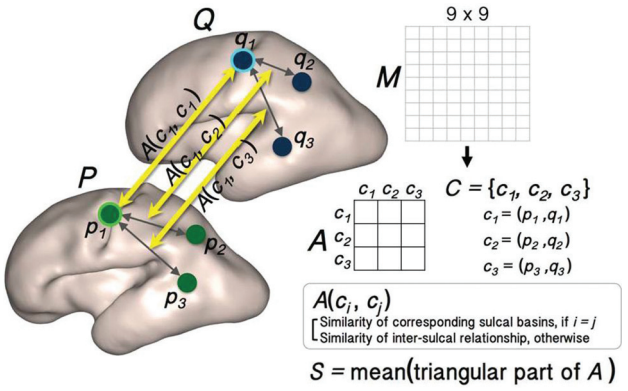
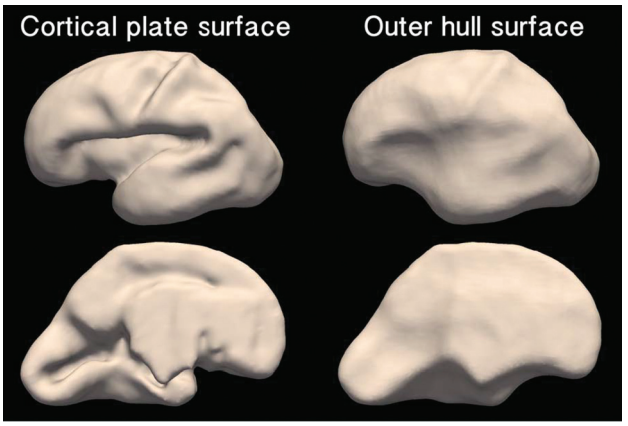
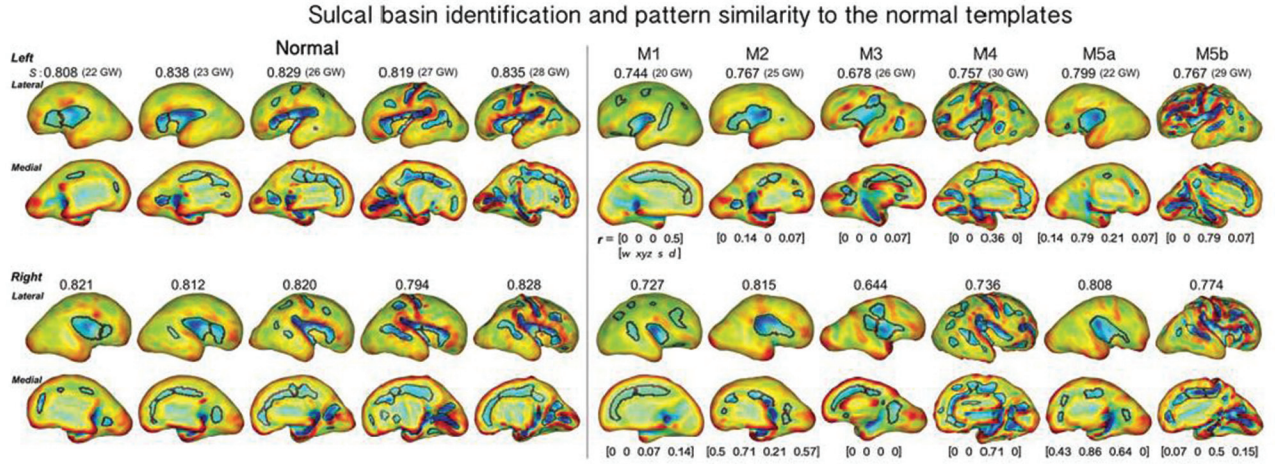


ON-LINE FIG 1. Description of sulcal pattern matching and similarity measurement between different 2 brains. *M* is a matrix to store the similarities of all candidate assignments (9 [= 3 nodes × 3] × 9) and their pair-wise similarities. The *M* is used to choose a subset matrix *A* of the consistent assignments set *C*. The c_1, c_2, and c_3 are consistent assignments (optimally matched pairs). $A(c_1, c_1)$ is a similarity of the assignment c_1 of p_1 and q_1, and $A(c_1, c_2)$ 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).



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).