Current methods for calculating the normal tissue complication probability use various models for reducing the dose volume histogram of the organ of interest to an equivalent dose-volume step function.

These methods reduce the spatial information about dose distribution. For example two distinct hot spots can yield a DVH identical to a single hot spot of equal volume. Furthermore the dose limits physicians recommend are usually of the type "no more than x gray, to no more than y percentile of the organ".

We propose a model for calculating the complication probabilities for normal organs based on the size and topology of hot spots.

The underlying supposition is that a complication will occur if a connected subvolume of the organ of interest accumulates enough damage. Dose average over the subvolume of interest measures the extent of the tissue damage. We use a linear expansion of the biological dose response curve around the average dose. Because of this assumption we are able to ignore the details of this curve. Complication will occur when the average dose exceeds a volume dependent threshold. The model uses the power law to scale the dose average for the different volumes. The model for the distribution of the complication threshold in the population is a logistic distribution.

The model implicitly allows the existence of threshold volumes.

We applied this method to a group of 74 patient treated for prostate carcinoma and estimated the model parameters and the size of the hot spot for each patient.