The Abstract "Formula"

An effective abstract has six components:

1. **General Background:** Something that everyone in your audience cares about.
2. **Specific Background:** Zoom in from the thing everyone cares about to the thing you did.
3. **Statement of Problem or Knowledge Gap:** What specific problem or phenomenon do we not understand in this field of study?
4. **Here we show:** One sentence about how you met the demonstrated need.
5. **Results:** Only the very highest-level results. Sometimes a summary of approach comes before the summary of results.
6. **Implications:** So what? What do your results mean for the thing everyone cares about?

This example abstract has been highlighted to indicate the six universal components of a successful abstract:

Ecology drives a global network of gene exchange connecting the human microbiome.

Horizontal gene transfer (HGT), the acquisition of genetic material from non-parental lineages, is known to be important in bacterial evolution. In particular, HGT provides rapid access to genetic innovations, allowing traits such as virulence, antibiotic resistance and xenobiotic metabolism to spread through the human microbiome. Recent anecdotal studies providing snapshots of active gene flow on the human body have highlighted the need to determine the frequency of such recent transfers and the forces that govern these events. Here we report the discovery and characterization of a vast, human-associated network of gene exchange, large enough to directly compare the principal forces shaping HGT. We show that this network of 10,770 unique, recently transferred (more than 99% nucleotide identity) genes found in 2,235 full bacterial genomes, is shaped principally by ecology rather than geography or phylogeny, with most gene exchange occurring between isolates from ecologically similar, but geographically separated, environments. For example, we observe 25-fold more HGT between human-associated bacteria than among ecologically diverse non-human isolates ($P = 3.0 \times 10(-270)$). We show that within the human microbiome this ecological architecture continues across multiple spatial scales, functional classes and ecological niches with transfer further enriched among bacteria that inhabit the same body site, have the same oxygen tolerance or have the same ability to cause disease. This structure offers a window into the molecular traits that define ecological niches, insight that we use to uncover sources of antibiotic resistance and identify genes associated with the pathology of meningitis and other diseases.

General Background
Specific Background
Statement of problem or knowledge gap
"Here we show..." one sentence summary of what was done/learned
Detailed summary of high-level results
Implications