Write a draft of your Statement of the Problem section of the proposal. (If you are working on a manuscript, this will still be useful for developing your Introduction section.) Your peers will review this draft and help you to keep developing it through your writing process.

Remember that the Statement of the Problem tells your audience about what the problem is and why they should care about it enough to approve your research.

**Guidelines on the Statement of the Problem**

Be as direct as you can be (2-3 sentences) about the problem your research addresses and exactly what is to be investigated. To amplify the statement, consider the:

* The scope or limitations of the problem;
* Either one or more hypotheses that the research seeks to test or the objectives expected as a result of the study.
* Major assumptions that underlie both the study as a whole and the methodology to be followed should be indicated.

Your draft can be longer than the recommended 2-3 sentences and be revised after it has been reviewed.

For additional guidelines and examples, consult the Graduate School's resources on theses-dissertations: https://web.uri.edu/graduate-s...

Who’s your audience?

* My peers in the writing group
  + Have little to no experience with reduced representation sequencing
  + Good understanding of fundamentals of biology and possibly evolution
  + Interested in writing effectively
* My committee
  + Lots of subject specific knowledge
  + Expert grasp of reduced representation sequencing
  + Understands that gap in research
  + Needs more specific in what EecSeq can offer

Problems?

* NGS techniques are currently limited by sample size
* Reduced representation techniques implemented to increase samples size are not targeted
* Targeted capture approaches require a build up of resources not available for understudied species
* Few sequencing workflows are tested from the lab bench to the bioinformatic deliverables

So what?

* Designing cost-effective and targeted sequencing projects is challenging
* Even with advances in Genome sequencing of animals such as the 1000 genome project, we do not have the resources for many organisms to benefit from targeted approaches

Solutions?

* Conduct molecular combinations of EecSeq probe and capture pool characteristics to provide a guide for others to quickly optimize their own studies
* Cost-benefit analysis and comparing the evolutionary outcomes from each NGS technique including commercial capture probe design can validate the EecSeq is a competitive approach
* Open source bioinformatic pipelines are integral to sharing quick and accurate data analysis.

Benefits?

Issue?

CARS model

Move 1: Establishing a territory [the situation]

Move 2: Establishing a Niche [the problem]

Move 3: Occupying the Niche [the solution]

Final Statement:

Next generation sequencing (NGS) techniques, like whole genome sequencing and RNA sequencing, have greatly increased our capacity to explore issues of genetic conservation and adaptation, but are costly and time-intensive to accurately assess regional population diversity and adaptation. Target capture sequencing allow us to reduce cost and selectively enrich only the specific expressed exons, but this design requires a robust and well-annotated genome. We are developing a novel sequencing technique called Expressed Exome Capture Sequencing (EecSeq) to sequence the exome of any organism rapidly and cost-effectively. Our research will improve and optimize our de novo exome capture laboratory protocols, validate EecSeq against other NGS approaches, and publish a reproducible and open-source data analysis pipeline to provide researchers with the information needed to implement EecSeq for their own questions.

Next generation sequencing (NGS) approaches, like whole genome sequencing and RNA sequencing, have greatly increased our capacity to explore issues of genetic conservation and adaptation, but are costly and time-intensive to accurately assess understudied populations. Target capture sequencing allow us to reduce cost and selectively enrich only the specific regions of the genome that are expressed, called the exome.

Genomic sequencing technologies have significantly altered our approach to exploring the adaptive potential of species in the face of climate change.

Next generation sequencing techniques have greatly increased our capacity to explore issues of genetic conservation and adaptation. Yet technologies like whole genome sequencing and RNAseq are costly and time-intensive to build up the needed resources for understudied species, many of which are the most at risk due to anthropogenic climate change. Targeted capture approaches are an alternative that selectively enrich specific regions of the genome before sequencing, increasing the number of individuals researchers can assess, but the downside to this approach is prior genomic resources are required to design good capture probes. We are developing a novel sequencing technique called Expressed Exome Capture Sequencing (EecSeq) to sequence the exome of any organism rapidly and cost-effectively without the need for prior genomic resources.