How much information does simulation data contain about a biological process?

If the simulation data turns out to be highly compressible via some transform, could we then hope to produce the simulation data more efficiently?

In particular, could we do so, in the absence of prior knowledge of the exact type of compressibility in the final data?

Suppose we are interested in answering certain high-level queries about the outcome of a simulation.

The answers will depend on computing certain functionals and predicates on the variables computed by the simulation.

If we knew in advance these functionals or predicates, could we compute their values, or good approximations to them, without running a full simulation?