



29th IBA CONFERENCE

**Bridging Science, Practice,
and Community Engagement
for Human–Bear Coexistence**

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**Rewilding
Apennines**

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THURSDAY 14:45 – 14:59 · POPULATION ESTIMATION AND DEMOGRAPHY

Cost-effective actionable data for conservation and management: combining high-throughput sequencing, demographic modelling and citizen science for a large-scale brown bear monitoring programme

Tomaž Skrbinšek, Matej Bartol, Barbara Boljte, Nuša Hrga, Tilen Hvala, Aleksandra Majić Skrbinšek, Elena Pazhenkova, Miha Predalič, Gregor Simčič, Marjeta Konec, Klemen Jerina

Genetic monitoring is for many bear populations the only approach that can provide robust, precise tracking of population abundance. But despite its many advantages, high costs, substantial field effort, and long time to results often make practical application challenging. In Slovenia, we started with brown bear genetics in 2004, which evolved into national-scale monitoring in 2007. In 2015 we switched to genotyping-by-sequencing to improve cost effectiveness, increase reliability, and considerably shorten field-to-results time. We also set the periodicity of genetic sampling to every eight years. Sampling is conducted through citizen science, with results carefully communicated to all stakeholders and participants. As management and conservation decisions require annual data, we developed a demographic model calibrated with genetic estimates and parameterized with the other demographic data. The model is re-run annually using new mortality data and rebuilt with each new genetic sampling. During the third monitoring session in autumn 2023, we collected 2,864 noninvasive genetic samples. Most samples were collected by hunters and foresters. High-throughput sequencing enabled rapid and cost-effective analysis, with laboratory work completed within eight months. The entire study, including capture–mark–recapture modelling, was finalized within ten months. We obtained a population estimate with a narrow confidence interval (Autumn 2023: 737, 695–797; Spring 2023: 1001, 959–1061). The demographic model closely matched the genetic estimate, confirming its usefulness. Over the last 20 years, genetic monitoring has evolved into robust, cost-effective cornerstone of brown bear management. In 2015 Slovenia partnered with Croatia to establish coordinated transboundary monitoring, and in 2026 we launched LIFE DinPin Bear to extend this across the Dinaric–Pindos population. We believe the knowledge gained and methods developed are applicable to other populations as well.

SYDNEY STEPHENS

University of Trento



THURSDAY 15:00 – 15:14 · POPULATION ESTIMATION AND DEMOGRAPHY

No News is Good News: Estimating Latent Recovery from a Managed State within a Survival Model for Grizzly Bears

Sydney Stephens, Mark Haroldson, Matthew Gould, Andrea Corradini, Cecily Costello, Justin Dellinger, Francesca Cagnacci, Frank T. van Manen

Demographic studies of large carnivores often deal with mixed data of individuals with different risk profiles. Management actions can change both an animal's true mortality hazard and its probability of being observed. Obtaining unbiased estimates of survival for the entire population from such data can be challenging. In the Greater Yellowstone Ecosystem (GYE), all grizzly bears (*Ursus arctos*) may be randomly sampled for research, but those involved in human-bear conflicts are targeted for capture and thus represent a biased subpopulation. However, being a 'managed' bear is not a static state; for bears that are released rather than removed, their risk profile may transition to that of an 'unmanaged' bear after a period without subsequent conflict. Yet, during this transition bears are often not collared and thus timing is unobserved (latent). To estimate spatially-explicit survival in the GYE, we adapted a multi-state modeling framework often used in biomedical research to wildlife: using latent states to link observation patterns to state-specific risks. Using a large dataset ($n=600$ bears, F:222, M:378) spanning 15-years (2009–2024), we developed and validated a Bayesian model to jointly estimate (1) bidirectional transitions between managed and unmanaged states and (2) spatially explicit survival in each state, yielding appropriately weighted population-level estimates. Simulations showed that modeling bidirectional state dynamics reduced bias in survival estimates compared with stratified, single-state or one-direction recovery models. Field data indicated a mean recovery rate from a managed state of 26.9 months. The instantaneous hazard of mortality in a managed state ($\lambda=0.0236$) was 472x greater than that of an unmanaged state ($\lambda=0.00005$). This is the combined hazard of management removal ($\lambda=0.0167$) and other mortalities ($\lambda=0.0069$). Our findings highlight the need to integrate state-varying risks on population-level estimates of survival and other events.