Alignment issues in X-ray cone-beam microtomography

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The resolution and reconstruction accuracy in X-ray cone-beam microtomography[1] not only depend on the source size, but also the alignment of the source-specimen-detector assembly (Fig 1). There are degrees of movement freedom in the specimen and detector orientations, namely roll, yaw and pitch as well as linear translation of the detector about the center axis[2]. Hardware alignment becomes increasing difficult as the magnification and resolution increase. We have investigated the possibility of obtaining geometrical misalignment information from 2D projections and 3D reconstructed data, then, system alignment can be made by hardware adjustment and in software pre-process compensation to achieve optimal reconstruction accuracy. Our current software allows detailed analysis of the system alignment and reports important alignment parameters which can be used in both hardware and post-accusation realignment.

Fig 1: Geometry of the cone-beam tomographic system. Fig 2 and 3: Cross sectional images of an optimally aligned (Fig 2) and a detector linear-translational-misaligned (x axis) (Fig 3) snail shown in Fig 6. Fig 4 and 5: 3D reconstructions of maize and rice spikelets respectively. Fig 6 and 7: 3D reconstructions of small snails. (60.5kV, source size 5um)


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