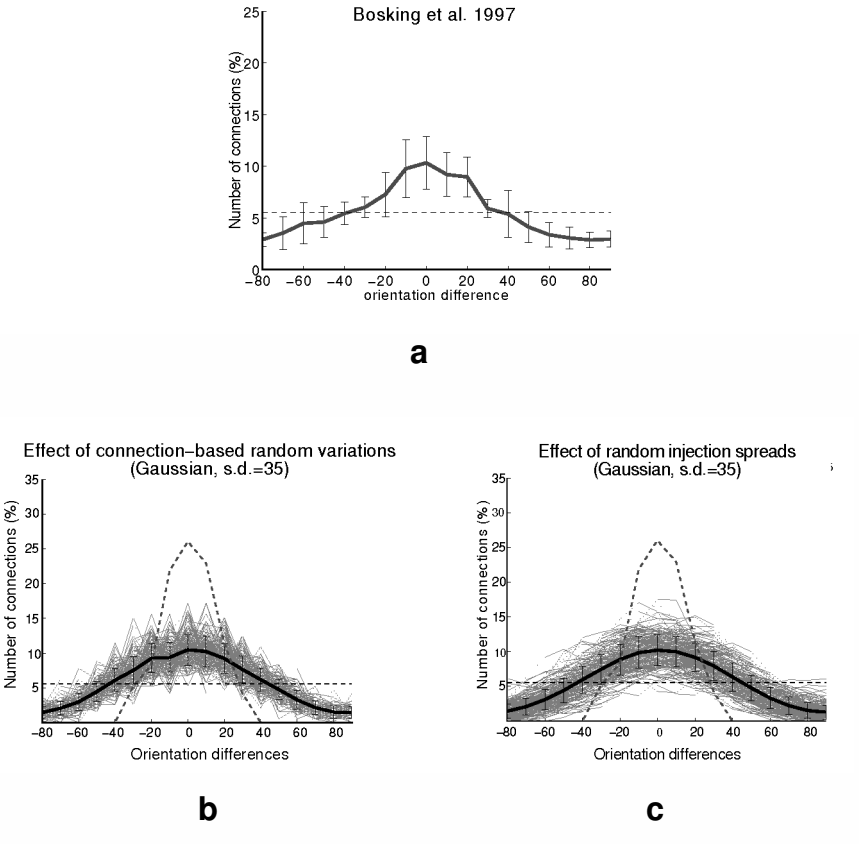

Figure 3: Results of a statistical pertubation of collinear connectivity distribution. (a) Mean connection distribution computed from the data in Bosking et al. (1997), shown here for reference. Error bars are ±1 standard deviation. Note the unimodal distribution that peaks at approximately 11%, the wide spread, crossing of the uniform distribution (dashed horizontal line) around ±40 degrees, and the nonmonotonic variance. Can all these features be replicated by applying noise to the base distribution induced by the standard colinearity model? (b) Result of simulating physiological deviation at the individual connection level. The dashed line is the base collinear distribution. The gray region is the superposition of individual applications of the noise model to the base distribution. The solid graph is the expected distribution, and error bars are ±1 standard deviation. Permitting large enough developmental variations (shown here is the result of wrapped gaussian independent and identically distributed noise of s. d. = 35°) in the connections to model the first-order statistics significantly violates the underlying connectivity principle of good continuation but still cannot model the second-order statistics. (c) Results of simulating measurement errors due to leakage in the injection site. All parts are coded as in *b*. Again, permitting large enough injection spread to model the first-order statistics (shown here is the result of gaussian noise of s.d. = 35° and assuming 20 cells per injection site; (Bosking et al., 1997) cannot model the second-order statistics