



Figure 1.2: The phenomenon of enzymatic adaptation revealed in bacterial growth curves. (A) Optical density measurements of *Bacillus subtilis* cultures grown in a mixture of sucrose and either glucose (blue points) or arabinose (green points). Biphasic growth can be observed in the sucrose/arabinose mixture where the pause in growth (white shaded region) corresponds to enzymatic adaptation. Data digitized from Monod (1941). (B) Diauxic growth curves of *Escherichia coli* cells grown on a mixture of glucose and sorbitol in different proportions. Data digitized from Monod (1947). Periods of enzymatic adaptation are highlighted by white vertical lines. In both plots, a univariate spline interpolation was used to draw lines to reflect data presentation of original literature. The [Python code \(ch1_fig2.py\)](#) used to generate this figure can be accessed via the thesis [GitHub repository](#).

nature of allosteric transitions (Loison, 2013; Monod et al., 1963, 1965), a topic that will feature prominently in the remainder of this thesis.

The diauxic growth transitions shown in Fig. 1.2 illustrate adaptive processes across the biological scales, as were schematized in Fig. 1.1. While it was not known to Monod at the time, we now know that many cases of enzymatic adaptation are driven by the regulation of gene expression. As the bacterial culture approaches the auxic shift, the presence or absence of the substrate is sensed by regulatory molecules that control whether the genes encoding the enzymes for metabolism of the substrate are expressed. This represents the level of *molecular adaptation* where, given binding or unbinding of the substrate molecule, the activity of the regulatory protein is modulated. The amino acid sequence of these proteinaceous regulators are the product of billions of years of evolution with regions of the protein (such as the DNA-binding and inducer-binding domains) under-