

Mass Transfer Nodal Results

The mass transfer nodal results (.UMN) are the concentration of each specie.

Main Header:

The main header appears once in the results file and has the following format:

| Variable | Type | Description |
|---------------------------------|----------------|--|
| TimeStepCount | 4-byte integer | The number of time steps in the results file. |
| SpeciesCount | 4-byte integer | The number of active species in the results file. Note that the model may have other species defined that are inactive (are not used in any part). |
| ResultsPerNode | 4-byte integer | The number of results per node. |
| NodeCount | 4-byte integer | The total number of nodes in the model. |
| Version | 8-byte real | The version number of the results file. This documentation is for Version = 1.0. |
| NDYN | 4-byte integer | The analysis code |
| ICode | 4-byte integer | The active direction code |
| Reserved(1) through Reserved(4) | 4-byte integer | Four values reserved for future development. This creates a "buffer" so that the length of the header can remain fixed. |

Total length of Main Header = 36 bytes. [Constant in all models]

Results:

The results consist of the specie concentration for all time steps, all species, all nodes. The data is ordered as follows:

```

Time Step #
  Specie #
    Node #
      Result 1 through result "ResultsPerNode"
        Next Node #
          Next Specie #
            Next Time Step #

```

The results at each node are as follows:

| Variable | Type | Description |
|---------------|-------------|--|
| Concentration | 8-byte real | The concentration of the specie at the node. If the specie does not exist at the node, the value will be NaN (not a number). |

Total length of all results = TimeStepCount x SpeciesCount x NodeCount x 8 bytes