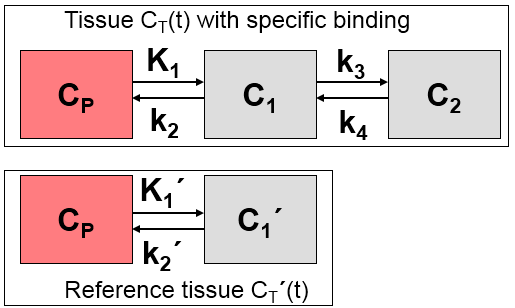
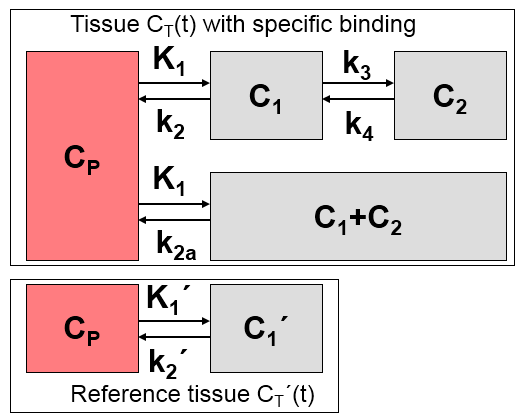
**Simplified Reference Tissue Model (SRTM) for PET Receptor Studies**

**Full Reference Tissue method**

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C\_Model(t) = R\_1 { C\_T‘(t) + aC\_T‘(t)(\*)exp[-ct]+ bC\_T‘(t)(\*)exp[-dt]}

**vs. SRTM**

Defining

R\_1=K\_1 / K\_1‘

C\_Model(t) = R\_1C\_T‘(t) + {k\_2 – R\_1k\_2 / (1+B\_NP)}C\_T‘(t) (\*) exp[-k\_2t/(1+BP\_NP)]

Assumptions:

distribution volume is the same for the tissue of interest and the reference volume:

K\_1/k\_2 = K\_1‘/k\_2‘

tissue TAC can be fitted by a 1-tissue compartment model

Unknowns:

R1, k2, BP\_ND

k\_2‘ and k\_2a are provided