This talk will outline the essentials of training in computational skills in bioinformatics and beyond. The need for such training is clear: researchers need to be able to work independently and efficiently using a variety of computational tools. The skills which they require include the ability to automate tasks and build reproducible research pipelines, understand and be able to apply good programming practices in a programming language of choice, as well as being familiar with those software engineering tools that provide relevant support for computational research, such as version control. The skills should scale up enabling researchers to use large computational resources and cloud infrastructure such as Amazon EC2 or Microsoft Azure. The talk will also discuss how much of the training in computational skills is common across biosciences, and how and when it needs to be adjusted for the particular purposes of different disciplines. The example of the successful model of Software Carpentry training shows that building on a common curriculum base makes possible to develop and deliver useful training packages.