Supplementary material for "Fiber estimation and tractography in diffusion MRI: Development of simulated brain images and comparison of multi-fiber analysis methods at clinical *b*-values"

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This supplement contains details of results presented in the main body of the paper. The material presented here uses the same definitions, acronyms, and color-coding of plots that were introduced therein.

1. Single-fiber per voxel estimation

Fig. S1 illustrates the same mean values (filled markers) as in Fig. 3 of the main paper, with error bars to indicate spread. The error bars extend to the mean of values above and below the filled marker.

2. Two-fibers per voxel estimation

Figs. S2-S7 illustrate the same mean values (filled markers) as in Figs. 4 and 5 of the main paper, with error bars to indicate spread. The error bars extend to the mean of values above and below the filled marker.

3. Three-fibers per voxel estimation

Fig. S8. illustrates the same mean values (filled markers) as in Fig. 6 of the main paper, with error bars to indicate spread. The error bars extend to the mean of values above and below the filled marker.

Overall, Figs S1-S8 show consistent decreases in mean error (filled markers) and spread with increasing number of diffusion-weighting directions, N, as would be expected. In general the significant reductions in mean error and spread are obtained from $N = 20$ to $N = 60$, with diminishing improvements up to $N = 120$.

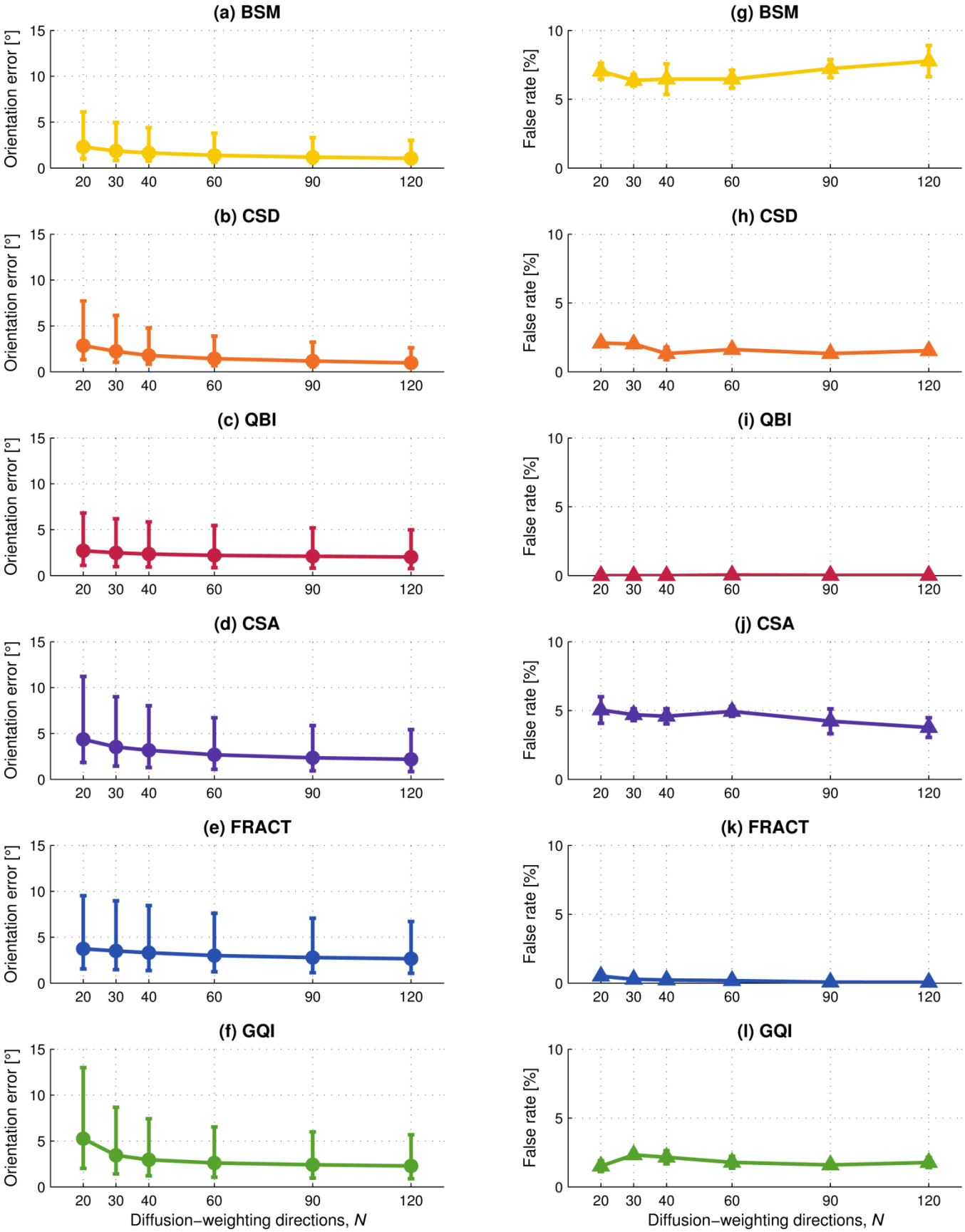

Fig. S1. Single-fiber estimation versus number of diffusion-weighting directions, *N*. Error bars extend to the mean of samples above and below the filled marker (mean of all data points). (a)-(f) Individual fiber orientation error for each method. (g)-(l) Corresponding false-positive rate.

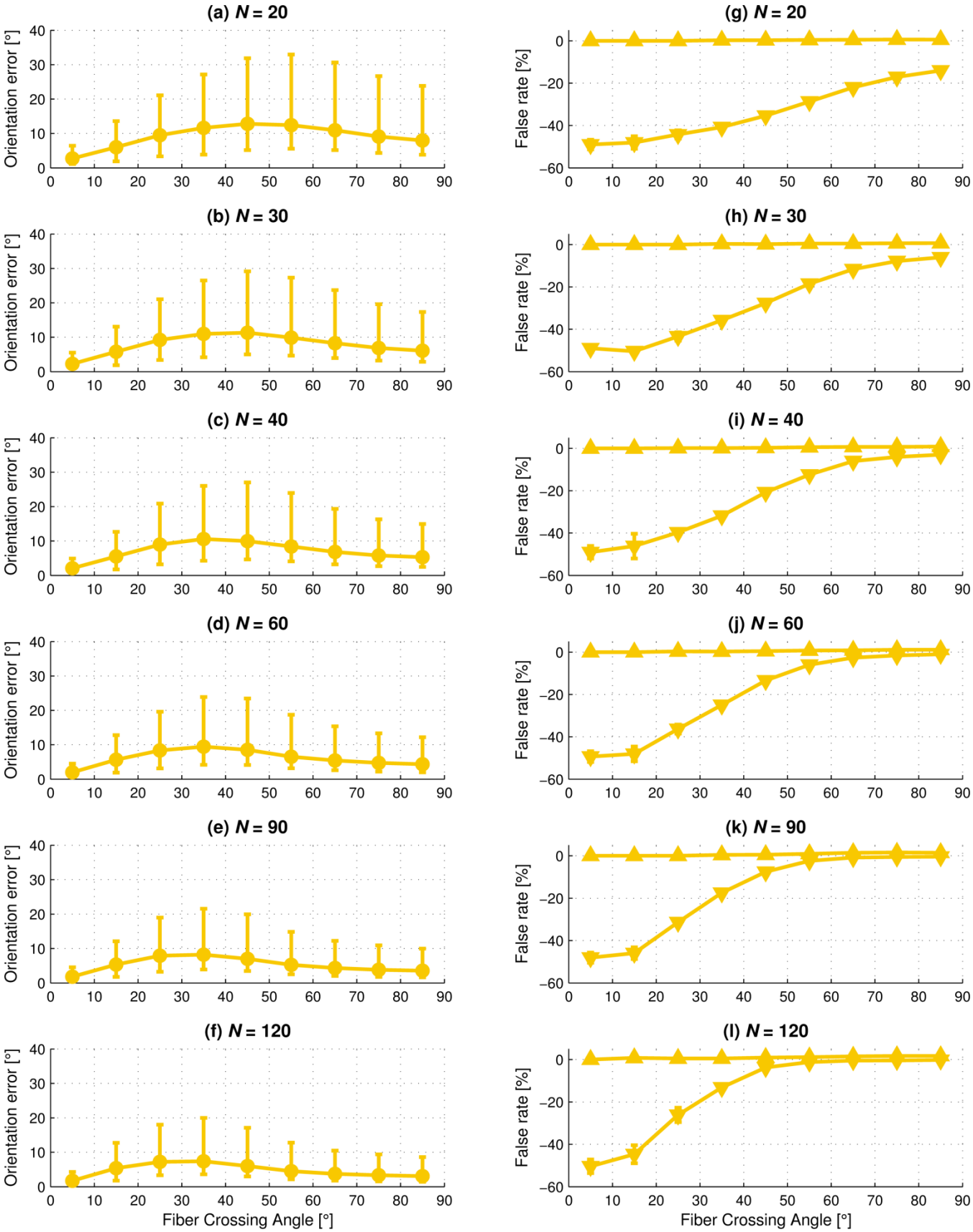

Fig. S2. Two-fiber estimation versus fiber crossing angle, for BSM method. Error bars extend to the mean of samples above and below the filled marker (mean of all data points). (a)-(f) Individual fiber orientation error, with increasing *N*. (g)-(l) Corresponding false-positive (▲) and false-negative (▼) rates.

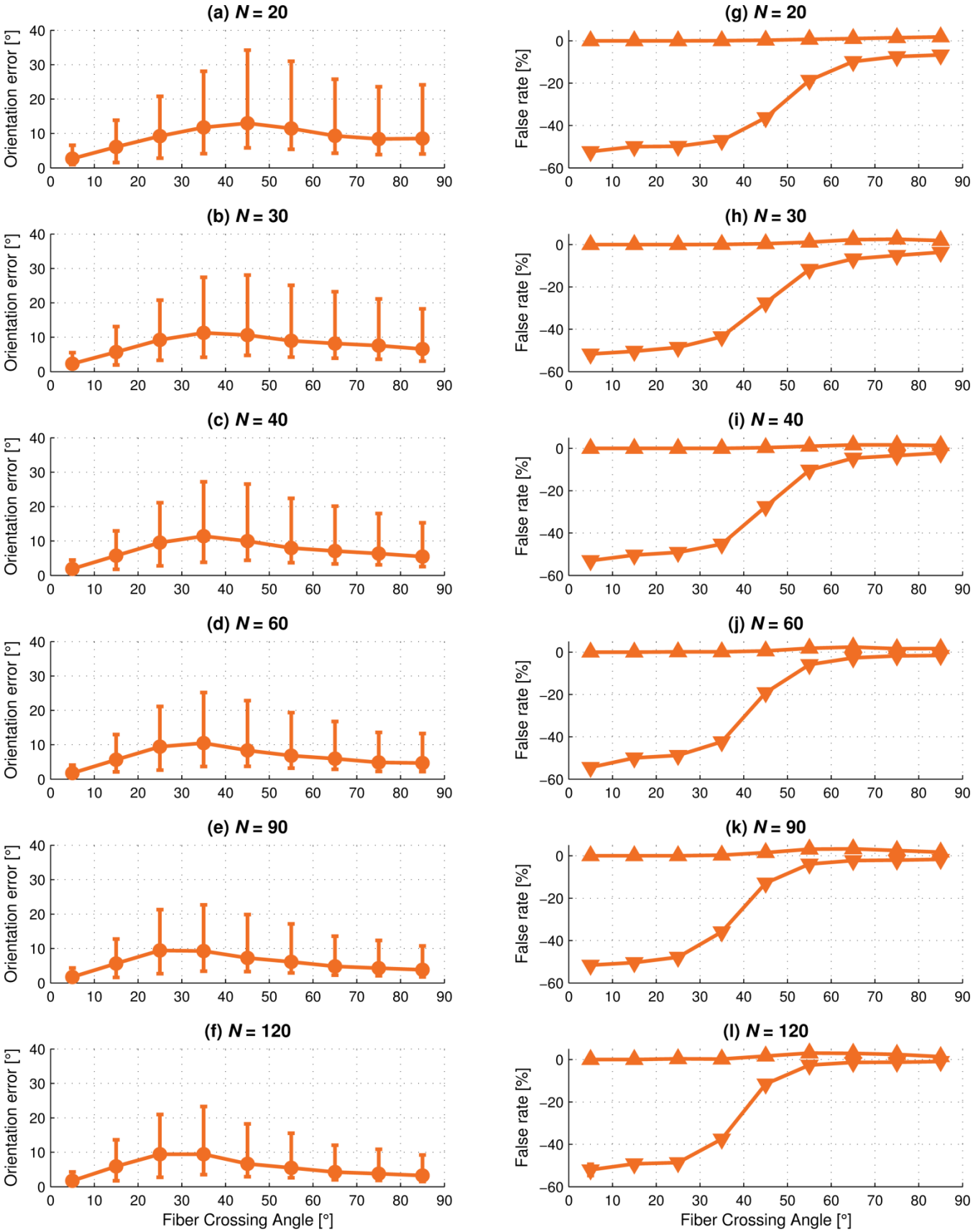

Fig. S3. Two-fiber estimation versus fiber crossing angle, for CSD method. Error bars extend to the mean of samples above and below the filled marker (mean of all data points). (a)-(f) Individual fiber orientation error, with increasing *N*. (g)-(l) Corresponding false-positive (▲) and false-negative (▼) rates.

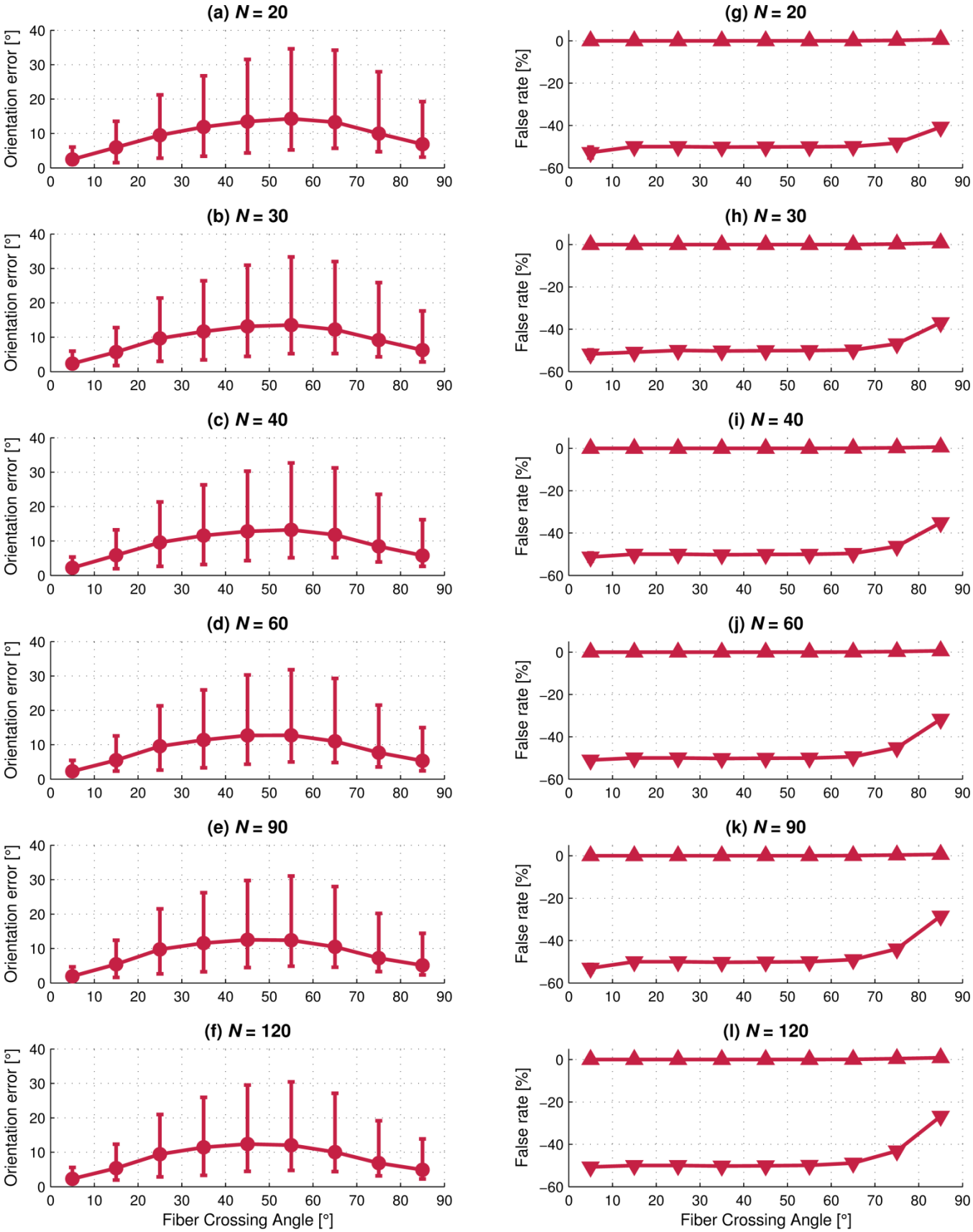

Fig. S4. Two-fiber estimation versus fiber crossing angle, for QBI method. Error bars extend to the mean of samples above and below the filled marker (mean of all data points). (a)-(f) Individual fiber orientation error, with increasing *N*. (g)-(l) Corresponding false-positive (▲) and false-negative (▼) rates.

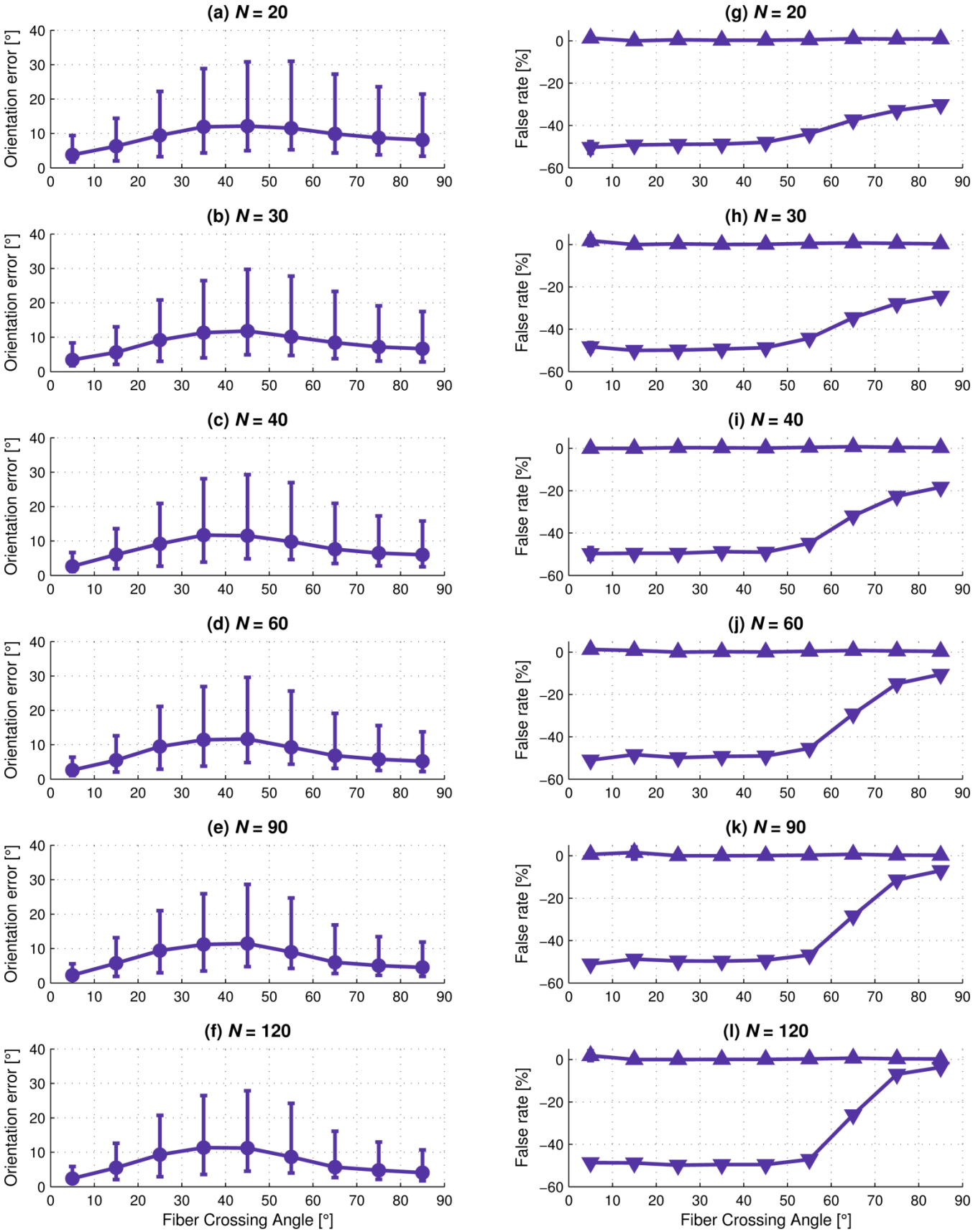

Fig. S5. Two-fiber estimation versus fiber crossing angle, for CSA method. Error bars extend to the mean of samples above and below the filled marker (mean of all data points). (a)-(f) Individual fiber orientation error, with increasing *N*. (g)-(l) Corresponding false-positive (▲) and false-negative (▼) rates.

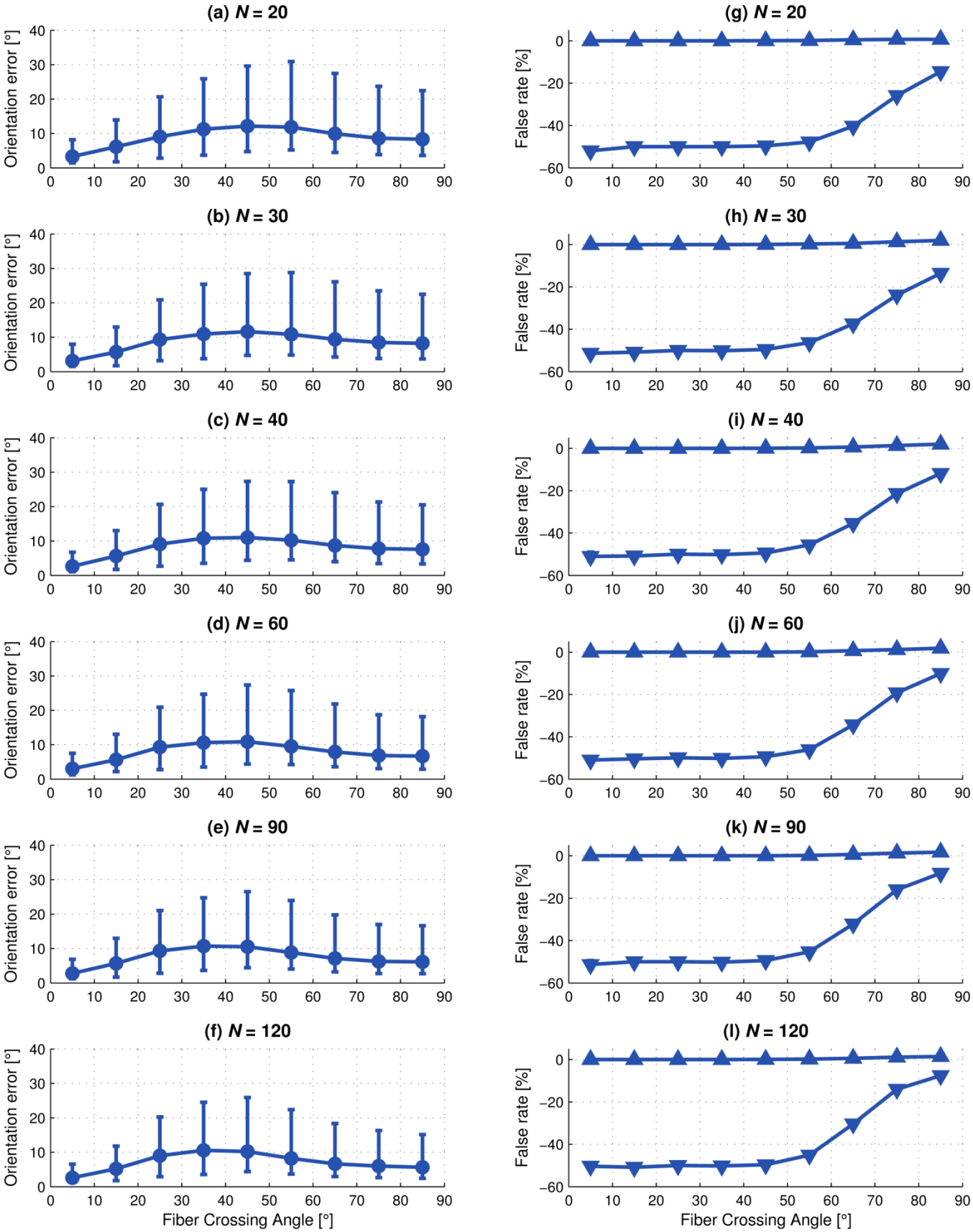

Fig. S6. Two-fiber estimation versus fiber crossing angle, for FRACT method. Error bars extend to the mean of samples above and below the filled marker (mean of all data points). (a)-(f) Individual fiber orientation error, with increasing *N*. (g)-(l) Corresponding false-positive (▲) and false-negative (▼) rates.

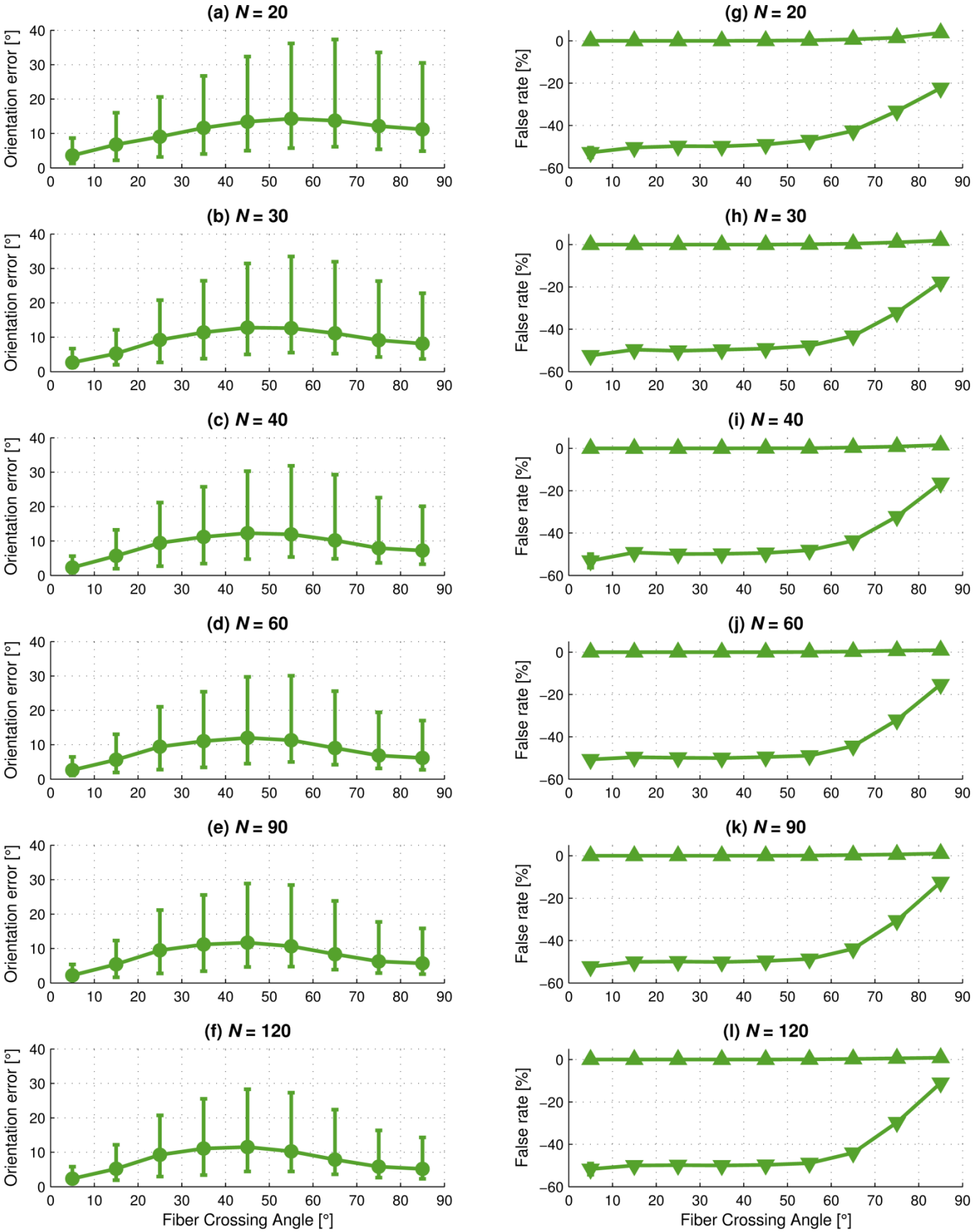

Fig. S7. Two-fiber estimation versus fiber crossing angle, for GQI method. Error bars extend to the mean of samples above and below the filled marker (mean of all data points). (a)-(f) Individual fiber orientation error, with increasing *N*. (g)-(l) Corresponding false-positive (▲) and false-negative (▼) rates.

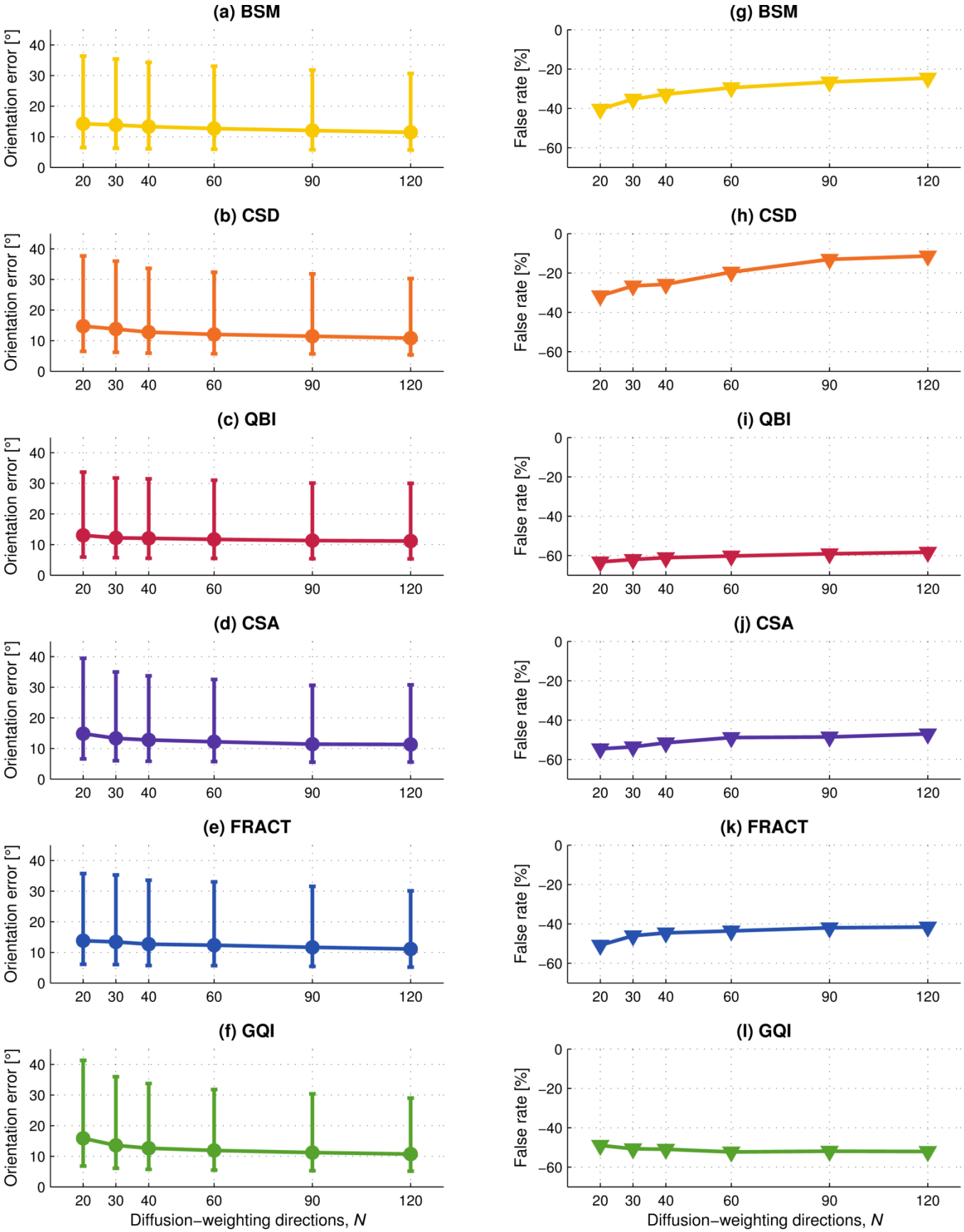

Fig. S8. Three-fiber estimation versus number of diffusion-weighting directions, *N*. Error bars extend to the mean of samples above and below the filled marker (mean of all data points). (a)-(f) Individual fiber orientation error for each method. (g)-(l) Corresponding false-negative rate.