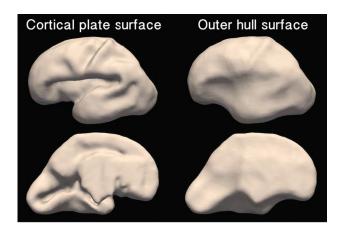


**ON-LINE FIG 1.** Description of sulcal pattern matching and similarity measurement between different 2 brains. M is a matrix to store the similarities of all candidate assignments (9 [= 3 nodes  $\times$  3]  $\times$  9) and their pair-wise similarities. The M is used to choose a subset matrix A of the consistent assignments set C. The  $c_n$ ,  $c_2$ , and  $c_3$  are consistent assignments (optimally matched pairs).  $A(c_n$ ,  $c_1$ ) is a similarity of the assignment  $c_1$  of  $p_1$  and  $q_1$ , and  $A(c_n$ ,  $c_2)$  is a similarity that measures how much the relationship between  $p_1$  and  $p_2$  is similar to the relationship between  $q_1$  and  $q_2$ . S is a global similarity between sulcal sets P and Q.



**ON-LINE FIG 2.** An example of cortical plate and outer hull surfaces for an individual fetal brain (27 GW).

## Normal M2 МЗ M4 М5а M<sub>5</sub>b s:0.808 (22 GW) 0.838 (23 GW) 0.829 (26 GW) 0.819 (27 GW) 0.835 (28 GW) 0.767 (25 GW) 0.678 (26 GW) 0.799 (22 GW) 0.767 (29 GW) [0 0 0.36 0] [0.14 0.79 0.21 0.07] [0 0 0.79 0.07] $r = [0 \ 0 \ 0 \ 0.5]$ [w xyz s d] [0 0.14 0 0.07] [0 0 0 0.07] 0.727 0.774 0.812 0.820 0.815 0.644 0.736 0.808

Sulcal basin identification and pattern similarity to the normal templates

**ON-LINE FIG 3.** Sulcal pattern similarity (*S*) to the templates measured with the whole set of features for 5 normal and all abnormal fetal brains. The ratios (*r*) are the quantification of the deviation from the normal controls with the whole feature set and each of the 3 components (*w*: whole feature set; *xyz*: 3D position; *s*: sulcal basin area; *d*: sulcal depth).

[0 0 0.07 0.14] [0.5 0.71 0.21 0.57]

[0 0 0.71 0]

[0 0 0 0]

[0.43 0.86 0.64 0] [0.07 0 0.5 0.15]