After reading “Capturing Heterogeneity in Gene Expression Studies by Surrogate Variable Analysis” by J. Leek and J. Storey, please respond to the following questions.

1. The authors state that expression heterogeneity (EH) due to technical, genetic, environmental, or demographic variables is common in gene expression studies. What is actually meant by expression heterogeneity? And what did the authors propose for dealing with it?

2. It is common to classify uncertainty depending on its source (e.g. noise, environmental, modeling simplifications, etc…). If we were to classify EH as a type of uncertainty, what category (or categories) would it fall under? What uncertainty in other fields would be comparable to EH in genomics?

3. The authors propose Surrogate Variable Analysis (SVA) as a way for detecting and handling EH. How can SVA be used to manage uncertainty in other fields?