

VOX:	based on counting voxels
DT:	based on distance transformation (filling structure with spheres)
TRI:	based on triangularization of surface (thus one more interpolation step in comparison to VOX)

Indices

TV:	total volume [mm ³]
BV:	bone volume [mm ³]
BV/TV:	relative bone volume [1] ("Percent")
Conn.D.:	connectivity density, normed by TV [1/mm ³]
SMI:	structure model index: 0 for parallel plates, 3 for cylindrical rods
Tb.N:	trabecular number [1/mm]
Tb.Th:	trabecular thickness [mm]
Tb.Sp:	trabecular separation = marrow thickness [mm]
DT-Tb.1/N.SD:	standard deviation of local inverse number [mm]
DT-Tb.Th.SD:	standard deviation of local thicknesses [mm]
DT.Tb.Sp.SD:	standard deviation of local separations [mm]

Note

These DT indices are calculated without assuming anything about the shape of the bone (i.e. without plate model assumption). SDs: with the DT operation, a local thickness/separation for every voxel within bone is calculated. A histogram of local thickness/separation values can be obtained, and a mean and SD of this distribution is calculated. [Explanation for Tb.1/N.SD: First answer: forget about it, take Tb.Sp.SD. Detailed answer: For DT-Tb.N, the histogram is actually of the local separation of the skeletonized structure, thus 1/N. The mean value can be inverted to give Tb.N, but the SD only makes sense as Tb.1/N.SD]

Mean1:	Mean voxel values of everything within volume of interest (mixture of bone and background). If scan was calibrated for bone, then the mean voxel value is in units of Hydroxyapatite density [mg HA/ccm], otherwise in linear attenuation coefficient [1/cm], Hounsfield [HU] or native file number [1] units Mean1: Mean of bone AND marrow -- 'apparent density' 'BMD'
Mean2:	Mean of segmented region, thus lin.att. only of what was considered bone Mean2: Mean of what was considered bone only --- 'material density:'TMD' or 'DMB'