| Baseline (t_1) | Pre-treatment (t_2) | Post-treatment (t_{3D}) |

Y_i^{t1} Y_i^{t2} Y_i^{t3D}

1   N   2N   3N

$Ht(\pi_i^{t2}, \pi_i^{t3D})$

$Ht(\pi_i^{t1}, \pi_i^{t3D})$

Y_i^{t1} Y_i^{t2} Y_i^{t3D}

1   N   2N   3N

$Ht(\pi_i^{t1}, \pi_i^{t2})$

$Ht(\pi_i^{t1}, \pi_i^{t3D})$ & $Ht(\pi_i^{t2}, \pi_i^{t3D})$ $\overset{?}{>}\overset{?}{>}$ $Ht(\pi_i^{t1}, \pi_i^{t2})$

N: length of genome sequence of interest
$Ht(\pi, \pi')$: transformed Hellinger distance between distributions π & π'