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The Science Daily article “Small Babies, Big Data” discusses how scientists discovered new information about molecular changes during the first week of human development. In the past, it has been hard for scientists to gather information about the first week of development because babies are too vulnerable for large amounts of blood sampling. However, scientists recently developed methods to analyze newborn development using uncommonly small blood samples (less than 1 ml of blood). With these samples, scientists found thousands of molecular changes. These changes included those in gene expression, immune defense, neutrophil function, and complement pathways. Scientists found these changes in two distinct cohorts of babies and therefore suggest that similar developmental paths may be present in all newborns. The article expresses how these findings may create a baseline for future medical studies involving newborn babies.

While the Science Daily (or non-science) article “Small Babies, Big Data” accurately summarizes the main implications from its scientific journal counterpart, it also simplifies how the experiment was organized. The non-science article correctly states that scientists analyzed “complex data” to find molecular changes during the first week of newborn life. However, the non-science article fails to explain how scientists studied four distinct developmental areas before using computer software to integrate their data in a systems biology approach. By simplifying how the experiment was structured, the non-science article does not fully convey how the methods were crucial in uncovering the experimental results. The article needed to outline the scientists’ step-by-step approach for the reader to grasp the significance of the experimental findings.

The four developmental areas laid out in the science journal article (Lee et al., 2019) were the immune system, transcriptomics, proteomics, and metabolomics. After initial data collection, scientists used software to combine information from these four developmental areas. Finally, after data integration, the most important biological pathways to emerge were interferon, neutrophil, and complement pathways. These pathways were not considered important before the data integration step, as before integration it was not possible for scientists to see any hierarchy or relationships in the individual data sets. In contrast, the non-science article reports that interferon, neutrophil, and complement pathways are simply a few examples of many possible developmental changes. The non-science article therefore does not explain how these biological pathways became significant only from analyzing the data in two distinct phases.

The non-science article leaves the reader with the impression that the experimental methods are too complex to understand. The science journal article instead breaks down the experimental processes, allowing the reader to see for themselves how important it is to understand the parts vs. the whole. The non-science article could have taken more steps to help readers understand that individual molecular components purposefully work together to create larger systems involved in human development.

References:

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