# Modeling Yeast in Suspension Part 2: The Efficacy of Applying Models to Commercial Quality Control Data.

TL;DR: I want to try and apply the models for the dynamics of yeast in suspension that I implemented in a previous paper to real commercial brewery QAQC data and see if it actually works. I need your help, via supplying data and professional input for this project, and hopefully going forward as I work to develop more free analytical tools in R for breweries to use in their QAQC programs.

## Project Description

The dynamics of yeast populations during brewery fermentations are important in determining the quality of the final product. Many environmental aspects (temperature, specific gravity, pH, etc.) as well as demographic factors (yeast pitching rate, age, health, etc.) and genetics (yeast strain, flocculin mutations) can impact the population dynamics of yeast, ultimately impacting the flavor of the beer. As a result, maintaining consistent conditions that result in consistent yeast population dynamics will result in consistent product quality. A lot of effort from the QAQC program goes into ensuring that these consistent conditions are well maintained in the hopes of keeping the fermentation remains consistent. However, there are not really any good analytical tools available to determine how successful these attempts are at maintaining consistent yeast population dynamics. Developing such a tool is the goal of this project.

Yeast populations grow logistically during fermentation, reaching a plateau in population growth once they have depleted available sugars. Typically, the total population size would be inferred from determining the density of cells in suspension, however, in commercial brewery fermentations, there is a second process at play, flocculation, that also influences population dynamics. Flocculation is the process by which yeast cells (aided via cell surface adhesin proteins) clump together forming flocs which rapidly precipitate out of solution. This results in the observed pattern of cells in suspension not resembling logistic growth, but rather some form of hump shaped population curve.

I’ve previously tried to describe the shape of that curve using a variety of models (with good success, see the attached paper if interested), but that was limited to data collected from a laboratory setting, in which there were tightly controlled conditions, and very frequent sampling. From that data, I simulated “brewery” data sets with fewer data points that would be more typical in a commercial data set, but this approach is likely of limited applicability. For example, difficulties in getting accurate cell counts, either due to issues with sampling from the tanks (due to extra yeast clumps aggregating around sample valves), or in the counting method used could result in significant irregularities in the results. Additionally, none of the now common brewing practices and process aids (like dry hopping, cold crashing, filtering, centrifuging, etc.) were included or considered.

I have been working with Bertille Smith (who I will introduce later) to get the models implemented with a data set from First Magnitude Brewery here in Gainesville, and we’re pretty much ready to go. We’d like to look at this from the perspective of several brewery sizes, thus wanting to bring people from multiple QAQC programs as well. For this project, we mostly just need help in providing the data, which includes all the knowledge around how the data is generated, methods and brewing practices used, etc. (no small feat). Ultimately, we’ll all be authors on the manuscript for this project that I’m planning on submitting to the ASBC journal. I am hopeful it won’t be too much of a time sink for anyone and provide cool results in the end.

## Future directions

In the future, I am also planning to continue this research on to the next natural steps. For example, I have been implementing similar models for specific gravity and pH, and I want to put together a framework to simplify making comparisons across fermentations to track consistency (rather than just tracking OG and FG for example). And on from there. This includes implementing these and other useful methods in a new brewing data analysis package for R (currently called brewnalysis, which is in the early development stage with this project), which will be freely available. I know that R has a significant learning curve, but I’m hoping to make the package easy to use in general and develop tutorials on how to use it so that more people get interested.

But I want to make sure it is useful, so I’m hoping to get continued input (and data for analysis/validation of the methods) in the future too, so if this project works out for everyone, I’m hoping to keep on working.