5.1 - Linear Program

We interpret *G* with each edge Unknown macro: 'mathinline' colored by read mappings as a flow network, considering the read volume assigned to every (super-) edge as a flux created by the expression of the underlying supporting transcripts *T*.Consequently, given an edge Unknown macro: 'mathinline' the contribution of the supporting transcripts Unknown macro: 'mathinline' to the flux Unknown macro: 'mathinline' observed along e can be described by a linear equation

Unknown macro: 'mathinline'

(**Equation 1**)

where f_i represents a factor that expresses the fraction of the respective transcript expression t_i observed between $tail_e$ and $head_e$. In the trivial case, f_i corresponds to the proportion of the interval [$tail_e$; $head_e$] in comparison to the entire length of the processed transcript. The correction factor Unknown macro: 'mathinline' in Eq.1 is to compensate for divergence from the expectation created by stochastical sampling intrinsic to RNA-Seq experiments.

The crux of the flux is that an RNA-Seq experiment provides a series of observations on the underlying expression level t_i along the transcript body. Following tradition in transportation problems, we model all of these observations as a system of linear equations by inferring Equation 1 on all Unknown macro: 'mathinline'. Subsequently, the linear equations spanned by a locus are resolved by the objective function

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(**Equation 2**)

Solving the linear program (Eq.2) imposed by a locus intrinsically provides an estimate for the expression level t_i of all alternative transcripts that are annotated.