We aim to:

- model the emergence of cultural stages in ICE ethnoscapes as experienced by both short- and long-term populations;
- identify those elements of ICE ethnoscapes that are specific to an individual season and those that are repeated;
- relate how the temporal and content stages of ICE ethnoscapes interact with risk, behavior, and injury; and
- demonstrate the utility of electronic and distance-based assisted ethnography in the conduct of social research in ICE environments of Antarctica and, possibly, in space.

We will begin with key informant interviews and focus groups conducted throughout the United States with people who have spent at least one season on the ice in the past 3 years. The purpose is to elucidate the behaviors, risks, and health events that residents face, particularly in the emergence of ethnoscapes. The next phase has us residing in Antarctica for an extended period and conducting participant observation and interviews at two different sites. This phase will include the Self-Disclosure Technique (SDT), an anthropological method for identifying the conceptual structure of a cultural event. SDT will be used to describe cultural dynamics in occupational, recreational, spiritual, and other group activities. Fieldwork will involve both short- and long-term residence. The data will be processed, and models will be tested for validity with informants on the ice.

This research could contribute to the development of screening procedures for long-term residence in ICEs and context-sensitive explanatory models of culture and injury risk, as well as illustrate the utility of distance-based ethnography. (B–027–M; NSF/OPP 01–25893)

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Genomic networks for cold-adaptation in embryos of polar marine invertebrates.

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Although the cold ocean ecosystems comprise 72 percent of Earth's biosphere by volume, they remain sparsely inhabited and relatively unexploited, particularly the metazoan phyla. Consequently, the few animals that can exist at this border of intracellular freezing are ideal for exploring genomic-level processes of environmental adaptation. Understanding life at the margin will convey significant insights into the processes essential for survival under intense selection pressures.

Our study of adaptive mechanisms in genomic networks focuses on a system that faces a formidable challenge at cold temperatures: embryonic development of two antarctic echinoderms, the seastar *Odontaster validus* and the sea urchin *Sterechinus neumayeri*, at sea water temperatures of -1.8°C. We will quantify temperature effects on gene expression and protein turnover networks during early development by using a Bayesian network analysis (a method of statistical analysis) to identify clusters of genes and proteins whose levels of expression are associated in fixed, synergistic interactions. Ultimately, the question to be addressed is whether it is more or less difficult (complex) for an embryo to develop in an extreme environment. To answer this question, we will decipher network topologies and subnet structuring to uncover gene connectivity patterns associated with embryonic development in this polar environment. We also intend to interest students in the developing field of environmental genomics by increasing the awareness of career opportunities within the field and increasing the racial diversity of those attracted to it.

Working in a remote, extreme environment such as Antarctica is always a challenge, but the adventurous nature of the work can be used to establish educational and outreach components of high interest to both undergraduate students and the public. We will bring the experience of working in Antarctica to a larger audience by

- incorporating environmental genomics into a new bioinformatics curriculum being developed at the University of Delaware,
- implementing an intern program to involve minority undergraduates in summer research in the United States and then to bring them to Antarctica to participate