

Geno.cpp:243: LOGGER << filterprompt << "." << std::endl;

Geno.cpp:248: LOGGER << "Switch to the full dosage compensation mode." << std::endl;

Geno.cpp:252: LOGGER << "Switch to the no dosage compensation mode." << std::endl;

Geno.cpp:366: //LOGGER << "num\_blocks: " << num\_blocks << ", count extract: " << marker->count\_extract() << std::endl;

Geno.cpp:433: if(filterByMaf)LOGGER << " " << extract\_index.size() << " SNPs remain after MAF filtering." << std::endl;

Geno.cpp:796: //LOGGER << "before: " << (void\*)g\_buf << std::endl;

Geno.cpp:1559: LOGGER << nFinishedMarker << " SNPs have been processed." << std::endl;

Geno.cpp:2195: LOGGER << "Error index: " << i << ", raw index: " << curRawIndex << std::endl;

Geno.cpp:2196: LOGGER << "Error buffer:" << static\_cast<void \*>(g\_buf) << std::endl;

Geno.cpp:2404: LOGGER << "1.gbuf size: " << bsize << ", mask size: " << msize << ", raw ct: " << rawCountSamples[0] << ", keep ct: " << gbuf->n\_sample << ", nMarker: " << numMarker << std::endl;

Geno.cpp:2763: LOGGER << "Old bgen 2 bed" << std::endl;

Geno.cpp:2781: LOGGER << "samples: " << num\_raw\_sample << ", keep\_sample: " << index\_keep.size() << std::endl;

Geno.cpp:2782: LOGGER << "Markers: " << num\_markers << std::endl;

Geno.cpp:3309: LOGGER << "0. gbuf size: " << bsize << ", mask size: " << msize << ", raw ct: " << num\_raw\_sample << ", keep ct: " << num\_keep\_sample << ", nMarker: " << cur\_num\_marker\_read << std::endl;

Geno.cpp:3732: LOGGER << nFinishedMarker << " SNPs have been processed." << std::endl;

Geno.cpp:3791: LOGGER << num\_valid\_marker\_processed << " SNPs have been processed." << std::endl;

Geno.cpp:3809: LOGGER << "Computing allele frequencies and saving them to [" << name\_out << "]..." << std::endl;

Geno.cpp:3823: LOGGER << "Saved " << numMarkerOutput << " SNPs." << std::endl;

Geno.cpp:3839: LOGGER << "Recoding genotypes and saving them to [" << name\_out << "]..." << std::endl;

Geno.cpp:3876: LOGGER << "Saved " << numMarkerOutput << " SNPs." << std::endl;

Marker.cpp:97: LOGGER << "Get " << extractlist.size() << " SNPs from list [" << options["extract\_file"] << "]." << std::endl;

Marker.cpp:103: LOGGER << "Get " << excludelist.size() << " SNPs from list [" << options["exclude\_file"] << "]." << std::endl;

Marker.cpp:879: LOGGER << outputs << std::endl;

Marker.cpp:1004: LOGGER << count\_chr\_error << " SNPs excluded due to filtering of chromosomes. " << std::endl;

Marker.cpp:1007: LOGGER << "Total SNPs included: " << num\_var\_added << "/" << num\_marker << "." << std::endl;

Marker.cpp:1073: LOGGER << "Extracting biallelic SNPs from bgen [" << bgen\_file << "]..." << std::endl;

Marker.cpp:1084: LOGGER << n\_variants << " SNPs, ";

Marker.cpp:1087: LOGGER << n\_sample << " samples in the bgen file." << std::endl;

Marker.cpp:1104: LOGGER << "bgen version ";

Marker.cpp:1107: LOGGER << "1.1, ";

Marker.cpp:1110: LOGGER << "1.2, ";

Marker.cpp:1113: LOGGER << "unkown, ";

Marker.cpp:1117: LOGGER << "no compress";

Marker.cpp:1120: LOGGER << "compressed by zlib";

Marker.cpp:1123: LOGGER << "compressed by zstd";

Marker.cpp:1126: LOGGER << "unknown format";

Marker.cpp:1128: LOGGER << "." << std::endl;

Marker.cpp:1138: LOGGER << "Looking for biallelic alleles..." << std::endl;

Marker.cpp:1173: //LOGGER << options\_i["start\_chr"] << " " << options\_i["end\_chr"] << " " << (int)chr\_item << " count\_chr\_error:" << count\_chr\_error << std::endl;

Marker.cpp:1221: LOGGER << count\_chr\_error << " SNPs excluded due to filtering of chromosomes." << std::endl;

Marker.cpp:1222: LOGGER << count\_multi\_alleles << " SNPs excluded due to multiple alleles." << std::endl;

Pheno.cpp:78: LOGGER << "Get " << keep\_subjects.size() << " samples from list [" << options["keep\_file"] << "]." << std::endl;

Pheno.cpp:84: LOGGER << "Get " << remove\_subjects.size() << " samples from list [" << options["remove\_file"] << "]." << std::endl;

Pheno.cpp:133: LOGGER << index\_keep.size() << " individuals to be included. " << index\_keep\_male.size() << " males, " << index\_keep\_sex.size() - index\_keep\_male.size() << " females, " << index\_keep.size() - index\_keep\_sex.size() <<" unknown." << std::endl;

Pheno.cpp:318: LOGGER << "Checking other sample files..." << std::endl;

main.cpp:289: LOGGER << key << " ";

main.cpp:291: LOGGER << element << " ";

main.cpp:293: LOGGER << std::endl;

main.cpp:331: LOGGER << "Peak memory: " << mem << " GB; Virtual memory: " << vmem << " GB." << std::endl;

main.cpp:336: LOGGER << "Overall computational time: " << time\_str << "." << std::endl;