The pseudocode of procedure Heu-Label

**Input:** A weighted similarity graph $G_H$.

**Output:** A labeling $l$ of $G_H$.

**Step 1:** for each vertex $i$ of $G_H$ do { $l(i) = \sim$; }

**Step 2:** for each homozygous constraint edge $c_{ij}$ of $G_H$ do

$\alpha =$ an HLA gene type in the constraint of $c_{ij}$; $l(i) = l(j) = \alpha$; delete $c_{ij}$ from $G_H$;

**Step 3:** build a graph $G$ by deleting all constraint edges and the similarity edges whose weights are small than $T_s$ from $G_H$;

**Step 4:** find all connected components of $G$ by depth first search;

**Step 5:** for each connected component $comp$ (from the largest to the smallest) do

**Step 5.1:** for each HLA gene type $\alpha$ in $C(G_H)$ do { $N(\alpha) = 0$; }

**Step 5.2:** for each vertex $i$ in $comp$ do

if $l(i) \neq \sim$ then $N(l(i)) ++$;
else

$\{ (\alpha, \beta) =$ the constraint of the constraint edge adjacent to $i$ in $G_H; N(\alpha)+++; N(\beta)+++; \}$

**Step 5.3:** $\gamma = \text{argmax}(N(\alpha))$;

**Step 5.4:** for each vertex $i$ in $comp$ do

$(\alpha, \beta) =$ the constraint of the constraint edge $c_{ij}$ adjacent to $i$ in $G_H$;

if $l(i) = \sim$ then

if $\alpha = \gamma$ then $l(i) = \alpha; l(j) = \beta$; delete the constraint edge $c_{ij}$ from $G_H$;
delete vertices $i$ and $j$ from $G$;
if $\beta = \gamma$ then $l(i) = \beta; l(j) = \alpha$; delete the constraint edge $c_{ij}$ from $G_H$;
delete vertices $i$ and $j$ from $G$;

**Step 6:** repeat Steps 4 and 5 until there are no more vertices can be labeled.