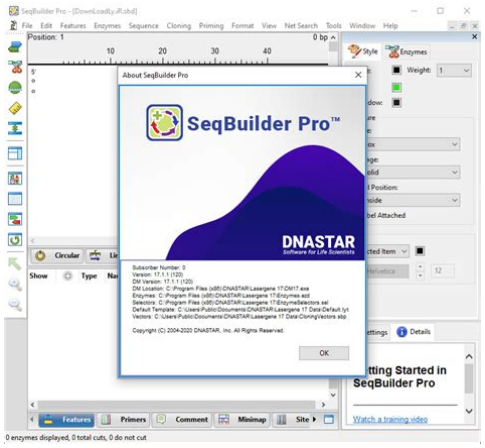
Dnastar Lasergene 8 Manual



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Book Descriptions:

Dnastar Lasergene 8 Manual

Lasergene provides sequence analysis functionality to researchers. The software is available on Windows and Macintosh platforms. The Lasergene product suite includesStandalone and network licenses are available. To take advantage of Vanderbilts 75% discount, visit.We will combine our transformative learning programs and compelling discoveries to provide distinctive personalized care. DNASTAR develops and sells software for sequence analysis in the fields of genomics, molecular biology, and structural biology.Advantage Business Media. By using this site, you agree to the Terms of Use and Privacy Policy. You can easily adjust the parameters with the userfriendly interface. Versatile Tools for the Analysis of Sequence Data After completing the assembly, your analysis is facilitated by numerous tools included with the software, such as a dynamic method for evaluating SNPs, reports for identifying large insertions and deletions, multiple options for automatically annotating your consensus sequence with existing or new features, the ability to design primers for regions of low coverage, the creation of highquality images of your annotated consensus, and more. This license is for commercial users. An academic license 4462914 is also available. For Research Use Only. Not intended for any animal or human therapeutic or diagnostic use.Not for use in diagnostic procedures. I do not think it is any more difficult to use than any other software on the market. It is good that the programs work together and there is no need to change formatI only need the basic Seqman, Editseq and possibly Megalign. Why do I have to pay for what I do not require. Questions to the support are answered fast.http://www.winnerjudo.pl/zdjecia/fck/canon-sure-shot-70-manual.xml

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Industry News DNASTAR Software Identified as Most Accurate NGS Aligner and Variant Caller 09 Oct 2015 James Brindle Easy It’s quick and simple to do Fast Your inquiry will be delivered straight to the manufacturer Free You’re under no obligation Secure We only pass your details on to trusted suppliers at your request Save time Submit your details once and make multiple inquiries. Lasergene provides sequence analysis functionality to researchers. The software is available on Windows and Macintosh platforms. Standalone and network licenses are available. Up until now, this software used an Installer VISE installer, which required me to completely repackage the software for deployment. However, as of Lasergene 13.x, DNAStar has switched to using Bitrock’s InstallBuilder for the Lasergene installer. This tool does not produce standard installer packages, but InstallBuilder installer applications do support installation and uninstallation via the command line. That allows me to run an installation or uninstallation of the Lasergene suite by using the commands shown below That makes it an improvement over the handcrafted installers I previously had to create for Lasergene. So if you install Lasergene as your local admin, that may mean that your users aren’t able to run the Lasergene applications because they may not have permission to run the applications or access one or more of the application data files. For more details, see below the jump. You’ll want to make sure that the your information is correctly set here if you don’t know what to put in, check the Help menu for the Packages User Guide.In the case of my project, I want to install with root privileges and not require a logout, restart or shutdown. For this, you’ll need a postinstall script. Here’s the one I’m using The end result should be that Lasergene installs with the correct permissions. We both can agree that you should not have to perform such grand measures to modify an installer to meet your needs.http://www.pszczelimiod.pl/uppics/canon-sure-shot-sd1000-manual.xml

If you are willing, please contact DNASTAR support , mention my name, and we can work toward

fixing the issues you have discovered. We changed the permissions scheme for the Chemical Component Library in the last release to resolve this crash issue. I am sorry you had to discover a workaround on your own just to launch Protean 3D. Notify me of new posts via email. Published by Oxford University Press. This is an Open Access article distributed under the terms of the Creative Commons Attribution NonCommercial License , which permits noncommercial reuse, distribution, and reproduction in any medium, provided the original work is properly cited. Abstract Advancements in highthroughput nucleotide sequencing techniques have brought with them stateoftheart bioinformatics programs and software packages. Given the importance of molecular sequence data in contemporary life science research, these software suites are becoming an essential component of many labs and classrooms, and as such are frequently designed for noncomputer specialists and marketed as onestop bioinformatics toolkits. Although beautifully designed and powerful, userfriendly bioinformatics packages can be expensive and, as more arrive on the market each year, it can be difficult for researchers, teachers and students to choose the right software for their needs, especially if they do not have a bioinformatics background. This review highlights some of the currently available and most popular commercial bioinformatics packages, discussing their prices, usability, features and suitability for teaching. Although several commercial bioinformatics programs are arguably overpriced and overhyped, many are well designed, sophisticated and, in my opinion, worth the investment. If you are just beginning your foray into molecular sequence analysis or an experienced genomicist, I encourage you to explore proprietary software bundles.

They have the potential to streamline your research, increase your productivity, energize your classroom and, if anything, add a bit of zest to the often dry detached world of bioinformatics. Keywords bioinformatics software, CLC bio, Geneious, genome assembly, nucleotide alignment, phylogenetics software INTRODUCTION Most mornings I wake up to a slew of spam email from biotech companies offering unbeatable bargains on nextgeneration sequencing NGS. These irritating emails underscore an important point massively parallel sequencing has arrived to the masses. Anyone who has ever had something sequenced, such as a genome, transcriptome, gene or PCR product, or used nucleotide or protein sequence data in their research has probably dabbled in bioinformatics. Given the breadth and depth of questions that can be addressed with primary biological sequence information, many of these programs have become immensely popular. Today’s omicsobsessed scientific marketplace is overflowing with bioinformatics programs. Whatever your sequence analysis problem assembling, aligning, annotating, folding, etc., there is probably a program or online application to solve it—skim through the communitymaintained list of bioinformatics software at SEQanswers.com to see what I mean. There are, however, various commercial alternatives, which bring together multiple bioinformatics programs into userfriendly standalone packages. Although beautifully designed, these software suites can come with a hefty price tag, meaning that most researchers, teachers and students are lucky if they can afford just one. Like buying a car, choosing between different suites can be challenging, and there is surprisingly little information appraising the different programs. Here, I describe my own experiences with using commercial bioinformatics packages, focusing on their cost, functions and educational utility.

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A bioinformatics magic bullet During my PhD I spent hours a day at the computer assembling and analysing organelle genomes. Like any decent genomics junkie, I usually had half a dozen different bioinformatics applications running concurrently. Sensing my angst, a colleague recommended that I invest in a commercial, crossplatform, GUIbased bioinformatics package, arguing that it would streamline and simplify my work. I was reluctant to take his advice. I felt that paying for such programs went against the spirit of academic research and that using GUI software would weaken

my computational skills. However, after failing for the fourth time to correctly install and run an opensource genome assembly algorithm, I gave in and bought a userfriendly bioinformatics bundle, and have not regretted it. Show me the money In 2007, with the grant support of my former PhD supervisor, I purchased my first bioinformatics software package. After testing an assortment of programs, I decided on Geneious Biomatters Ltd., Auckland, New Zealand, which was first released in 2005 and is now among the more widely used crossplatform commercial bioinformatics packages Table 1 . I chose Geneious not because it was necessarily better than other software, but because the company offered, and continues to offer, student discounts. As Geneious increases in popularity, so does its price tag. Prices were taken directly from company websites as of 1 June 2014 or were obtained by sales representatives sometime between January and June 2014. Many companies offer a range of pricing and licensing options, and frequently have promo deals.In some cases, de novo assembly features are missing. In several cases, the costs of these software suites were not listed on the company websites or anywhere else online. To get pricing details, I had to request quotes from sales representatives.

On a number of occasions, after requesting quotes or free trial access, I was bombarded with emails and phone calls by sales agents asking whether I had come to any decisions about purchasing the software or whether I needed more information; one time a representative even called a laboratory where I used to work, asking for my current contact details—so if you request a quote, be prepared to be pestered. What do you get for your money and for how long. Purchasing a commercial sequence analysis suite is not as simple as a onetime payment followed by a lifetime of bioinformatics bliss. There can be hidden unexpected costs and clauses associated with running the software and continuing to use it in the future. Most commercial packages include 12 months of free maintenance, upgrades and support. Shortly after I bought my student license for Geneious, the firm released a new version of the software. Because this occurred within 1 year of my purchasing the program, I was able to upgrade to the newest version for free. Although costly, subscribing to the maintenance agreement can be wise. Commercial bioinformatics programs Table 1 , such as Geneious, CLC Genomics Workbench and Lasergene, frequently undergo major changes, which can significantly improve the software. In the past, I have regretted not renewing certain software, and more than once I have bought programs anew at full price because I let the maintenance period expire. Before investing in a bioinformatics package, there are other important details to consider. I suggest asking about the rules on moving the software to another computer, in case, for example, you buy a new laptop or your old one breaks down. I have found that most companies allow users to transfer their software license to a different computer.

But doing so normally requires contacting user support for a new software activation key, and if you have let your maintenance agreement expire, then you might have to renew it before being able to migrate the software. Similarly, if you update your computer operating system—from Apple OS X 10.8 to 10.9, for instance—your bioinformatics package might have to be upgraded as well. Most bioinformatics companies offer their software for both Windows and Apple platforms, and some, including Geneious and CLC bio, have Linux versions too, so in most cases, it is possible to switch operating systems completely and continue running the program. The number of people that can log on depends on the number of floating licenses that were purchased. Floating licenses can also be convenient for groups that have a high turnover—such as those with a lot of summer students and undergraduate volunteers—as they allow software key codes to be issued to individual lab members and then taken back once the member leaves. Sequencher can then be loaded onto as many computers as the owner wants—all that is required to activate the software is plugging in the USB key. But, as I can attest, USB dongles are easy to misplace and, if issued from Sequencher, expensive and inconvenient to replace. Companies like DNAnexus, InterpretOmics, and others are selling bioinformatics as a service, whereby consumers buy online access to powerful computers and

their associated software tools, analysis pipelines and data storage and sharing capabilities. Alternatively, the popular webbased platform Galaxy is a free, opensource, cloudbased bioinformatics tool. It is safe to assume that bioinformatics clouds will only grow larger and more popular over the next few years and are where the most innovative new software will be based. But what does the software actually do. You have paid your money and decided on the best maintenance and licensing options for your needs, now what.

Well, it is time to start examining molecular sequence data and making some big discoveries, of course. Commercial bioinformatics packages bring together, into a single browserbased platform, a diversity of nucleotide and protein analysis tools Figure 1 . These tools do everything from simple pairwise alignments to restriction site and gene predictions to whole genome and transcriptome assemblies. Given the prevalence of highthroughput sequencing in life science research, many of the tools are designed for analysing, visualizing and arranging NGS information.One of the most sought after and marketed features of commercial bioinformatics software is their ability to perform fast, efficient and highquality de novo assemblies of NGS data—taking millions, even billions, of single or pairedend sequencing reads and assembling them into contigs. These kinds of claims are often associated with a white paper describing the software's de novo assembler, including its algorithm, speed and accuracy, how well it performs on standard datasets, such as the human genome, and how it stacks up against other brandname and opensource assemblers. White papers, however, do tend to present commercial software in an overly positive light and—unlike opensource programs—only a few of the widely used proprietary tools have undergone peer review. Commercial browserbased assemblers once had a reputation for being slow, memoryexpensive and inferior to the free opensource alternatives. Early on, I admittedly struggled to generate quality assemblies, even of small genomes, using commercial programs. In recent years, however, proprietary assembly algorithms have improved immensely and are now used by some of the top academic and industrial research laboratories in the world. With software like CLC Genomics Workbench v7, I have been able to assemble draft genome and transcriptome sequences of microalgae from my laptop computer, which has 16 GB of memory and an Intel Core i7 processor.

Many teams are using proprietary tools to assemble complex eukaryotic nuclear genomes, including those of land plants. But these kinds of assemblies require large amounts of time, resources and computing power. Commercial assemblers, unlike certain opensource ones, are also great at handling data from different sequencing platforms, such as assembling a mixture of Illumina, 454, PacBio and Sanger reads Table 1 ; in fact, for many researchers, this is a key selling point. Read mapping, which is when sequencing reads are aligned to a reference, such as an entire chromosome or genome, is another core feature of commercial bioinformatics packages. Like with the de novo assemblers, bioinformatics companies regularly boast about their highly tuned, ultrafast mapping algorithms for referenceguided alignments. The claims can be overstated, but in my experience commercial read mappers are as good as or outperform many of the opensource alternatives. The ultimate test for any assembler or read mapper is whether it is cited in peerreviewed journals. There is no question that opensource programs are cited more than proprietary ones. But citations for commercial software suites, especially their assembly and mapping algorithms, are on the rise and catching up to their opensource counterparts. Skimming through these publications, it is obvious that most papers citing proprietary programs reference a range of opensource ones as well, and that contemporary genomics research often involves a hodgepodge of commercial and free bioinformatics software. More than just browserbased assemblers and mappers Commercial sequence analysis suites, in addition to assembling and mapping NGS data, are designed to carry out the daytoday bioinformatics tasks involved in molecular, evolutionary and genome biology Figure 1 . Although it might sound trivial, one of the more useful features of commercial packages is visualizing, organizing and storing molecular sequence information.

The intuitive graphical interfaces of commercial software allow users to easily build folder hierarchies and dropdown lists of sequence data, move or export these data to different folders and change file formats for use in other applications. In most cases, the software can connect to online resources, such as the National Centre for Biotechnology Information NCBI and UniProt, providing quick direct access to vast amounts of nucleotide and protein sequence information, which can then be downloaded, interpreted and analysed through interactive sequence viewers. My research on organelle DNA has benefited greatly from these types of search tools—in minutes, using commercial software, I can download all of the completely sequenced mitochondrial and chloroplast genomes from GenBank, extract their annotations, sort and search them based on a range of features and transfer them to subfolders for downstream analyses. The applications within commercial bioinformatics suites that I tend to use most often are for evolutionary analyses and comparative genomics. Most packages come with software for aligning nucleotide and amino acid sequences and entire chromosomes as well as tools for inferring evolutionary relationships among sequences and constructing phylogenetic trees and distance matrices. Other useful tools include protein structure prediction, nucleotide repeat and motif finders and primer prediction software. An advantage to performing these kinds of analyses within commercial software is that the results—be they genome maps, alignments, nucleotide sequence dot plots or phylogenetic trees—are depicted in colourful and editable graphics, which can be exported and used for figures in lectures and publications. I regularly build genome maps with Geneious and then export them to a graphicsediting program for further polishing.

The interactive graphical visualization tools of commercial suites are excellent for exploring large genomic data sets often depicted in stacked views and allow for quick navigation to regions or contigs of interest. Plugins are downloadable applications that provide additional features to software packages—similar to apps for smartphones and tablets. For bioinformatics software, plugins add an array of new sequence analysis tools ones that complement existing tools or that add novel functions, greatly improving the package. Companies are constantly designing new plugins for their software, which means that the repertoire of tools within bioinformatics packages is continually expanding. Plugins work in two ways they allow users to add more features to the software, but they also allow developers to design their own apps for the software. More plugins means more functions and sometimes more money. This way you can set up a workflow to go through for example read mapping, using the mapped reads as input for variant detection, and perform filtering of the variant track’. Workflows can save researchers huge amounts of time and are becoming more widespread among commercial bioinformatics packages. If you do not want to fork out the big bucks, check out The Galaxy Project —a free, webbased and userfriendly bioinformatics workflow management system, which provides access to a large number of data integration and analysis programs. Bringing bioinformatics into the classroom Students today are reared on a digital diet of smartphones, tablets and ultrasleek retinadisplay laptops filled with intuitive software apps, which integrate seamlessly across platforms and devices. Thus, when these students are introduced to bioinformatics and molecular evolution, one would expect them to engage more easily and enthusiastically with easytouse GUI software than with barebones commandlinedriven tools.

Commercial bioinformatics suites, given their browserbased pointandclick interface, lend themselves to teaching and learning. From a lecturer’s perspective, the highend graphics, visual aids and tutorials built into proprietary software are great for communicating bioinformatics topics, themes and procedures, from sequence alignments to contig assemblies to blasting proteins against GenBank. I regularly incorporate bioinformatics software suites into my undergraduate lectures and conference presentations. With my notebook computer connected to a projector, I can use a program like Geneious to effectively communicate to a large audience the procedures and output of various bioinformatics analyses. With the same software, I can design, distribute and evaluate bioinformatics

assignments to be completed inside or outside of the classroom. These assignments typically involve a range of sequence analysis tools where the results of one tool are used as input for another. I almost always receive positive feedback from students when using userfriendly bioinformatics—some students have even said that it has inspired them to pursue a career in bioinformatics. Obviously, the biggest barrier to bringing commercial software into the classroom is the high financial cost of the programs. It is unreasonable to ask students to pay hundreds of dollars for proprietary software, and most undergraduate departments are unable or unwilling to invest thousands of dollars into bioinformatics teaching resources—although with institutes like Northwestern buying campuswide access to proprietary programs, this might be changing. One strategy for using commercial bioinformatics in a course is to get all of the students to apply for a free trial version of the software. Again, there is nothing preventing instructors from investing in a personal copy of the software and using it for lectures.

Give it try and give us your feedback Going forward, innovations in molecular sequencing techniques will result in ever more sophisticated bioinformatics programs, and it is crucial that these programs are accessible to a broad range of users. We might soon be at a point where walkin medical clinics have genome sequencing and bioinformatics desks, where patients can play an active role in interpreting their gene sequences and contributing to genetic treatments, and where highschool students assemble and analyse genomes for homework. The increasingly integral role of bioinformatics in research, medicine and society also means that it will become an increasingly larger, more lucrative industry and one where users will have to pay for the best products. My own experiences with proprietary bioinformatics software have been positive. The tools I have purchased have made my laboratory group and me more productive, and I certainly enjoy using standalone GUIbased programs more than commandline driven ones. This productivity and ease of use, however, has come at a cost, both intellectually and financially. Although I use sequence analysis tools almost every day, my bioinformatics skills, in certain respects, have plateaued. Moreover, the licensing and upgrading costs of using commercial software represent a significant proportion of my laboratory’s operating budget. But as bioinformatics software and algorithms become increasingly complex, it might be unrealistic to expect students to have a strong grasp of the math, theory and computer science that underpin those processes. If you are considering commercial programs, I recommend taking advantage of the free trials that most of the bioinformatics companies offer. Wherever you stand on the topic, I urge you to share your opinions and experiences with others—and best of luck with all of your bioinformatics endeavours.

Key Points Innovations in molecular sequencing techniques, and the popular use of these technologies, have given rise to a range of userfriendly commercial bioinformatics software suites. Often marketed as onestop bioinformatics toolkits, these software packages can be expensive, and it can be difficult for consumers to choose between the different programs. This review explores some of the currently available proprietary bioinformatics packages, comparing their prices, usability, functions and suitability for teaching. Some commercial bioinformatics programs are arguably overpriced and overhyped, but many are well designed, sophisticated and, in my opinion, worth the investment. I encourage readers to explore commercial bioinformatics packages; they have the potential to streamline your research, increase your productivity and energize your classroom. FUNDING This work was supported by a Discovery Grant to DRS from the Natural Sciences and Engineering Research Council NSERC of Canada. References 1. Metzker ML. Sequencing technologies — the next generation. Artemis an integrated platform for visualization and analysis of highthroughput sequencebased experimental data. A survey of tools for variant analysis of nextgeneration genome sequencing data. Vincent AT, Charette SJ. Freedom in bioinformatics. Larkin MA, Blackshields G, Brown NP, et al. Darling AC, Mau B, Blattner FR, et al. Ronquist F, Huelsenbeck JP. MrBayes 3 Bayesian phylogenetic inference under mixed models. DNASTAR press release, 31 March 2014 Northwestern University adopts DNASTAR Lasergene software. 1 June 2014, date last

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