# Test

Keith T. Smith,[1] A. N. Other,[2] and Third Author[2,3]

[1]Affiliation 1
[2]Affiliation 2
[3]Affiliation 3

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Figure 1: *Figure 1 (?, ?)*

## 1 Tables

Table 1: **Cross-validation accuracy.** The percentage of correctly imputed two-field alleles is shown for each method at each HLA locus in each of four major populations from the cross-validation analysis with the multi-population reference panel. The number of individuals used for validation in each population at each HLA locus is also shown. *Method does not support this locus.

| Population | HLA locus | No. validation individuals | Method | | | |
|---|---|---|---|---|---|---|
| | | | HIBAG | HLA*IMP:02 | HLA*IMP:03 | SNP2HLA |
| African-American / African | *A* | 203 | 94.1 | 92.9 | 95.1 | 88.1 |
| | *B* | 235 | 88.3 | 85.1 | 90.0 | 77.4 |
| | *C* | 203 | 93.3 | 92.4 | 94.6 | 79.8 |
| | *DQA1* | 355 | 97.5 | 94.8 | 96.3 | 77.6 |
| | *DQB1* | 531 | 85.2 | 82.8 | 86.0 | 63.0 |
| | *DRB1* | 550 | 91.8 | 89.8 | 94.9 | 90.0 |
| | *DRB3* | 338 | * | 95.6 | 99.0 | * |
| | *DRB4* | 337 | * | 98.2 | 99.4 | * |
| | *DRB5* | 342 | 99.1 | 99.4 | 99.6 | * |
| Asian | *A* | 749 | 86.2 | 91.5 | 92.6 | 88.9 |
| | *B* | 852 | 89.9 | 86.2 | 91.6 | 85.8 |
| | *C* | 759 | 97.8 | 96.6 | 97.7 | 86.7 |
| | *DPA1* | 452 | 99.3 | 99.1 | 99.3 | 91.5 |
| | *DPB1* | 452 | 88.4 | 89.0 | 89.3 | 83.6 |
| | *DQA1* | 487 | 96.6 | 96.1 | 97.4 | 84.8 |
| | *DQB1* | 767 | 86.7 | 86.0 | 88.2 | 72.4 |
| | *DRB1* | 845 | 87.8 | 86.8 | 91.2 | 88.4 |
| | *DRB3* | 12 | * | 87.5 | 100.0 | * |
| | *DRB4* | 11 | * | 100.0 | 100.0 | * |
| | *DRB5* | 14 | 100.0 | 100.0 | 100.0 | * |
| Europeans | *A* | 6,685 | 97.7 | 97.6 | 97.7 | 96.4 |
| | *B* | 7,999 | 95.8 | 94.2 | 95.7 | 93.7 |
| | *C* | 6,642 | 98.3 | 98.1 | 98.2 | 94.0 |
| | *DPA1* | 5,615 | 99.7 | 99.7 | 99.9 | 97.5 |
| | *DPB1* | 5,686 | 95.0 | 95.1 | 95.6 | 92.5 |
| | *DQA1* | 5,899 | 99.3 | 98.8 | 99.3 | 91.4 |
| | *DQB1* | 7,325 | 98.0 | 97.1 | 98.0 | 88.2 |
| | *DRB1* | 7,918 | 94.1 | 93.6 | 95.0 | 94.2 |
| | *DRB3* | 165 | * | 96.7 | 98.5 | * |
| | *DRB4* | 197 | * | 97.5 | 99.2 | * |
| | *DRB5* | 217 | 99.5 | 99.8 | 99.5 | * |
| Latino | *A* | 217 | 91.5 | 92.4 | 92.4 | 89.4 |
| | *B* | 350 | 78.3 | 73.6 | 78.9 | 70.7 |
| | *C* | 220 | 96.1 | 94.5 | 96.4 | 90.2 |
| | *DPB1* | 26 | 84.6 | 86.5 | 86.5 | 82.7 |
| | *DQA1* | 42 | 100.0 | 98.8 | 98.8 | 84.5 |
| | *DQB1* | 232 | 91.6 | 90.5 | 94.4 | 81.0 |
| | *DRB1* | 339 | 83.9 | 82.2 | 88.8 | 84.4 |
| | *DRB3* | 23 | * | 93.5 | 97.8 | * |
| | *DRB4* | 11 | * | 100.0 | 100.0 | * |
| | *DRB5* | 33 | 100.0 | 100.0 | 100.0 | * |

Table 2: **Summary of HLA reference panel.** For each HLA locus the table displays: the number of individuals typed at two-fields in each dataset (CEU+58, GSK, YRI, 1000G, T1DGC, KC, PA, SW) and in total; the number of SNPs in the xMHC for the dataset formed by merging all individuals typed at that HLA locus; and the number of two-field alleles present in the dataset. MIM number – Mendelian Inheritance in Man number. *HLA-DRB4* does not have a MIM number; the HUGO Gene Nomenclature Committee (HGNC) ID is given instead.

| HLA locus | A | B | C | DQA1 | DQB1 | DRB1 | DRB3 | DRB4 | DRB5 |
|---|---|---|---|---|---|---|---|---|---|
| MIM number or HGNC ID | 142800 | 142830 | 142840 | 146880 | 604305 | 142857 | 612735 | HGNC:4952 | 604776 |
| No. individuals in each dataset | | | | | | | | | |
| CEU+58 | 890 | 1,490 | 836 | 61 | 1,017 | 1,122 | – | – | – |
| GSK | 379 | 1,365 | 398 | 302 | 498 | 1,191 | 158 | 182 | 265 |
| YRI | 23 | 23 | 23 | 23 | 22 | 18 | – | – | – |
| 1000G | 927 | 927 | 926 | – | 925 | 927 | – | – | – |
| T1DGC | 5,192 | 5,192 | 5,192 | 5,192 | 5,192 | 5,192 | – | – | – |
| KC | – | – | – | 332 | 330 | 331 | 332 | 332 | 332 |
| PA | 443 | 439 | 449 | 450 | 450 | 448 | – | – | – |
| SW | – | – | – | 423 | 421 | 423 | 48 | 42 | 9 |
| Total individuals | 7,854 | 9,436 | 7,824 | 6,783 | 8,855 | 9,652 | 538 | 556 | 606 |
| No. SNPs in merged dataset | 1,672 | 1,672 | 1,672 | 1,357 | 1,162 | 1,162 | 2,254 | 2,253 | 2,291 |
| No. two-field alleles | 91 | 174 | 54 | 20 | 28 | 94 | 6 | 3 | 4 |

Table 3: **Imputation accuracy in T1DGC validation set.** The percentage of correctly imputed two-field alleles is shown for each method at each HLA locus in the T1DGC validation set. Publicly available pre-trained models were used for HIBAG and MAGprediction. Two sets of results are presented for HLA*IMP:02 and HLA*IMP:03: the cross-validation analysis with the multi-population reference panel, and trained with all samples except T1DGC. The number of individuals available for validation at each HLA locus also shown. *Method does not support this locus.

| HLA locus | No. validation individuals | HIBAG Pre-trained | MAGprediction Pre-trained | HLA*IMP:02 | | HLA*IMP:03 | |
|---|---|---|---|---|---|---|---|
| | | | | CV | Excl. T1DGC | CV | Excl. T1DGC |
| A | 5,192 | 95.2 | 41.2 | 97.4 | 95.5 | 97.5 | 96.6 |
| B | 5,192 | 91.5 | 46.6 | 93.3 | 91.5 | 95.1 | 93.8 |
| C | 5,192 | 97.2 | 56.2 | 98.3 | 97.1 | 98.4 | 97.7 |
| DPA1 | 5,192 | * | * | 99.7 | 98.3 | 99.8 | 98.8 |
| DPB1 | 5,190 | 89.9 | 86.9 | 95.0 | 88.4 | 95.6 | 92.3 |
| DQA1 | 5,192 | 98.4 | * | 98.8 | 98.2 | 99.4 | 98.8 |
| DQB1 | 5,192 | 97.1 | 67.2 | 97.5 | 95.3 | 98.4 | 95.2 |
| DRB1 | 5,192 | 88.8 | 37.6 | 93.6 | 90.1 | 95.3 | 93.7 |

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Figure 2: *Figure 1 (?, ?)*