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The user has the option to provide a custom pathways database to HUMAnN 3.0 and to use all pathways instead of the minimal pathways computed by MinPath. To account for non-linearity in the conversion of gene copy number to pathway copy number, we define a "compression constant" (k) equal to the total pathway abundance divided by the total ...

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where k is the size of the alphabet (e.g. 4 for DNA, 20 for amino acids) and the values 1 to k correspond uniquely to one of the characters. O_j is the character frequency in the sequence tested. E_j is the overall character frequency from the entire alignment.

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