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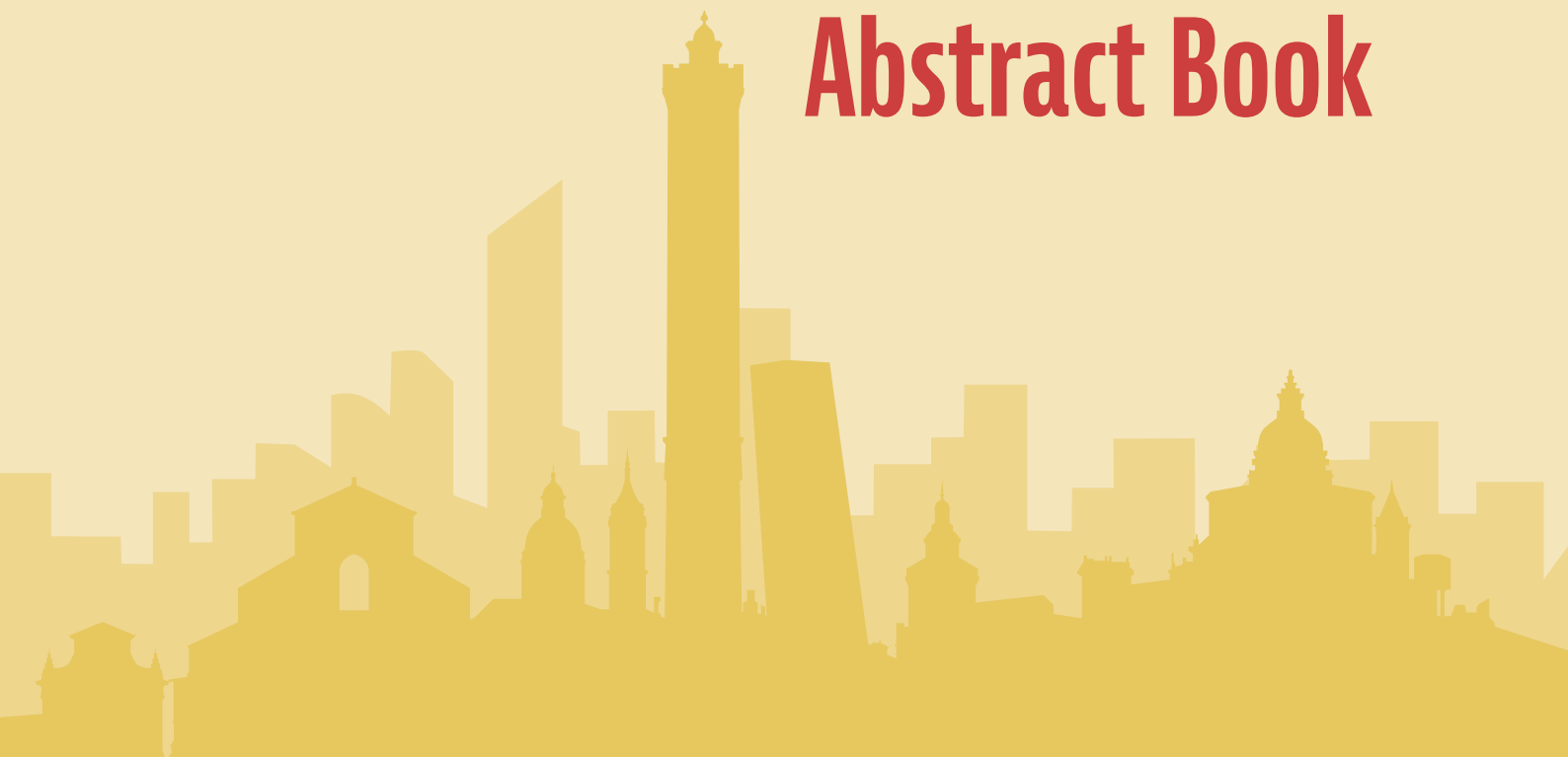
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Like foraging bees

We seek novelty, we need cooperation
and we profit from diversity

Abstract Book



COMPARATIVE POPULATION GENOMICS OF WILD AND MANAGED HONEY BEES

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Abstract

The Western honey bee (*Apis mellifera*) has been kept in hives for millennia and is therefore generally regarded as a managed bee. However, the species has a dual nature, with wild (including feral) colonies being more than twice as abundant as managed ones globally. Since honey bee queens naturally mate with multiple drones drawn from a vast area, and beekeepers have limited breeding control, it is generally unclear whether, or to what degree, managed honey bee populations have been functionally changed by humans. This study aims to quantify genomic signatures of modern beekeeping at a global scale by jointly comparing the genomes of pairs of self-sustaining wild and managed honey bee populations from 15 regions in Europe, Africa, Australia, and North America. We analysed whether wild and managed honey bee populations differ in genome-wide levels of genetic diversity, how the species' original geographic lineages are represented in each group, and whether there are any signatures of adaptation to managed conditions. This study will reveal whether wild honey bee populations harbour additional genetic diversity compared to managed populations and provide insights into whether beekeeping per se leads to honey bee domestication.