Feature comparison Matching engines

Educational webinars

- 12 November 2020: slides | video
- 22 March 2021: slides | video
- 1 September 2022: slides | video
- 5 December 2023: slides | video

Feature	Optimatch	HAP-E	ATLAS
AB search	Yes (separate search)	No. Technically possible, but turned off for performance reasons.	No. Not possible because donors without DRB1 are not accepted by ATLAS as valid donors.
ABDR search	Yes	Yes	Yes
AB Antigen, DRB1 allele match (for cord matching)	Yes	Yes	Not planned. Lack of community interest. requires fundamental code changes.
Sorting performed by Matching Engine	Yes	No. WMDA Search and Match performs sorting.	Yes, but WMDA will override with own sort parameters
Information about probability of match at other allele at already mismatched locus	No	Yes	Yes
Flexible scaling to accommodate periods of high and low use of the engine	No	Yes	Yes
g group level matching	Yes	Yes	Yes (actually "P" group matching)
G group level matching (leading to less populations and lesser performance for some of populations, but better matching for other populations).	No	No	Yes, but turned off at the moment in favour of g group matching.
automatic refresh of patient searches	Yes	Yes	Yes
differential results from matching algorithm. algorithm tells what has changed.	No	Yes	Yes
HLA validation of DRB3, DRB4, DRB5, DQA1 and other loci not considered for matching	Possible in Optimatch. Not implemented in WMDA setup for Search & Match v1.	Yes	Loci other than A, B, C, DRB1, DQB1 and DPB1 are not validated or imported by ATLAS and therefore also not returned.
Performing a mismatch search will return also (potentially) matched results	Yes	Yes	Yes
Consider combination of serological and DNA typing for match probability	Yes	No	No
support for > 2 mismatches	Possible in Optimatch. Not implemented in WMDA setup for Search & Match v1.	Not yet. Will also be 2 or more mismatches on ABDRB1. >=4/8 all loci to be considered need to be typed at high resolution for patient.	yes, but only for cords >= 4/8
HLA imputation based on patient organisation and/or pool	Possible in Optimatch. Not implemented in WMDA setup for Search & Match v1.	Yes.	Available at go-live.
mismatches per locus can be sent directly to matching engine?	Yes, during actual search and during retrieval.	No. Server side filtering needed for API and GUI	Yes, but not fast. For performance reasons WMDA will perform server side filtering for GUI use.
null allele handling	Only considers null alleles with allele frequency higher than 0% in donor population or high resolution null allele.	Will return donors which match haplotype with known null allele or high resolution null allele.	?

TCE handling for DPB1	Allele frequency based TCE3	Allele frequency based TCE3 The determination of permissiveness follows the logic described in Crocchiolo et al., 2009. The TCE group assignment is based on functional distances as described in Crivello et al., 2016 Crocchiolo_Blood_2009 nonpermissive DPB1 outcomes.pdf Crivello_Blood_2016_Functional distance between recipient and donor HLA-DPB1 determines nonpermissive mismatches in unrelated HC.pdf	TCE3
match grade handling when multiple potential ARDs in donor typing	When only 1 ARD in ambiguity list occurs in the known haplotypes allele match ("A")	Always "Potential" even if there is only 1 ARD in known haplotypes (100% potential match)	
broad serology level matching	yes	No. Split serology will only match same split serology or when donor/patient is broad serology. Not matched when patient/donor has split serology that is different but both share same broad serology. e.g. • 26 -> split serology 26, broad serology 10 • 66:XX -> split serology 66, broad serology 10 • Hap-E does not consider the shared broad serology as a match • Optimatch seems to consider them a match	AB Antigen, DRB1 allele match not supported.
Lowest probability in search results	1 (0 is very rare circumstances). 0% match probability for haplotype frequency matching displayed as 1% if allele frequency based matching indicates possible match.	0	0
matching probability when donor haplotype cannot be explained	No match probabilities displayed.	No match probabilities displayed.	No match probabilities displayed.
directionality of DPB1 nonpermissive mismatch indicated?	Yes	Yes	Yes
Indicate in search result that it is unclear whether allele or antigen mismatch	Yes	No	No
donors returned with A, B and C and /or DQB1, but not DQB1	Yes in AB search	yes but filtered out	donors without DRB1 are never returned
HLA typing other than A, B, C, DRB1, DQB1 and DPB1 (e.g. DRB3/4/5 or DPA1) available in search results and full report	Yes	yes, only in full report due to design choice in Search & Match	no.
Meaning of locus-specific match probability	Locus match probability no matter the amount of overall mismatches	Locus match probability in the case of additional mismatch additional info	Locus match probability no matter the amount of overall mismatches
Handling of "NEW" alleles (alleles that do not yet have an official allele name). See https://onlinelibrary.wiley.com/doi/10.1111/tan.15048	?	Supported for Donors and Patients. Search & Match including Dataupload currently only supports NEW alleles for Patients (so Search & Match).	Not currently supported. Support will be added in the future using ticket https://github.com/Anthony-Nolan/Atlas/issues/876
Homozygous mismatch: how many mismatches		Configurable. Currently set to "2" in WMDA Search & Match.	2?