



# Similarity network fusion for the integration of multi-omics and microbiomes in respiratory disease

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Shareable abstract (@ERSpublications)

**Similarity network fusion (SNF) is increasingly employed for multi-omics and microbiome data integration and assists patient endotyping. This Methods article describes its performance and explores current and future applications in respiratory medicine.** <https://bit.ly/3gtoYq9>

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Advances in platform technologies facilitate the design of large-scale “multi-omic” studies that encompass genomic, transcriptomic, proteomic, epigenomic, metabolomic and microbiomic components, each representing different views of a single biological specimen [1]. While useful, this is analogous to the “Flatland” *jeu d’esprit*, where the same reality (*i.e.* a sphere of constant diameter) is subject to different interpretations (*i.e.* circles of varying diameter) depending on one’s point of view (from various two-dimensional cross sections). Although each -omics approach has value, they can be even more useful if holistically modelled through appropriate integration. While “mono-omic” analysis has been extremely beneficial, from a systems medicine perspective, this may fail to capture the emergent properties of an individual system and hence may yield limited understanding of non-linear and dynamic features, all of which are increasingly evident in the pathogenesis of respiratory disease [1]. There is clearly a growing need for a more holistic “all in” integration methodology that leverages each distinct -omic dataset derived from multi-omic studies (figure 1). Although several integrative methodologies are available (*e.g.* mixOmics, Anvi’o and integrOmics), similarity network fusion (SNF) has emerged as an appropriate, applicable and robust method in respiratory disease [2–4].