df_ShiftRaw

ID	chr	window_old	window	frac_sampleName	div_sampleName	
Chr + window_old	chr name		shifted to global position on genome	fraction of window for which div could be evaluated + "Sample Name" e.g. vu-bb-15-1	$\pi / \theta / D$ for this window	ea,
NC_003279.85000	NC_003279.8	5000	5000	0,967	0,0024	

df_ShiftNorm

stays · multiplied per window

	divNorm_sampleName
	0,0023

Overview

ID	institution	treatment	inst_treat	week	rep	div_mean	div_std	divWeight_mean	divWeight_std
Sample ID = Institute + treatment + week + replicate									
VU_bn5_15_2	vu	bn5	vu_bn5	15	2	0,0016	0,0031	0,00163	0,00309

div_mean/div_std: simple mean for all diversity values in df-shiftRaw (& std)

divWeight_mean/divWeight_std:
$$\text{div}_{weight} = \frac{\sum_{i=1}^{n} \text{div}_i \cdot \text{frac}_i}{\sum_{i=1}^{n} \text{frac}_i}$$
→ Calculated using df-ShiftNorm