Pencil Beam Dose Calculation Algorithm

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The following description is meant to give the reader a simple conceptual grasp of the pencil beam dose calculation algorithm. It is not exhaustive in its detail and practical implementations obviously incorporate many more details and complexities than are described here.

The “pencil beam” algorithm is dose calculation technique. It assumes that any collimated photon beam hitting (incident) on the patient is actually a conglomeration of lots of smaller, narrow “pencil beams”. Each of these pencil beams has a central axis ray along which it deposits some dose. The dose deposition pattern varies with the intensity and the spectrum of the beam that is incident on the patient.

The arrangement and weighting of the pencil beams is defined by the field shapers (linac jaws, blocks, multileaf collimators). Where the linac beam profile is non-uniform or modulated (e.g., IMRT) the weighting of each pencil beam is adjusted appropriately. In practice this weighting includes the primary photon intensity at the entry point on the patient and also electron contamination. The total incident energy in the pencil beam is referred to as the *primary energy fluence*.

But we should start by thinking about just one pencil beam in isolation. This pencil beam will have a very small diameter on the surface (a wise guy might say it could be infinitesimal!). When that pencil beam hits the surface, there will be dose deposited under the surface (water if it is a phantom). That dose will have a definite spatial distribution in the water, and it will happen according to the basic scattering and absorption processes that the photons and secondary electrons undergo. Which is to say, it will be spread out. This tear-drop/pear-shaped distribution of dose arising from a pencil beam incident on an absorber is referred to as the *pencil beam dose kernel* or simply the *dose kernel*. For our purposes the dose kernel can be thought of as simply the isodose plot arising from one infinitely narrow pencil beam of photons.

How could we work out what the dose kernel looks like? While in principle it might be possible to set up an experiment with a very small collimator and use very small radiation detectors to map out the resulting dose distribution in water, or some other phantom material, in practice this is a complex undertaking. The more common and more accurate approach is to use Monte Carlo simulations to calculate what the dose distribution from a pencil beam in water would be. These simulations also allow us to generate dose kernels for different photon energy spectra very easily.

How do we use the dose kernel pencil beams to calculate the total dose for a radiotherapy beam? At this point it might help to think of the dose kernel as a little table of dose values representing the dose at each point in space around the incident pencil beam. In order to get the dose distribution for the whole radiotherapy beam we need to add up the dose contribution to each point from each of the adjacent pencil beams which make up the whole beam. The volume of the patient is divided up into dose voxels (sometimes called a “dose grid”) and the tabulated dose values for each pencil beam kernel are superimposed on these. At each voxel in the volume the dose contribution from all the surrounding pencil beams is summed up to yield the total dose at that point. This calculation process is called *superposition*.

In the simplest situation where the dose kernels are all considered to be the same (ie no change of kernels to account for different photon spectra at different points in the beam) and the patient is

considered to be uniform density a mathematical shortcut called “Fourier *transform convolution”* can be applied to speed up the superposition calculation of the dose. For the more general situation however this approach cannot be followed and superposition must be calculated by applying each pencil beam to the dose voxels one by one and adding up the total dose in each voxel.

Real patients have *inhomogeneities*. By this we mean that different parts of the anatomy have different densities (bone, lung, airways, muscle, etc.). Different densities lead to different photon attenuations and dose absorptions. To be useful the pencil beam calculation needs to take this into account. Based on the planning CT image dataset, the density of each voxel in the patient is known. The pattern of dose deposition for each pencil beam (I.e., the “dose kernel”!) can be modified to take these density changes into account. Using the total density of all the material between the point of incidence of the pencil beam and the voxel where we wish to know the dose a scale factor is derived to “stretch” or “squash” the shape of the pencil beam dose kernel. It stretches if the density has been reduced (like with lung), or squashes if the density has been increased (like with bone) In a region of low density the pencil beam dose kernel would in effect be elongated, whereas in a high density region its dimension would contract to account for the higher attenuation coefficient. These corrections are applied to the dose kernel for each pencil beam depending on the local density variations that affect that pencil beam. After that, the same superposition process of summing up the contributions to each voxel from all the nearby pencil beam kernels is followed. Despite these corrections the pencil beam algorithm still suffers from inaccuracies around inhomogeneities.

In practice there are many versions of the pencil beam dose calculation process and each commercial treatment planning system will have a slightly different approach but what has been described above are the main conceptual elements of the scheme. The description above has been given in the context of photon beams but similar approaches can be utilised for electron beams as well.

That in a nutshell is the story of the kernel and the pencil beam algorithm.