# FIGURE 1 (J). REFEREES POSITION ON MAT 87 pdf

## 1: Professional wrestling holds - Wikipedia

*techniques learned during senior referee mentoring sessions, mat side situation discussions with fellow referees and PIKE POSITION Figure 1 Figure 2. 7.*

No competing interests were disclosed. The author s declared that no grants were involved in supporting this work. This is an open access article distributed under the terms of the Creative Commons Attribution Licence , which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. R package for bcbio RNA-seq analysis [version 2; referees: We have added a new figure Figure 1 to describe in more detail the structure of the object the package uses. It has been adapted from the RangedSummarizeExperiment object and shows where the different count data and metadata are stored. We have updated the package to use the GRanges structure to store the genomic position of genes. This should help to integrate gene expression with epigenetic information, such as ChIP-Seq data, when trying to find features close to genes using the already available methods for Granges object. We have updated the name of some functions to match the Bioconductor style. This section focuses on how to work with the data generated from the other templates to complete a functional analysis. We have focused only on the first few steps as the functional analysis follows published workflows. All figures and code lines have been updated to match the version of the package. We have added a discussion section after the quality control section to give examples of possible interpretations of the figures the package produces. The intention is to provide guidelines to the user on how to act accordingly based on the information generated in the figures. We have added a link to the session info from the computer used to run the code shown in the article. The new version of the article contains the following updates: Automating a full analysis from raw sequence data to functionally annotated gene results requires the coordination of multiple steps and tools. From the first data processing steps to quantify gene expression, to the data quality checks necessary for identification of differentially expressed genes 2 and functionally enriched categories, RNA-seq analysis involves the repetition of commands using various tools. This is done on a per-sample basis, and each step can require varying degrees of user intervention. As a bioinformatics core facility that processes a large number of RNA-seq datasets, we have developed a Bioconductor BioC 3 package called bcbioRNASeq to aggregate the outputs of tools for RNA-seq quality control QC , differential expression and functional enrichment analysis as much as possible, while still retaining full, flexible control of critical parameters. This package relies on the output of bcbio , a Python framework that implements best-practice pipelines for fully automated high-throughput sequencing analysis including RNA-seq, variant discovery, and ChIP-seq. We briefly describe some of the tools included in the bcbio RNA-seq pipeline to help our users understand the outputs of bcbio that are used in the bcbioRNASeq package. To ensure that the library generation and sequencing quality are suitable for further analysis, tools like FastQC 4 examine the raw reads for quality issues. Cutadapt 5 can optionally be used to trim reads for adapter sequences, along with other contaminant sequences such as polyA tails and low quality sequences with PHRED 6 , 7 quality scores less than five. Salmon 8 generates abundance estimates for known splice isoforms. In parallel, STAR 9 aligns the reads to the specified reference genome, and featureCounts 10 generates counts associated with known genes. Finally, MultiQC 12 generates an interactive HTML report in which the metrics from all tools used during the analysis are combined into a single dynamic file. The next stages of an RNA-seq analysis include assessing read and alignment qualities, identifying outlier samples, clustering samples, assessing model fit, choosing cutoffs and finally, identifying differentially expressed genes. These steps often occur in multiple iterations, and require more active analyst involvement to integrate multiple tools that accept input data with incompatible formats and properties see Use Case section. For example, the featureCounts gene counts from STAR-based alignments a simple matrix are useful for quality control, providing many more quality metrics than the quasi-alignments from Salmon. However, the quasi-alignments from Salmon which are imported by tximport into a list of matrices have been shown to be more accurate when testing for differential gene expression 13 , Managing these disparate data types and tools can make analyses unnecessarily time consuming, and increases the risk of inconsistency between analyses.

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Given the complexity of the analysis, it is essential to report the final parameters and associated results in a cohesive, reproducible manner. The package offers multiple R Markdown templates that are ready-to-render after configuration of a few parameters and include example text and code for quality control metrics, differential expression, and functional enrichment analyses. Although other packages have been developed to solve similar issues, bcbioRNASeq allows for tight integration with the bcbio framework, and provides a unified package with objects, functions and pre-made templates for fast and simple RNA-seq analysis and reporting. Additional information about the bcbio RNA-seq pipeline is available on readthedocs. At the end of a bcbio run, the most important files are stored in a separate directory specified by the user in the bcbio configuration YAML file under the "upload: Within this directory, there is a dated project directory containing quality metrics, provenance information, and data derived from the analysis that have been aggregated across all samples, e. In addition, there is a directory corresponding to each sample that contains the binary alignment map BAM files and Salmon count data for that sample. Once the bcbio run is complete, you can open an R session and load the bcbioRNASeq package source code is available at our GitHub repository. Use the bcbioRNASeq constructor function see example below to create a structured S4 object that contains all of the necessary information for downstream analysis. The only required argument when creating this object is uploadDir, which specifies the path to the bcbio final upload directory. Note that bcbioRNASeq will transform all sample metadata column names to lowerCamelCase format without spaces, dashes, periods or underscores; therefore the interestingGroups argument should be specified in the same format. Additionally, specifying the organism of the dataset is strongly recommended, and must use the full Latin name e. Mus musculus ; this enables automatic downloading of gene annotations from Ensembl. Once the S4 object is assigned, use the saveData function to write the dataset to disk as an R Data file. Note that the following code block does not need to be run to reproduce the figures in this paper; its purpose is to describe how to load the data from a bcbio analysis into R using this package, facilitating use of the downstream functions. Non-working example demonstrating how to load a bcbio run. Load the pre-saved object instead See use case below. From here, you can use various functions in bcbioRNASeq to perform analyses, make figures, and generate data tables and results files as we describe in later sections. This object is also used as the input for the R Markdown templates for report generation. First, we begin by describing the object in more detail. The assays slot contains Salmon quasi-alignment data imported with tximport 13 , and automatically generated DESeq2 16 count transformations that provide support for quality control plots. These matrices are described in more detail below: ShallowSimpleListAssays containing count matrices derived from Salmon quasi-aligned counts imported with tximport and processed with DESeq2. Also accessible with assay. Normalized counts, with DESeq2 sizeFactors applied. GRanges describing the rows genes of the count matrices slotted in assays. When organism is specified in the bcbioRNASeq function call, gene annotations will be downloaded from Ensembl using AnnotationHub and ensembldb. DataFrame describing the columns samples of the count matrices slotted in assays. Also contains sample quality metrics from bcbio analysis, generated from aligned counts produced by STAR and featureCounts. These aligned counts are not saved in the object. Version of bcbioRNASeq package used to generate the object. Whether counts are loaded at gene default or transcript level. Caller used to generate the counts. Parameter used when reading transcript abundance with tximport. Path to bcbio final upload directory. Paths of sample directories contained in bcbio upload directory. Path to custom sample metadata file. Can be used to override the sample metadata saved in the bcbio run YAML, but is not normally needed. Path to project directory in bcbio upload. Name of YAML file used to configure bcbio run. Date of bcbio run completion. Groups of interest to use by default for quality control plot colors. Latin species name e. Ensembl release version e. Metadata describing the ensembldb package used with AnnotationHub to define the rowRanges. Transcript annotation file path, if used instead of Ensembl metadata. Number of flow cell lanes used during sequencing. Genome versions used by bcbio. Program versions used by bcbio. Whether the object contains all samples from the run. The assays slot contains several matrices with sample IDs as column names and gene IDs as row names, including raw counts and various derivations of the raw counts, and can be accessed via the assays function. Gene IDs tie these assays to additional information about the genes stored as a GRanges object, and can be accessed via the rowRanges function. Similarly,

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sample IDs tie the assays to further sample information such as run metrics from bcbio and experimental factors also stored as a DataFrame, and can be accessed via the colData function. Non-gene or sample specific metadata about the entire run such as tool versions and genome builds is stored as a list and can be accessed via the metadata function. Use case To demonstrate the functionality and configuration of the package, we have used an experiment from the Gene Expression Omnibus GEO public repository of expression data as an example use case. From this dataset, we are using a subset of the samples for our use case: A pre-computed version of the example bcbioRNASeq object used in this workflow bcb. First, load the bcbioRNASeq object and a few other libraries to demonstrate how to access the different types of information contained in the object. Read counts for each sample in the dataset are aggregated into a matrix, in which columns correspond to samples and rows represent genes. Multiple normalized counts matrices are saved in the bcbioRNASeq object, and are accessible with the normalized argument: Exporting quantified data The package contains multiple convenience functions to extract the expression abundances described above. Outlined below are the steps to save these counts external to the bcbioRNASeq object. These steps utilize functions from the DESeq2, edgeR and tximport packages both directly as well as within wrapper functions. For discussions on RNA-seq data normalization methods and count formats see 18 ; we typically save at least the DESeq2 normalized counts library size adjusted and transcripts per million counts gene length adjusted for further analyses. Most of the data required to make these assessments is automatically generated by bcbio; the bcbioRNASeq package makes it easier for users to access it. For instance, the Qualimap tool runs as part of the bcbio pipeline and generates various metrics that can be used to assess the quality of the data and consistency across samples. The output of Qualimap is stored in the bcbioRNASeq object, and the package has several functions to visualize this output in a graphical format.

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## 2: Performance Trends KRK78 Bed Mat El Camino Black Rubber Each | eBay

*tain adenosine as their first nucleotide (Figure 1c, e, at position 1), while the remaining cDNAs show an enrichment of thymidines (Figure 1b, d, at position 1).*

Thessen, Arika Virapongse Competing interests: The author s declared that no grants were involved in supporting this work. This is an open access article distributed under the terms of the Creative Commons Attribution Licence , which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. A new paradigm for the scientific enterprise: Declining public funding for basic science 1 , 2 has led academic institutions to change their business models 3 , 4 ; the administration of universities is becoming increasingly corporatized 5. The evolving funding landscape at academic and research institutions has had a major impact on career opportunities for scientists, particularly those who are early-career. As a result of grant dollars being increasingly awarded to a disproportionately small number of established investigators and institutes 11 , intellectual discovery has become captured by a privileged few 12 , leading to greater bias in scientific research, diminished scientific productivity 13 , and less potential for breakthrough discoveries 14 ,  Such a lack of social diversity and equity is a major challenge in science, technology, engineering, and mathematics STEM 16 ,  The career pipeline envisions a straight career path, from higher-education training to a coveted permanent position, and then up a career ladder until retirement Figure 1. While such a direct path to success may be optimal for some, it does not reflect the reality of typical career development Box 1. The pipeline includes formal scientific training and different scientific career paths. The pipeline is characterized as a set of distinct streams with little flow between each stream, and a career ladder within each sector. Indeed, training models for graduate students, and particularly for PhDs, in STEM often focus on delivering them to a tenure-track faculty position. Such a system has become a poverty trap for many graduate students and early PhDs, as they work long hours for low wages under the expectation that their participation in the pipeline will eventually lead to a permanent position in academia. Much of the discussion around career prospects for PhDs assumes that they must find a traditional position in a university in order to continue pursuing their scientific goals  Funding changes have also produced an academic structure that provides limited prospects for early-career scientists to advance their careers within academia 9. Postdoctoral training periods also continue to expand. While the increasing complexity of research may require longer training periods, it is unlikely that longer postdoc positions result in better researchers; many postdocs rarely get the appropriate direct training and mentoring to start an independent lab  It is unknown how many promising, early-career scientists become trapped in postdoctoral limbo, as the morass of titles given to postdocs disguises the scale of the scientific workforce that exists in this state  By presenting it as such, the pool of tenured faculty is limited to those who have the means to commit to such a lifestyle: This demographic is steadily decreasing proportionally across the whole scientific research community, so career advice solely targeting this group is increasingly irrelevant. Even after gaining a tenure-track position, the mechanics of gaining tenure can be just as rigid and unforgiving  The limitations of the pipeline as a conceptual model for education and careers is being recognized in both the tech industry 19 and science  The consequences of continuing to apply this outdated model is stalled career development in science, underemployment of some of the most highly educated people in our society, and overall loss of STEM professionals as they seek out career alternatives 21 â€”  Considering the governmental and individual investment that is made into higher STEM education each year, this is not just an academic conundrumâ€”it is a societal problem. By persisting with the assumption of the pipeline, we also miss engaging in conversations that address the fundamental cultural change that is occurring in science today. A new conceptual model is needed to help guide both early-career scientists and those who care about the scientific enterprise towards a more sustainable and resilient professional future. Then, we articulate our ecosystem metaphor by describing a series of design patterns that draw on peer-to-peer, decentralized, cooperative, and commons-based approaches to science. We finish by describing the related cultural shifts underway that can hasten a more diverse and fluid scientific enterprise into the 21st century. Proposed solutions tend to fall into one of three

categories: Here, we highlight some of the main issues facing these proposed solutions. Adjusting flow in the pipeline Alberts et al. Increasing the number of tenure-track-style positions, as desirable as that might be, seems unlikely given the current trends in science funding. By addressing the demand end, it has also been suggested that the size of individual labs should be decreased to reduce the number of trainees that must be moved into faculty positions 10 , While these proposed reforms are thoughtful and well-intentioned, they do not address the problems of an oversupply of talented researchers and funding models that rely on large numbers of low-paid trainees to get work done. Such a solution could certainly lead to fewer scientists with more career stability, but is this the future that we envision for science and our society? Many candidates must go to great lengths to make themselves more competitive. This is leading to a system that is even less accessible to those with lesser means 45 and may contribute even further to a bias towards hiring candidates from elite institutions Much of the energy, currently being devoted to preparing individuals to adapt to the system, could be redirected towards more collaborative and collective solutions. Finding another pipeline The paucity of traditional academic jobs has led to increased career advice about alternatives to academic careers, and there are encouraging indications that many PhDs are finding employment outside academia 47 , While these career options suit many people, the possibility of doing any future self-directed science outside of an academic or research position is rarely considered. Thinking outside the pipeline Much of the career advice on how to be successful in the academic science pipeline reflects the values and dynamics present in the job market when many senior scientists obtained their first positions e. Academics often fail to recognize the broad applicability and value of PhD degrees, or encourage their trainees to work outside the traditional academic pipeline. As such, early-career scientists occupy a passive role, waiting for change to come from the top, such as through institutional reform driven by senior leaders. Likewise, the scarcity of research positions is accepted as a given, limiting how much science can be done. New models are needed to help identify different ways for scientists to continue their work outside of a standard academic or agency job. The science ecosystem We propose an ecosystem as a conceptual model that is relevant both to the training of a scientist and their role as a professional Figure 2. The two most inner circles in the Figure depict the basic necessities, training, and professionalism of science. Here, traditional scientific labs may still have a role, but the networks of peer-to-peer collaborators that span both within and outside of institutions are emphasized. The two outermost circles are the impetus behind the changing context of science today. It is becoming more evident that a new systems-based approach is needed to allow science to adapt more quickly to the complex socio-political and biophysical context of today the outermost circle. There are, however, now new resources, tools, and infrastructure courtesy of STEM advances , such as lab space, journal access, and high-performance computing, either publicly available, or available for rent, that allow science to thrive outside of traditional institutions the orange, next outermost circle In addition, bottom-up changes are already being driven by early career scientists themselves in many different ways 57 â€” The inner circle beige represents the basic necessities needed to be a functioning member of society, as well as a scientist. The next circle purple shows the different groups that are often involved in the pursuit of knowledge and scientific progress. In addition, the borders between the different institutes are highly porousâ€”there is collaboration, reflection, and sharing of resources between them. The next circle orange represents different kinds of resources and infrastructure needed to support science. The outermost circle light blue represents the environmental context, including biophysical limitations, and the socio-political and economic landscape, that science and scientists must function within, adapt to, and seek to understand and affect. Many postdocs and adjunct scientists already have the majority of tools that they need to do independent science, such as deep training and understanding of their field, a body of work that demonstrates their scientific ability, pre-existing networks of colleagues with similar intellectual interests, and the Internet to collaborate and share. By moving beyond the existing pipeline model of academic science, the ecosystem vision provides the space, flexibility, and diversity that science needs to be more responsive to both local and broader complex scales affecting science. To demonstrate how an ecosystem model would work in practice, we present a set of conceptual design patterns loosely inspired by commons-based approaches 61 â€” 63 , systems-thinking approaches 64 , and the sustainable livelihoods framework We acknowledge specific social movements and grassroots changes that are occurring today, and

demonstrate how science now has the means to be more egalitarian, inclusive, and diverse by being less dependent on their institutional settings. We recognize, that major institutional reforms are needed to realize this vision to its fullest, so we also address the changing role of institutions within this vision. That said, we do not claim a one-to-one correspondence with biological ecosystems. Fundamental development of the scientist Basic necessities i. To truly allow independent scientists to develop, a strong set of progressive social policies, such as universal health care, basic income, and high-quality free education, are needed to strengthen the core of the ecosystem 66 , Instead, an individual learns foundational knowledge, explores ideas, and gathers experience through a journey that is influenced by a broad range of interests, a balance of personal and professional goals, and adaptation to the challenges of life overall. Such a student might attend the traditional classes expected in their field, explore other fields of interest e. Along the way, they might explore other career or life choices, and perhaps return to academia completely, or explore specific scientific questions from a new perspective in another career choice outside of traditional academic institutions. Overall, the ecosystem model emphasizes that there is no right way to become a scientist. The diversity of experiences and perspectives are key to advancing STEM development in novel and more inclusive ways. Multiplicity of niches Most importantly, the ecosystem model recognizes that every scientist is a person, meaning that people are more than their jobs and must balance a myriad of responsibilities, goals, and limitations that change as they move through life. While the conventional academic scientist pipeline assumes that individuals are functioning within a protected static environment i. Indeed, sustainable livelihood strategies 65 further emphasize this point by recognizing that people must be constantly making decisions to most efficiently use their resources human, natural, financial, physical, and social capital to meet their livelihood needs, and such decisions are often made within the context of the changing biophysical and socio-political conditions of the system that they live in. Furthermore, people must balance both non-monetary activities i. There is a lack of recognition of the importance of non-monetary activities in making livelihood decisions within conventional career models, as well as limited supporting economic and political structures to support these activities By contrast, the ecosystem model not only presents a flexible model that encompasses the dynamism of the system, it also thrives on social, economic, and experiential diversity. Income-generating activities in the ecosystem approach can be diverse different, contrasting with the expectation of there being a sole niche, such as tenure-track employment in university settings. For example, some independent scholars run consultancies involving their scientific expertise in a commercial setting, but reserve time to pursue their own research; their research and consulting activities help inform the other, resulting in more grounded research and science-informed solutions, respectively. Independent institutes and laboratories Organizations of independent scholars, such as the non-profit Ronin Institute for Independent Scholarship of which the authors are all members , the National Coalition of Independent Scholars , the Institute for Globally Distributed Open Research and Education , CORES Science and Engineering , Neurolinx Research Institute and research consortia such as the Complex Biological Systems Alliance 2 enable highly trained individuals to contribute to basic science outside the traditional academic setting. Independent labs focusing on more specific research questions or subject areas have also emerged, such as the Orthogonal Lab. Many such scholars also retain joint or visiting status with traditional universities, demonstrating the porousness between institutes as part of the overall scientific ecosystem. Through seminars, virtual meet-ups, and in-person unconferences, the Ronin Institute provides an essential community for independent scholars to trade ideas and identify new collaborations, so that they are not operating within a vacuum. For example, PhD graduates who work in private companies, government agencies, or the non-profit sector do not have to trade their scientific career for a profession. In addition, independent scholars can side-step some of the bureaucracy of the university, while maintaining their scientific identity that can be lost while working in full-time industry jobs. Thus, another step towards building the open ecosystem is to normalize the movement into and out of traditional university positions. The formal system for scientific training must value students, postdocs, or other researchers who leave and re-enter programs or jobs for their professional and diverse experiences, and the unique network of colleagues that they bring to programs or jobs. Such a change will reduce the fear that scientists have in diversifying their career experience. We expect that for some kinds of science i. Normalizing these movements

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as one of many flows within the overall scientific ecosystem would be a big step in the right direction Box 3 for both broadening and diversifying science, and creating new career opportunities for scientists. Shifting the dominant narrative A tenure-track job is still the dominant yardstick of legitimacy for a scientist 27 , and such a lack of vision for scientific careers makes institutional and cultural change in science difficult. Benderly offers one example where non-tenure-track early career scientists have been dismissed in biomedicine  Unfortunately not all in positions of power are good-faith participants in this conversation: However, many senior academics recognize the unsustainability of the current system  There are many steps that such sympathetic senior academics can take to support the ecosystem view. Here are just some: These small shifts will add up, especially if they originate from well-respected senior academics. Diversity of scales in pace and budget The increasingly all-consuming competitive nature of academic life often discourages speculation, innovation, and collaboration 73 â€”  Little time and energy is left for the reflection needed to develop original ideas

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## 3: A new paradigm for the scientific enterprise: nurturing the ecosystem - FResearch

*Open Peer Review Discuss this article Comments (0) WEB TOOL treeWidget: a BioJS component to visualise phylogenetic trees [version 1; referees: 1 approved, 1 approved with reservations].*

Stretches are usually employed to weaken an opponent or to force them to submit, either vocally or by tapping out: Chokes, although not in general stress positions like the other stretches, are usually grouped with stretches as they serve the same tactical purposes. Head, face, chin, and shoulder stretches[ edit ] Yoshihiro Tajiri applying a camel clutch to Rene Bonaparte The wrestler begins the hold by standing over a face-down opponent. A standing variation of the camel clutch is also used, with this variation popularized by Scott Steiner in the late s as he used it as his finisher dubbed the Steiner Recliner also A rolling variation of the camel clutch is also used with this variation popularized by Maryse Ouellet dubbed French pain. Leg-trap camel clutch[ edit ] The attacking wrestler stands over a face down opponent, facing the same direction. Stepover armlock camel clutch[ edit ] The attacking wrestler stands over a face down opponent, facing the same direction. The wrestler then reaches forwards and applies a chinlock as in a standard camel clutch, leaning backwards to apply pressure to the upper back and arm. The attacker then either pulls straight back on the chin or wrenches it to the side. Front chinlock[ edit ] A maneuver similar to a neck wrench where the wrestler faces a bent over opponent. As with a sleeper hold, this move can also be performed from a standing position. This can be transitioned into a clawhold STO. There is also double-handed version sometimes known as a head vise, the wrestler performing the hold approaches their opponent from behind and grip their head with both hands. While in the vise, the wrestler can control their opponent by squeezing the temples and bring them down to a seated position where more pressure can be exerted. It was invented and used by Baron von Raschke as well as many members of the Von Erich family , and Blackjack Mulligan. Mandible claw[ edit ] Mick Foley applying his mandible claw hold, with his sock puppet "Mr. Socko" present, on RJ City A maneuver which, when applied correctly against an individual, is purported to cause intense, legitimate pain. Usually performed with the attacking wrestler standing behind a seated opponent, it can also be executed to an opponent on their back enabling a pinfall. Other variations include squeezing either the side of the neck or the muscle in the front of the armpit, with the four fingers dug into the armpit and the thumb pressing into the front of the shoulder. Double underhook crossface[ edit ] This is a crossface combined with a scissored armbar. Straight jacket crossface[ edit ] Similar to a crossface this move sees a wrestler standing above a facedown opponent. Front chancery[ edit ] Also known as "Neck Wrench", the wrestler faces his opponent who is bent over. Similar in execution and function to a front chancery, this lock is often used as a setup for a suplex. Inverted facelock[ edit ] The wrestler stands behind his opponent and bends him backwards. The attacker then arches backwards, putting pressure on the opponents neck and spine. This move is often used on an opponent trapped within the ring ropes, but this makes the move illegal under most match rules. Chris Masters applies a standing side headlock to Shawn Michaels In this hold a wrestler who is facing away from an opponent wraps their arm around the neck of an opponent. This is also called a "reverse chancery". Though this is an often used rest hold, it is also sometimes the beginning of a standard bulldog move. Three-quarter facelock[ edit ] The wrestler stands in front of the opponent while both people are facing the same direction, with some space in between the two. Then, the wrestler moves slightly to the left while still positioned in front of the opponent. The move is also referred to as a "European headlock", due to its prominence in European wrestling. This hold is a staple of European style wrestling and technical wrestling influenced by European wrestling. The wrestler then tightens their grip to choke an opponent by compressing their throat. In professional wrestling this move is used to set up powerbombs or piledrivers.

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*Referee's position: The starting position in which one wrestler is in the top position and the other is on the bottom Takedown: A move during which you take your opponent down to the mat and gain control from the neutral position.*

Correspondence and Footnotes Abstract The aim of the present study was to determine the effect of volume and composition of fluid replacement on the physical performance of male football referees. Ten referees were evaluated during three official matches. In one match the participants were asked to consume mineral water ad libitum, and in the others they consumed a pre-determined volume of mineral water or a carbohydrate electrolyte solution 6. Total water loss, sweat rate and match physiological performance were measured. When rehydrated ad libitum pre-match and at half time participants lost 1. This parameter was significantly reduced when they consumed a pre-determined volume of fluid. Sweat rate was significantly reduced when the referees ingested a pre-determined volume of a carbohydrate electrolyte solution, 0. The high percentage  An increase in percent movement expended in backward running was observed when they consumed a pre-determined volume of carbohydrate solution, 7. The improved hydration status achieved with the carbohydrate electrolyte solution reduced the length of time spent in activities at low-speed movements and increased the time spent in activities demanding high-energy expenditure. Football referee; Dehydration; Sweat loss; Performance; Fluid replacement Introduction Football soccer , an endurance sport in which players perform activities of varying intensity during a min match, is one of the most popular pastimes in the world. Despite the importance of referees in a football match, most studies have focused on player performance 1. Although football players and referees are exposed to identical environmental conditions, they represent different populations because during a match each plays a different role involving specific physical and cognitive demands 2. The growing economic importance of football matches in recent years has increased the physical and psychological demands imposed on referees enormously, which in turn have stimulated studies on their physical, psychological and physiological status and performance 2,3. Several studies of referees have described movement patterns 4,5 , distance covered by assistant referees 6 , anthropometric parameters, heart rates 4,7 , and dehydration levels 8. Taken together, these results support a new specific training protocol for football referees 9. Dehydration often occurs during physical activity and is more pronounced in endurance activities. Dehydration can be aggravated by environmental conditions that promote fluid loss heat, humidity, lack of wind , by fluid deprivation and by high-intensity activities that require higher metabolic heat dissipation  Body fluid loss is promoted by physical activity during sports such as marathon races, American football, basketball, football, and hockey. Dehydration levels in football players during training sessions and actual games can oscillate between 1. In addition, dehydration and hyperthermia impair the cognitive performance of athletes 13 , an equally important point for football referees, who must often make crucial decisions during a game. Football refereeing is a highly intermittent exercise mode when approximately every 4 to 6 s the referee changes motion activity, covering total distances similar to those covered by midfield players 3. Thus, soccer referees experience a considerable physical demand that could be impaired by the dehydration levels observed during official matches. Several studies have reported that exercise performance is improved by the ingestion of water to offset the effects of dehydration. Also, in many situations, athletes benefit from the inclusion of carbohydrates in their rehydration protocols to supplement liver and muscle glycogen stores  Hypohydration can affect the physical performance of referees, but this question has not been thoroughly investigated. The aim of the present study was to determine the effect of fluid replacement on the physical performance of football referees during official matches, and the relationship of performance with the type of fluid ingested. Material and Methods Participants and ethical procedures Ten male football referees field or principal referees accredited by CBF Brazilian Football Confederation were used as subjects in this study. All were volunteers and were informed verbally and by an informed consent form describing the nature and demands of the study, as well as about eventual health risks, which all participants signed. The participants were submitted to the official physical tests used by FIFA to evaluate its referees and to a medical evaluation prior to the study  All subjects were approved in both evaluations. All matches were disputed at the

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same time, 4: Care was taken to ensure that subjects maintained their normal training and professional routines during the experimental period. The weather data were measured at fixed-site stations located in the area of the stadiums. Experimental design and measures of hydration The body water loss of the referees during an official match was studied on three separate occasions, in three different conditions, in an individually randomized order: The individual volume of the fluid allocations was estimated on the basis of a loss of approximately 1. The ingestion of this volume was divided into two periods, one 10 min before the start of the match and the other at half time. No food was consumed by the referees for 2. They were also instructed to consume no food and to drink only the fluid provided, from the time of the initial body mass measurement until 10 min after the match. The matches were separated by at least 1 week. Before and 10 min after the match the referees emptied their bladders and nude body mass was then determined to the nearest g using a digital balance Plena, Model MS, Brazil. The referees were instructed to collect any urine passed at half time into containers provided so that this could be taken into account in the calculation of total body water loss. The difference between post- and pre-match readings, plus fluid intake during half time and the urinary volume, was used to estimate total body water loss during the match. Sweat loss per hour was calculated from the change in body mass after correction for fluid intake and any urine passed during half time, using the following formula: The relatively small changes in mass due to substrate oxidation and other sources of water loss, like evaporative loss from the lungs, were ignored. We considered a body mass loss of 1 kg to be equivalent to a dehydration of 1 L  The measurement error was 0. Match analysis Match physiological performance of football referees is usually evaluated by a time motion analysis methodology 3, All matches were filmed using a digital camera Sony, model Handycam CCD-TRV , Japan attached to a tripod positioned at the side of the pitch, at the halfway line, at a height of about 15 m and at a distance of about m from the field. The camera filmed the referee close up to evaluate locomotive activities. The referees were observed during the whole match. The following locomotive categories were used: These categories were chosen based on a previous study 5 , whereas the mean speed for each category was determined after studies of the videotapes. The time for the subject to pass known distance pre-markers in the field was used to calculate the speed for each locomotive activity. The frequency and duration of each activity were digitally recorded by the same experienced observer. These data were used to calculate the distance covered by the referee in each activity. The total distance covered during each stage of the match was calculated by adding the distances covered in each motion activity. The total distance covered provides an overall index of work rate, based on the assumption that the energy expenditure during the match is directly related to total work output. Energy expenditure values were estimated from the time the referees spent in each motor activity. Oxygen uptake during walking, running and sprinting was calculated according to the equations suggested by the American College of Sports Medicine  Oxygen uptake during jogging and backwards running was calculated by the equation: Energy expenditure during the time subjects remained still was calculated by multiplying the basal metabolism constant 3. The value of O2 consumption was then transformed to kcal by multiplying it by 5. Blood lactate concentration was determined with a portable lactate analyzer Accutrend Lactate System, Roche Diagnostics, Switzerland. Statistical comparisons between two means were performed by the two-tailed Student t-test paired or unpaired, as applicable , whereas comparisons among multiple means were made by repeated-measures ANOVA, followed by the Student-Newman-Keuls multiple comparisons test, using the statistical software Instat 3. Correlation analysis was performed by least squares regression. Results The environmental conditions during the matches were warm, with an average temperature of  These parameters did not change significantly among the matches. The amount of mineral water ingested ad libitum was 0. Table 1 presents the fluid turnover data for the refe-rees. When the participants consumed mineral water ad libitum they lost 1. This percentage of body mass loss was significantly reduced when the participants consumed a pre-determined volume of fluid. Total body water losses averaged 2. This percentage of total body water loss was also significantly reduced with the consumption of a pre-determined volume of mineral water or carbohydrate electrolyte solution. Sweat rate was significantly reduced when the referees ingested a pre-determined volume of a carbohydrate electrolyte solution Table 1. The total distance covered during the two halves was not significantly different in any of the matches studied see Table 2 and Figure 1. The total

# FIGURE 1 (J). REFEREES POSITION ON MAT 87 pdf

distance covered by high-intensity activities, running and sprinting, was: There were no significant differences in these activities between the two halves in any of the experimental situations studied Table 2 , Figure 1. As shown in Table 2 and Figure 2 , there were no differences between the two halves for these activities. The referees spent reduced percentages of total time performing high-intensity activities running and sprinting. The differences between the two halves were also not significant see Table 2 and Figure 2. On the other hand, consumption of a pre-determined volume of carbohydrate electrolyte solution caused a significant increase in the percentage of time spent in an unorthodox directional mode, backward running 7. As shown in Figure 2 and Table 2 , only when the participants consumed a pre-determined volume of mineral water was the percentage spent in backward running during the second half significantly lower than in the first half: This energy expenditure was not modified by fluid supplementation: Blood lactate concentration Blood lactate concentration with mineral water ad libitum was 2. These concentrations were not significantly different from those observed when the referees ingested a pre-determined volume of fluids. Distances covered by football referees in different locomotive categories during the first half open bars and second half filled bars of a match. Hydration status parameters under the three fluid replacement conditions. Locomotive categories performed and distances covered by football referees under three fluid replacement conditions. The use of the carbohydrate electrolyte solution reduced the length of time spent in activities involving low-speed movements walking and jogging and increased the time spent in activities demanding high-energy expenditure backward running. The amount of fluid lost by sweating depends on exercise intensity, environmental conditions, baseline hydration status and individual differences. Athletes such as football players become dehydrated if sweat loss exceeds fluid intake  Changes in body mass are routinely used in field studies to assess the hydration status of athletes  In the present study, football referees lost 2. However, body mass was reduced by 1. Therefore, the moderate dehydration that occurred during the match was not compensated by spontaneous water intake. The fluid intake of 0. Therefore, referees did not realize that they needed fluid replacement. Our results corroborate this idea.

# FIGURE 1 (J). REFEREES POSITION ON MAT 87 pdf

## 5: bcbioRNASeq: R package for bcbio RNA-seq analysis - FResearch

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Genetic changes in RNA viruses result from genetic drift, erroneous replication processes, mutagenic agents and upon which natural selection acts Moya et al. Rapid replication and mutations generate an ensemble of mutant genomes that are comprised of both dominant and low frequency variants. This diversity has been shown to affect virus fitness landscape, transmission, colonization and replication Henn et al. Many recent studies Henn et al. A number of methods that incorporate both genomic and epidemiologic data to infer pathogen transmission have recently been developed Worby et al. These approaches rely partly on the accurate detection and quantification of minority variant populations from genomic samples. Several tools have been developed to identify and quantify minority variants from short-read data Koboldt et al. Nonetheless, these tools do not fully account for discrepancies that arise from sample collection, pre-processing and sequencing in addition to errors that are introduced during downstream bioinformatic analysis. In some cases, sequencing errors can be reduced by developing high-fidelity protocols and laboratory quality control measures Kinde et al. Additionally, the uncertainty resulting from random sequencing errors can be countered by sequencing larger populations at higher coverage Zukurov et al. A number of studies have extensively explored variants from somatic or tumour samples Hofmann et al. In this study, we evaluated four published minority variant detection tools using artificial short-read data with different error profiles. We show that concordance metrics are dependent on sample coverage and are influenced by the quality of input data. Methods Overall, we considered ten published, open-source tools with presumed ability to call minority variants from virus deep sequence data. A number of callers were excluded from the analysis for various reasons, for example, the GATK HaplotypeCaller primarily targets germline calling from human and not variant calling from viral samples. We experienced technical difficulties in setting up the Platypus caller and even after setup, Platypus did not provide calls across all levels of coverage in our datasets. Therefore, the following four tools were evaluated, FreeBayes version 1. A schematic diagram showing the overall approach is shown in Figure 1. A schematic diagram showing the variant calling workflow. ART-Illumina was took the reference RSV genome sequence as input and generated artificial reads using data derived error models to mimic sequence data. Each dataset comprised of eight samples with varying depth of coverage 20, 50, , , , , , and was generated using the methods described in Supplementary File 1 , section S1. The first dataset did not incorporate an error profile. This process was repeated with a separate set of positions that comprised a set of mutations with frequencies below 0. The default parameter options used in each tool are explicitly provided in Supplementary File 4. All output files were provided in the variant call format VCF or as a tabular file for the case of VarDict. Performance measures To evaluate the performance of the variant calling algorithms, we compared the sequence generated by each variant caller vc, denoted S.

## 6: Kelantan FA season - Wikipedia

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