SRS Tech Note

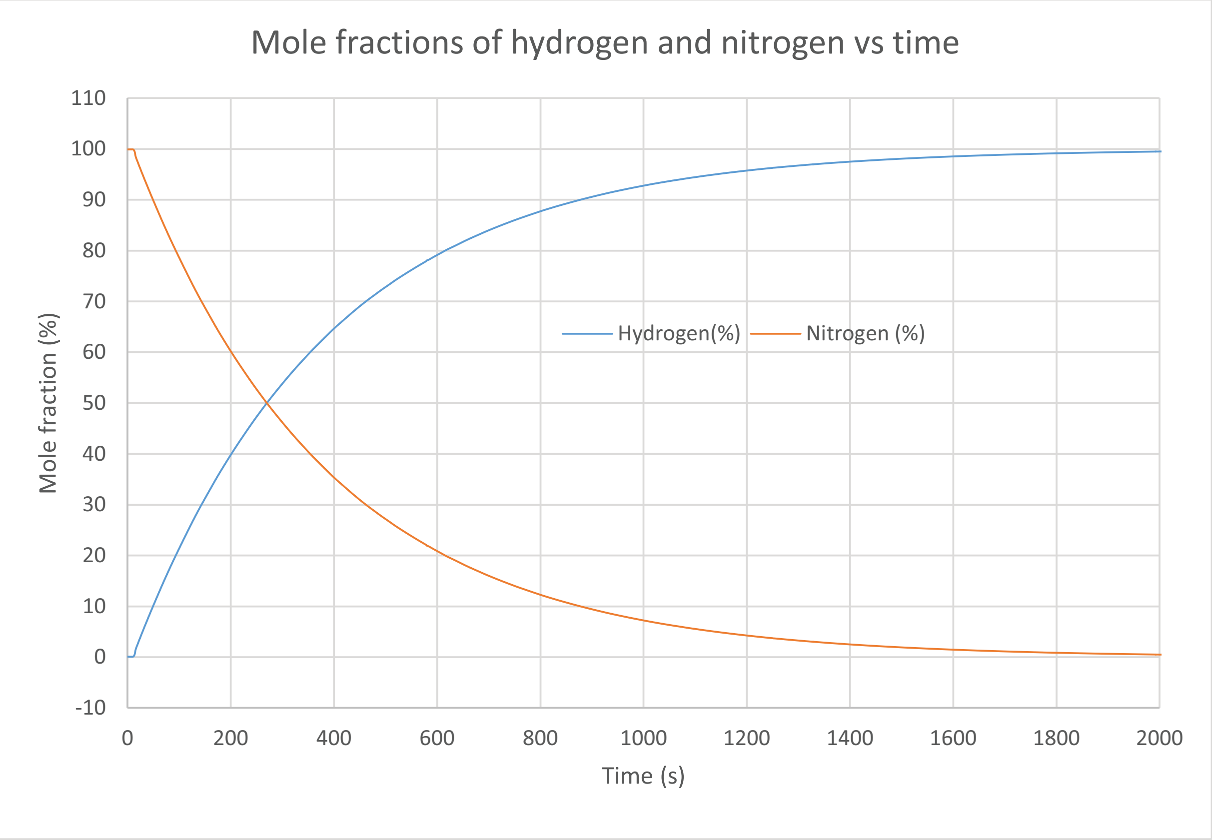
Accuracy of BGA244 for Measuring Mixtures of Nitrogen and Hydrogen

J. Willison, November 18, 2015

The BGA244 Binary gas analyzer can be used to accurately measure the composition of a wide variety of binary gas mixtures. The instrument's high resolution and stability (a few ppm for the speed of sound and the temperature), and its database of thermodynamic properties for about 500 gases, enables the instrument to make composition measurements of thousands of gas mixtures with a typical mole fraction accuracy of 0.1%.

The purpose of this application note is to demonstrate the accuracy of the BGA244 for mixtures of nitrogen and hydrogen. A simple arrangement was used to test the BGA244 over a wide range of mixtures: The BGA244's 130 cc acoustic cavity was filled with pure nitrogen, data recording was started, and (after about 10 seconds) a flow of 20 sccm of hydrogen was started. To prevent backflow, the cavity was vented through a narrow tube into the room at 14.7 psia. The hydrogen flow eventually purged the cell of nitrogen, exponentially converging to pure hydrogen with a time constant given by the (Cell volume) / (Flow rate) = 130 cc/20 sccm = 6.5 minutes = 390 seconds.

The SRS monitoring program, BGAMon, was used to record the BGA244's reported values of the mole fractions of nitrogen and hydrogen as the cell was purged. Actual data from the scan is graphed below:



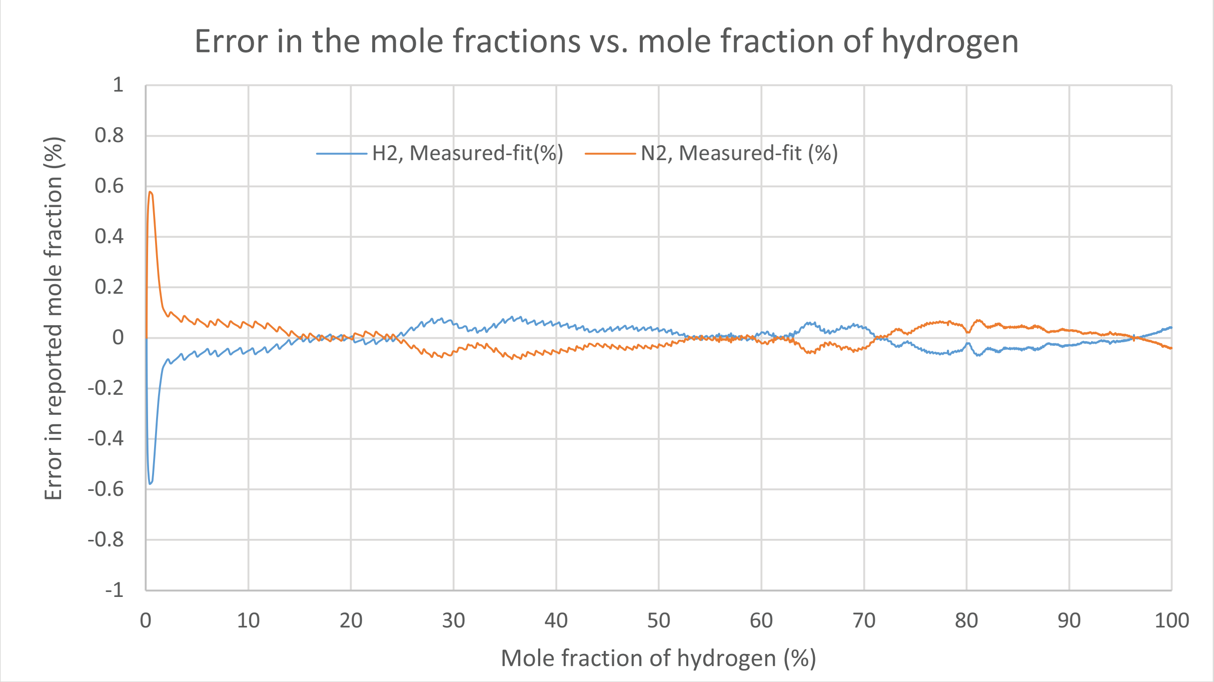
Analytic fit to exponential mixing

For $t \geq t_0$, (t_0 is the time when the hydrogen flow started) the mole fraction of nitrogen was expected to follow this equation:

$$Mole\ fraction\ of\ nitrogen(t) = A \cdot e^{-(t-t_0)/\Gamma}$$

We used $A = 100\%$ with $t_0 = 10\ s$ and $\Gamma = 390\ s$ as initial estimates. A least-squares fit of this equation to the measured mole fraction of nitrogen vs. time improved the initial estimates, finding $t_0 = 9.313\ s\ and\ \Gamma = 376.324\ s.$

With the assumption that the system conforms to the exponential mixing model, we can estimate the error in the reported mole fractions by taking the difference between the measured concentrations and the exponential fits. Those residuals are shown below:



Conclusions

The mole fraction errors are less than 0.1% over the entire scan. (The ±0.6% errors at the start of the scan, which are barely visible in the full scale mole fractions graph, are due to the temperature transient caused by starting the flow of hydrogen.) In cases where better accuracy is required close to 0% or

100%, the user can use the “Rel” feature of the instrument, declaring the current cell contents to be 0% or 100% mole fraction. After doing so the mole fraction accuracy will typically be ±10 ppm.