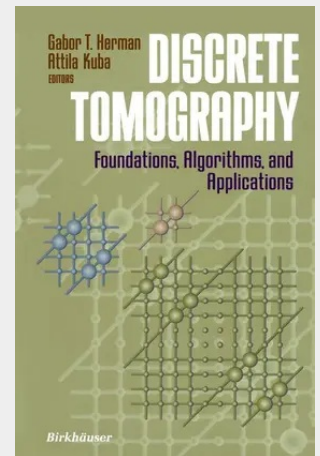


Discrete Tomography

Foundations, Algorithms, and Applications

Goals of the Book Over the last thirty years there has been a revolution in diagnostic radiology as a result of the emergence of computerized tomography (CT), which is the process of obtaining the density distribution within the human body from multiple x-ray projections. Since an enormous variety of possible density values may occur in the body, a large number of projections are necessary to ensure the accurate reconstruction of their distribution. There are other situations in which we desire to reconstruct an object from its projections, but in which we know that the object to be reconstructed has only a small number of possible values. For example, a large fraction of objects scanned in industrial CT (for the purpose of nondestructive testing or reverse engineering) are made of a single material and so the ideal reconstruction should contain only two values: zero for air and the value associated with the material composing the object. Similar assumptions may even be made for some specific medical applications; for example, in angiography of the heart chambers the value is either zero (indicating the absence of dye) or the value associated with the dye in the chamber. Another example arises in the electron microscopy of biological macromolecules, where we may assume that the object to be reconstructed is composed of ice, protein, and RNA. One can also apply electron microscopy to determine the presence or absence of atoms in crystalline structures, which is again a two-valued situation.

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