## Calculation of protein expectation value from peptide expectation values in $X$ ! Tandem:

Assume that an experiment has generated $s$ mass spectra. If a protein sequence is being inferred from the observation of $n$ unique peptide sequences, each of which has been assigned an expectation value $e_{j}$, then the expectation value for the protein, $E_{p r o}$, is given by:
$E_{\text {pro }}=\left(\frac{\beta^{n}(1-\beta)^{s-n}}{s N^{n-1}}\right) \times\left(\prod_{j=1}^{n} e_{j}\right) \times\left(\prod_{i=0}^{n-1} \frac{(s-i)}{(n-i)}\right)$
where
$\mathrm{N}=$ peptide sequences scored in to find the n unique peptides
$\beta=\mathrm{N} /($ total number of peptides in the proteome considered)
In the exceptional case that only one peptide has been observed, $E_{p r o}=\mathrm{e}_{1}$
The following page shows the code used by X ! Tandem to implement this equation.

```
/*
    * expect_protein is used to assign the expectation value for a
protein, if more than one peptide has been found for that
protein. the expectation values for the peptides are combined
with a simple Bayesian model for the probability of having two
peptides from the same protein having the best score in
different spectra.
    */
double mprocess::expect_protein(
    const unsigned long _c, // number of peptides found
    const unsigned long _t, // number of total spectra
    const unsigned long _n, // number of peptides considered
    const double _d // sum of log peptide expectation values
    )
{
    double dValue = _d+log10((double)m_tProteinCount);
    if(_c == 1 && _d < 0.0) {
        return _d;
    }
    else if(_c == 1) {
        return 1.0;
    }
    if(_c == 0) {
        return 1.0;
    }
    double dN = _n;
    double dK = _c;
    double dV = _t;
    unsigned long a = 0;
    while(a < _c) {
        dValue += log10((dV - a)/(dK - a));
        a++;
    }
    dValue -= log10(dV);
    dValue -= (dK-1.0)*log10(dN);
    double dP = dN/(double)m_tPeptideCount;
    if(dP >= 1.0)
        dP = 0.9999999;
    double dLog = dK*log10(dP)+(dV-dK)*log10(1.0-dP);
    dValue += dLog;
    return dValue;
}
```

