Associate Professor Narrative Statement Example B — *"The Investigator"*

Primary Area of Distinction: **Investigation**
A candidate who devotes a majority of effort (> 75%) to investigation with a minority of effort for education and academic service.

Expected Achievements:
- **Established** level in **Investigation**
- Entry level in Education
- Entry level in Academic Service

J.J. SAMPLE, PhD
Assistant Professor, Department of Biochemistry

I am trained in bioinformatics, the computational approaches necessary for analysis of genetic data. I was recruited to UMMS to direct the Department of Biochemistry's Bioinformatics Core and to apply my expertise to research projects in the department. My goals as a faculty member are to provide state-of-the-art resources in these areas for the department and school, to develop and refine technological approaches through my own research, and to educate my colleagues and their trainees on applying these techniques to their research projects. I seek promotion to Associate Professor based on my achievements in the Area of Distinction in Investigation, in Education, and in Academic Service.

Area of Distinction in Investigation

Over the last ten years since my arrival at UMMS, I have built a state-of-the-art Bioinformatics Core for the Department of Biochemistry. In addition to our strengths in computational analysis, we provide next-generation sequencing (NGS) with the acquisition of an Illumina MiSeq. Supported financially by the department and by external funds through research grants to faculty, the Core is self-sustaining and has been able to expand in both personnel and equipment. In the last year alone the Core conducted over 300 analyses and contributed to 23 funded research projects.

In addition to providing support through the Core, I collaborate with other department investigators where my expertise is essential for completing a project or securing external funding. Collaborative studies have included an analysis of mutations causing renal disease, variations in the immune response to influenza, and the mechanism of gene regulation underlying the development of neocortex. These studies have resulted in authorship on 12 peer-reviewed publications in the last five years, as well as 19 abstracts for presentations at national society meetings. My expertise is also in demand for funded research projects: currently, I am a co-investigator with department faculty members on two NIH R01 awards and a core director for a program project grant.

I also conduct an independent research program to develop novel computational approaches for NGS. I am particularly interested in developing algorithms that correct for the biases inherent in sequencing technology. The methods for preparing sample libraries and the choice of primers can introduce consistent errors in the sequence results, particularly in regions with high frequencies of single base repeats. I have developed a set of algorithms for the most common sequencing methods to test for potential errors and apply corrections. This study was recently published (Sample et al., 2017) in Bioinformatics and Genomic Research, a leading journal in bioinformatics. I also was co-author (Sample & Test, 2017) of a review on bias and error in NGS. These studies are funded by a grant from the Beckmann Foundation for which I am P.I.

Note: The information presented here is fictional and does not relate to any real individuals or scientific/medical fact.

I have presented my research at institutes within New England, including Tufts, UConn, and Brown. I was also an invited speaker at a recent meeting of the New England Bioinformatics Group and at the last annual meeting of the International Society for Computational Biology.

Education

One of my goals as a faculty member is to impart my expertise to others in the department. As Director of the Bioinformatics Core, I have developed and implemented a course, Next-Generation Bioinformatics, to train users of the core in the principles of bioinformatics applied to NGS. An average of eight students, postdocs and faculty take the course each year. I also give two lectures each year, on bioinformatics and deep sequencing, in the Biochemistry Program Molecular Methods course. In both cases, my teaching evaluations are above average. I also serve on the thesis committees for three graduate students in the Biochemistry Program. Much of my educational activity, however, is individual and informal—I have educated many students, postdocs and faculty in the methods of bioinformatics and advised them on the best approach to a specific research project. Hopefully, I am considered the "go-to expert" in this area for the department.

Academic Service

In addition to directing the Bioinformatics Core, I chair the department's Research Resources Committee and serve on the UMMS Research Computing Committee. I am an advisor to the UMMS Department of Pathology for development of clinical applications of NGS. I have also been invited as a consultant by departments at other schools (SUNY Upstate, UConn, MCW) to advise on establishing core facilities. I am a peer reviewer for the journals Trends in Biotechnology and Current Opinion in Biotechnology, top ten journals in my field. I am currently a member of the program planning committee for the New England Bioinformatics Group.

Summary

It has been truly rewarding to establish an essential research service and watch it grow and have a measurable impact on department research, in terms of discoveries made, awards funded, projects completed, and papers published. Furthermore, I sense that faculty, trainees and students are becoming increasingly sophisticated in their use of bioinformatics and that the department has been able to keep pace nationally with the development of this rapidly evolving area of science. I foresee continued growth as we tackle the complex genetics of human disease.