Erratum: Possibility of single biomolecule imaging with coherent amplification of weak scattering x-ray photons [Phys. Rev. E 78, 041906 (2008)]

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In my recent paper, Eq. (12) was mistakenly derived. The author would like to apologize for such a mistake, and present here a revised equation and additional explanation.

The improvement in S/N can be estimated as

$$\frac{S/N|_{\text{holography}}}{S/N|_{\text{direct}}} = \frac{\sqrt{I_1 I_4}/\sqrt{I_1}}{\sqrt{I_3 I_4}/\sqrt{I_3}} = 1. \tag{12}$$

Therefore S/N will not be improved nor deteriorated with this method. In the single biomolecule imaging, the average number of photon in each pixel is lower than 1, thus the signal level is lower than the noise level (Poisson noise). This situation cannot be improved by attaching the gold particle. The signal level increases as $\sqrt{I}$; at the same time, the noise level also increases $\sqrt{I}$. Thus the S/N ratio remains constant. As a consequence of constant S/N, the author would like to point out that there are no improvements in phase retrieval process based on the assumption of high S/N as originally claimed in Sec. V.

On the other hand, the signal amplification and the holographic fringes will help the classification of diffraction data, which is more important for the 3D structure reconstruction of biomolecules. After the classifications, averaging the diffraction data will improve the S/N ratio and provide better resolution.

The instrumental noise (CCD electrical noise, for example), and the background noises due to x-ray stray beams can be effectively reduced by introducing the gold particle.

