For a $r{\times}c$ frequency table, n_{ij} is the frequency in the ij cell, where $i = 1,\ldots, r$ and $j = 1,\ldots, c$. We denote the expected frequency (under the hypothesis of independence) in cell ij as m_{ij}.

Then, a saturated Log-Linear model for a two-dimensional table such as ours is:

$$log\left(m_{ij}\right) = u + u_{C(i)} + u_{S(j)} + u_{CS(ij)}$$

where u is the overall mean:

$$u = \sum^{r}\sum^{c} \frac{log\left(m_{ij}\right)}{rc}$$

$u_{C(i)}$ is the factor C (here, chromosomes) main effect:

$$u_{C(i)} = \sum_{1}^{c} \frac{log\left(m_{ij}\right)}{c} - u$$

$u_{S(j)}$ is the factor S (here, sites) main effect:

and $u_{CS(ij)} = log\left(m_{ij}\right) - u - u_{C(i)} - u_{S(j)}$ is parameter representing the interaction between the main factors *(CS)*.