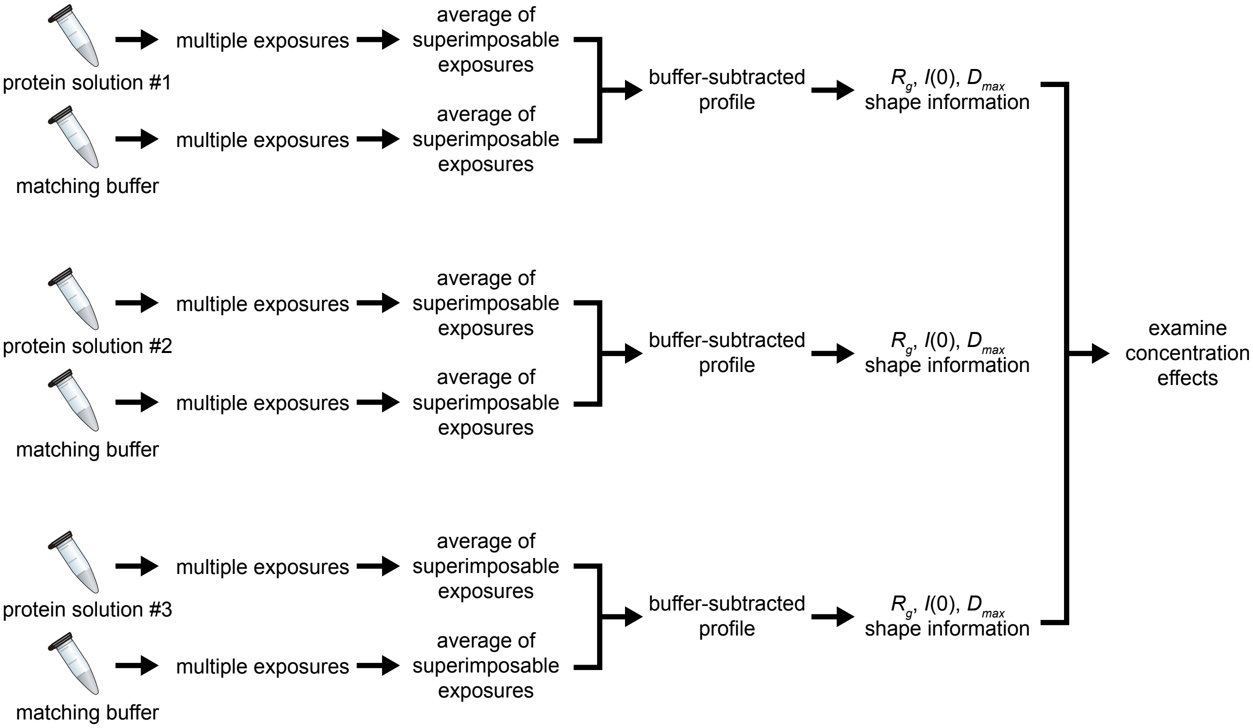

Planning a concentration series experiment. To perform a concentration series experiment, proteins solutions must be prepared at three or more protein concentrations in the same buffer (here, represented as protein solutions #1-3). For each sample, the total volume should be equal to or greater than the minimum volume required by the sample cell. Recipes should be designed such that mixing volumes can be pipetted accurately. Multiple X-ray exposures are collected on each protein solution and matching buffer as described in the Procedures. Data are then reduced (i.e. by averaging and subtraction) in order to produce a single background-subtracted scattering profile, from which structural information can be gained. Multiple background-subtracted scattering profiles at different protein concentrations are then required to examine concentration effects and estimate structural parameters, such as R_g at infinite dilution. As many exposures are generated in a single experiment, careful and detailed documentation is indispensable.