The Charlesworth Group
Servicos XML para as Revistas Brasileiras

17 de maio de 2013

The Charlesworth Group

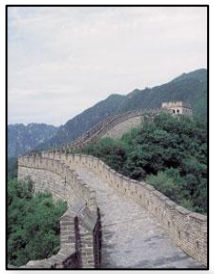
Uma empresa familiar, fundada em 1928, especializada em:

- **Inovação:** **Processo de produção e serviços editoriais**
- **Serviços editoriais: para autores e editores**
- **Globalização: Estratégias para o mercado internacional**

Escritórios:


Reino Unido


EUA 2004


China 1999

Parceria com:

CABOVERDE
SERVIÇOS ESPECIALIZADOS PARA REVISTAS CIENTÍFICAS

Experiência:

- 20 anos de experiência em XML, 80 anos em serviços editoriais
- Mais de 10.000 páginas em XML para o SciELO por ano (dados atuais)
- 300.000 páginas em XML para o PMC por ano
- 500.000 páginas em XML por ano

- **Mais de 6MM de páginas em XML já produzidas até hoje**

Domínio Tecnológico:

- Líder de mercado em Inovação Tecnológica
- Centenas de clientes pelo mundo – capacidade de adaptação a diversos *workflows*
- Participação em conferências pelo mundo
- Abordagem prática cliente a cliente – trabalhamos com suas necessidades
- Equipe dedicada para implantação e suporte ao cliente

Portfólio internacional:

IF: 36,8
Alta QUALIDADE

SCIENTIFIC REPORTS

PLOS ONE

IF: 4.092
Grande VOLUME -
2.400 Artigos por mês

Portfólio nacional:

Brazilian Journal
of medical and biological research

CLINICS

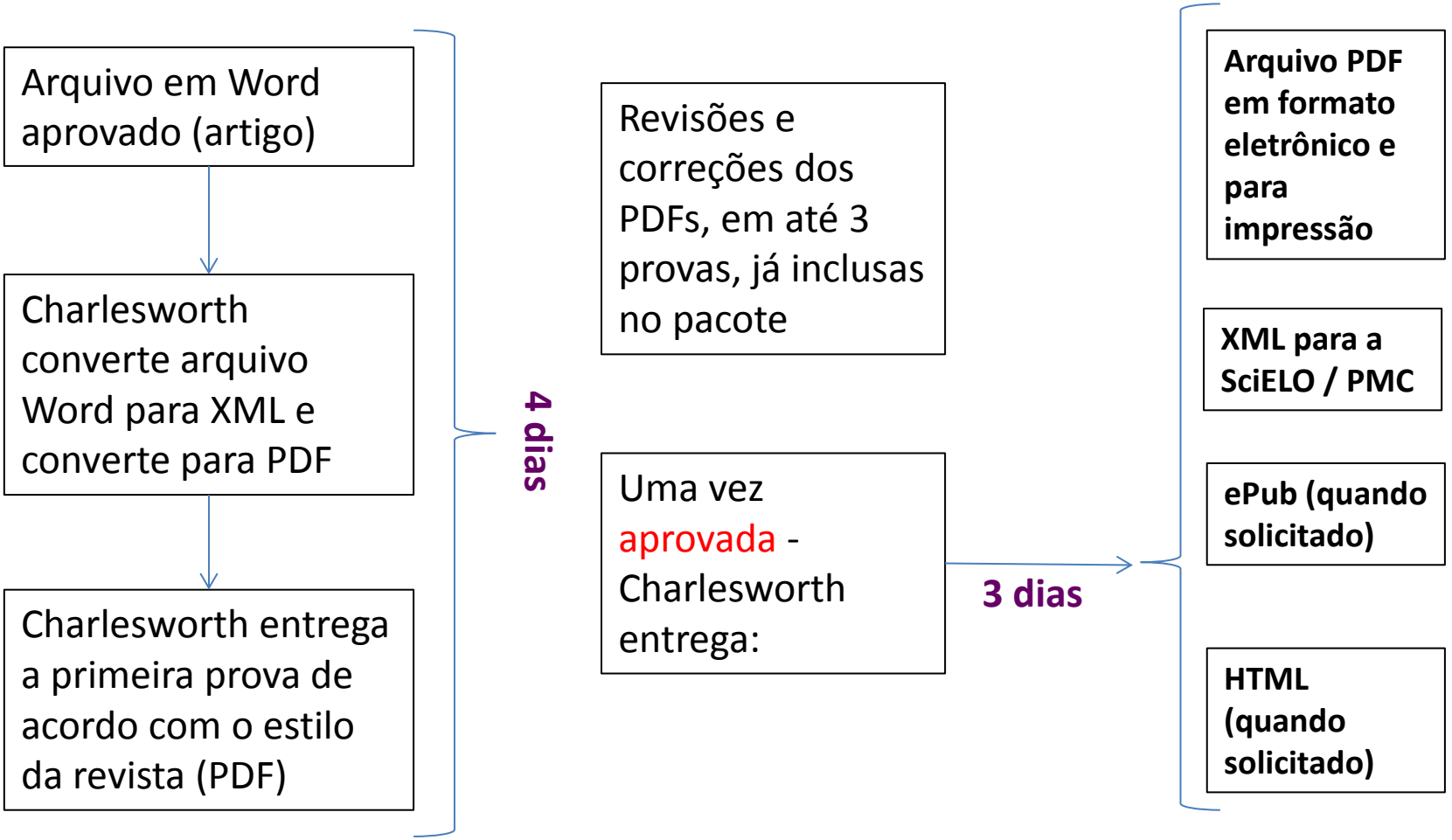
SciELO Brasil

Revista Brasileira de Psiquiatria
RBPPsychiatry

Como podemos ajudá-lo?

- **Processo editorial completo em XML** – envie arquivos em Word e receba artigos finais em PDF, XML, e/ou ePub, no estilo da sua revista, sem o uso de *InDesign* – primeira prova já a partir do XML.
- **Conversão de PDF para XML** – Publicações atuais ou acervos históricos
- **Fornecedor certificado** pela SciELO e pela PubMed Central
  - Sabemos exatamente o que eles querem: RESULTADO DE APROVAÇÃO GARANTIDO!
  - Trabalhamos diretamente com eles para atualizações e desenvolvimento de novos serviços

Processo editorial completo em XML



Exemplos de revistas que utilizam o *Processo XLM*

PLoS

CLINICS

Nature

OPEN ACCESS Freely available online

PLoS one

Clickstream Data Yields High-Resolution Maps of Science

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Abstract

Background: Intricate maps of science have been created from citation data to visualize the structure of scientific activity. However, most scientific publications are now accessed online. Scholarly web portals record detailed log data at a scale that exceeds the number of all existing citations combined. Such log data is recorded immediately upon publication and keeps track of the sequences of user requests (clickstreams) that are issued by a variety of users across many different domains. Given these advantages of log datasets over citation data, we investigate whether they can produce high-resolution, more current maps of science.

Methodology: Over the course of 2007 and 2008, we collected nearly 1 billion user interactions recorded by the scholarly web portals of some of the most significant publishers, aggregators and institutional consortia. The resulting reference data set covers a significant part of worldwide use of scholarly web portals in 2006, and provides a balanced coverage of the humanities, social sciences, and natural sciences. A journal clickstream model, i.e. a first-order Markov chain, was extracted from the sequences of user interactions in the logs. The clickstream model was validated by comparing it to the Getty Research Institute's Architecture and Art Thesaurus. The resulting model was visualized as a journal network that outlines the relationships between various scientific domains and clarifies the connection of the social sciences and humanities to the natural sciences.

Conclusions: Maps of science resulting from large-scale clickstream data provide a detailed, contemporary view of scientific activity and correct the underrepresentation of the social sciences and humanities that is commonly found in citation data.

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¤ These authors contributed equally to this work.

Introduction

Maps of science derived from citation data [1,2,3,4,5,6,7] visualize the relationships among scholarly publications or disciplines. They are valuable instruments for exploring the structure and evolution of scholarly activity. Much like early world charts, these maps of science provide an overall visual perspective of science as well as a reference system that stimulates further exploration. However, these maps are also significantly biased due to the nature of the citation data from which they are derived: existing citation databases overrepresent the natural sciences; substantial delays typical of journal publication [8,9,10] yield insights in science past, not present; and connections between scientific disciplines are tracked in a manner that ignores informal cross fertilization.

Scientific publications are now predominantly accessed online. Scholarly web portals provide access to publications in the natural sciences, social sciences and humanities. They routinely log the interactions of users with their collections. The resulting log datasets have a set of attractive characteristics when compared to citation datasets. First, the number of logged interactions now greatly surpasses the volume of all existing citations. This is illustrated by Elsevier's announcement, in 2006, of 1 billion (1×10^9) article downloads since the launch of its Science Direct portal in April 1999. In contrast, around the time of Elsevier's announcement, the total number of citations in Thomson Scientific's Web of Science from the year 1900 to the present does not surpass 600 million (6×10^8). Second, log datasets reflect the activities of a larger community as they record the interactions of all users of scholarly portals, including scientific authors, practitioners of science, and the informed public. In contrast, citation datasets only reflect the activities of scholarly authors. Third, log datasets reflect scholarly dynamics in real time because web portals record user interactions as soon as an article becomes available at the time of its online publication [8,9]. In contrast, a published article faces significant delays before it eventually appears in citation datasets: it first needs to be cited in a new article that itself faces publication delays [11,12], and subsequently those citations need to be picked up by citation databases.

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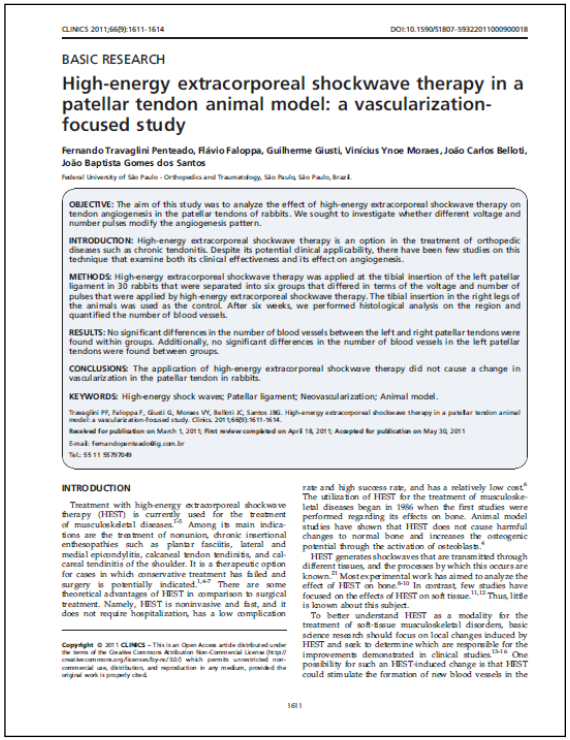

CLINICS 2011;66(9):1611-1614 DOI:10.1590/S1807-59322011000900018

BASIC RESEARCH

High-energy extracorporeal shockwave therapy in a patellar tendon animal model: a vascularization-focused study

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OBJECTIVE: The aim of this study was to analyze the effect of high-energy extracorporeal shockwave therapy on tendon angiogenesis in the patellar tendons of rabbits. We sought to investigate whether different voltage and number pulses modify the angiogenesis pattern.

INTRODUCTION: High-energy extracorporeal shockwave therapy is an option in the treatment of orthopedic diseases such as chronic tendonitis. Despite its potential clinical applicability, there have been few studies on this technique that examine both its clinical effectiveness and its effect on angiogenesis.

METHODS: High-energy extracorporeal shockwave therapy was applied at the tibial insertion of the left patellar ligament in 30 rabbits that were separated into six groups that differed in terms of the voltage and number of pulses that were applied by high-energy extracorporeal shockwave therapy. The tibial insertion in the right legs of the animals was used as the control. After six weeks, we performed histological analysis on the region and quantified the number of blood vessels.

RESULTS: No significant differences in the number of blood vessels between the left and right patellar tendons were found within groups. Additionally, no significant differences in the number of blood vessels in the left patellar tendons were found between groups.

CONCLUSIONS: The application of high-energy extracorporeal shockwave therapy did not cause a change in vascularization in the patellar tendon in rabbits.

KEYWORDS: High-energy shock waves; Patellar ligament; Neovascularization; Animal model.

Travaglini PF, Faloppa F, Giusti G, Moraes VY, Belloti JC, Santos JBG. High-energy extracorporeal shockwave therapy in a patellar tendon animal model: a vascularization-focused study. Clinics. 2011;66(9):1611-1614.

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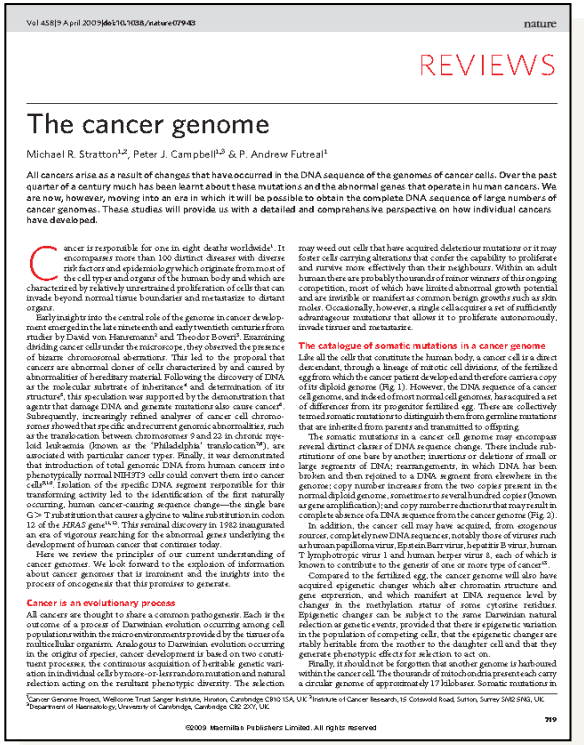
INTRODUCTION

Treatment with high-energy extracorporeal shockwave therapy (HEST) is currently used for the treatment of musculoskeletal diseases.[1,2] Among its main indications are the treatment of nonunion, chronic insertional enthesopathies such as plantar fasciitis, lateral and medial epicondylitis, calcaneal tendon tendinitis, and calcaneal tendinitis of the shoulder. It is a therapeutic option for cases in which conservative treatment has failed and surgery is potentially indicated.[3,4,5] There are some theoretical advantages of HEST in comparison to surgical treatment. Namely, HEST is noninvasive and fast, and it does not require hospitalization, has a low complication rate and high success rate, and has a relatively low cost.[6] The utilization of HEST for the treatment of musculoskeletal diseases began in 1986 when the first studies were performed regarding its effects on bone. Animal model studies have shown that HEST does not cause harmful changes to normal bone and increases the osteogenic potential through the activation of osteoblasts.[7]

HEST generates shockwaves that are transmitted through different tissues, and the processes by which this occurs are known.[8] Most experimental work has aimed to analyze the effect of HEST on bone.[9,10] In contrast, few studies have focused on the effects of HEST on soft tissue.[11,12] Thus, little is known about this subject.

To better understand HEST as a modality for the treatment of soft-tissue musculoskeletal disorders, basic science research should focus on local changes induced by HEST and seek to determine which are responsible for the improvements demonstrated in clinical studies.[13-16] One possibility for such an HEST-induced change is that HEST could stimulate the formation of new blood vessels in the



Vol 458|9 April 2009|doi:10.1038/nature07943 nature

REVIEWS

The cancer genome

Michael R. Stratton[1,2], Peter J. Campbell[1,2] & P. Andrew Futreal[1]

All cancers arise as a result of changes that have occurred in the DNA sequence of the genomes of cancer cells. Over the past quarter of a century much has been learnt about these mutations and the abnormal genes that operate in human cancers. We are now, however, moving into an era in which it will be possible to obtain the complete DNA sequence of large numbers of cancer genomes. These studies will provide us with a detailed and comprehensive perspective on how individual cancers have developed.

Cancer is responsible for one in eight deaths worldwide[1]. It encompasses more than 100 distinct diseases with diverse risk factors and epidemiology which originate from most of the cell types and organs of the human body and which are characterized by relatively unrestrained proliferation of cells that can invade beyond normal tissue boundaries and metastasize to distant organs.

Early insights into the central role of the genome in cancer development emerged in the late nineteenth and early twentieth centuries from studies by David von Hansemann[2] and Theodor Boveri[3]. Examining dividing cancer cells under the microscope, they observed the presence of bizarre chromosomal aberrations. This led to the proposal that cancers are abnormal clones of cells characterized by and caused by abnormalities of hereditary material. Following the discovery of DNA as the molecular substrate of inheritance[4] and determination of its structure[5], this speculation was supported by the demonstration that agents that damage DNA and generate mutations also cause cancer[6]. Subsequently, increasingly refined analyses of cancer cell chromosomes showed that specific and recurrent genomic abnormalities such as the translocation between chromosomes 9 and 22 in chronic myeloid leukaemia (known as the 'Philadelphia' translocation[7]), are associated with particular cancer types. Finally, it was demonstrated that introduction of total genomic DNA from human cancer into phenotypically normal NIH3T3 cells could convert them into cancer cells[8,9]. Isolation of the specific DNA segment responsible for this transforming activity led to the identification of the first naturally occurring, human cancer-causing sequence change—the single base G>T substitution that causes a glycine to valine substitution in codon 12 of the *KRAS* gene[9,10]. This seminal discovery in 1982 inaugurated an era of vigorous searching for the abnormal genes underlying the development of human cancer that continues today.

Here we review the principles of our current understanding of cancer genomes. We look forward to the explosion of information about cancer genomes that is imminent and the insights into the process of oncogenesis that this promises to generate.

Cancer is an evolutionary process

All cancers are thought to share a common pathogenesis. Each is the outcome of a process of Darwinian evolution occurring among cell populations within the micro-environment provided by the tumour of a multicellular organism. Analogous to Darwinian evolution occurring in the origins of species, cancer development is based on two constituent processes, the continuous acquisition of heritable genetic variation in individual cells by more-or-less random mutations and natural selection acting on the resultant phenotypic diversity. The selection may weed out cells that have acquired deleterious mutations or it may foster cells carrying alterations that confer the capability to proliferate and survive more effectively than their neighbours. Within an adult human there are probably thousands of minor winners of this ongoing competition, most of which have limited abnormal growth potential and are invisible or manifest as common benign growths such as skin moles. Occasionally, however, a single cell acquires a set of sufficiently advantageous mutations that allow it to proliferate autonomously, invade tissues and metastasize.

The catalogue of somatic mutations in a cancer genome

Like all the cells that constitute the human body, a cancer cell is a direct descendant, through a lineage of mitotic cell divisions, of the fertilized egg from which the cancer patient developed and therefore carries a copy of its diploid genome (Fig. 1). However, the DNA sequence of a cancer cell genome, and indeed of most normal cell genomes, has acquired a set of differences from its progenitor fertilized egg. These are collectively termed somatic mutations to distinguish them from germline mutations that are inherited from parents and transmitted to offspring.

The somatic mutations in a cancer cell genome may encompass several distinct classes of DNA sequence change. These include substitutions of one base by another; insertions or deletions of small or large segments of DNA; rearrangements, in which DNA has been broken and then rejoined to a DNA segment from elsewhere in the genome; copy number increases from the two copies present in the normal diploid genome, sometimes to several hundred copies (known as gene amplification); and copy number reduction that may result in complete absence of a DNA sequence from the cancer genome (Fig. 2).

In addition, the cancer cell may have acquired, from exogenous sources, completely new DNA sequences, notably those of viruses such as human papilloma virus, Epstein Barr virus, hepatitis B virus, human T-lymphotropic virus 1 and human herpes virus 8, each of which is known to contribute to the genesis of one or more type of cancer[10].

Compared to the fertilized egg, the cancer genome will also have acquired epigenetic changes which alter chromatin structure and gene expression, and which manifest at DNA sequence level by changes in the methylation status of some cytosine residues. Epigenetic changes can be subject to the same Darwinian natural selection as genetic events, provided that there is epigenetic variation in the population of competing cells, that the epigenetic changes are stably heritable from the mother to the daughter cell and that they generate phenotypic effects for selection to act on.

Finally, it should not be forgotten that another genome is harboured within the cancer cell. The thousands of mitochondria present each carry a circular genome of approximately 17 kilobases. Somatic mutations in

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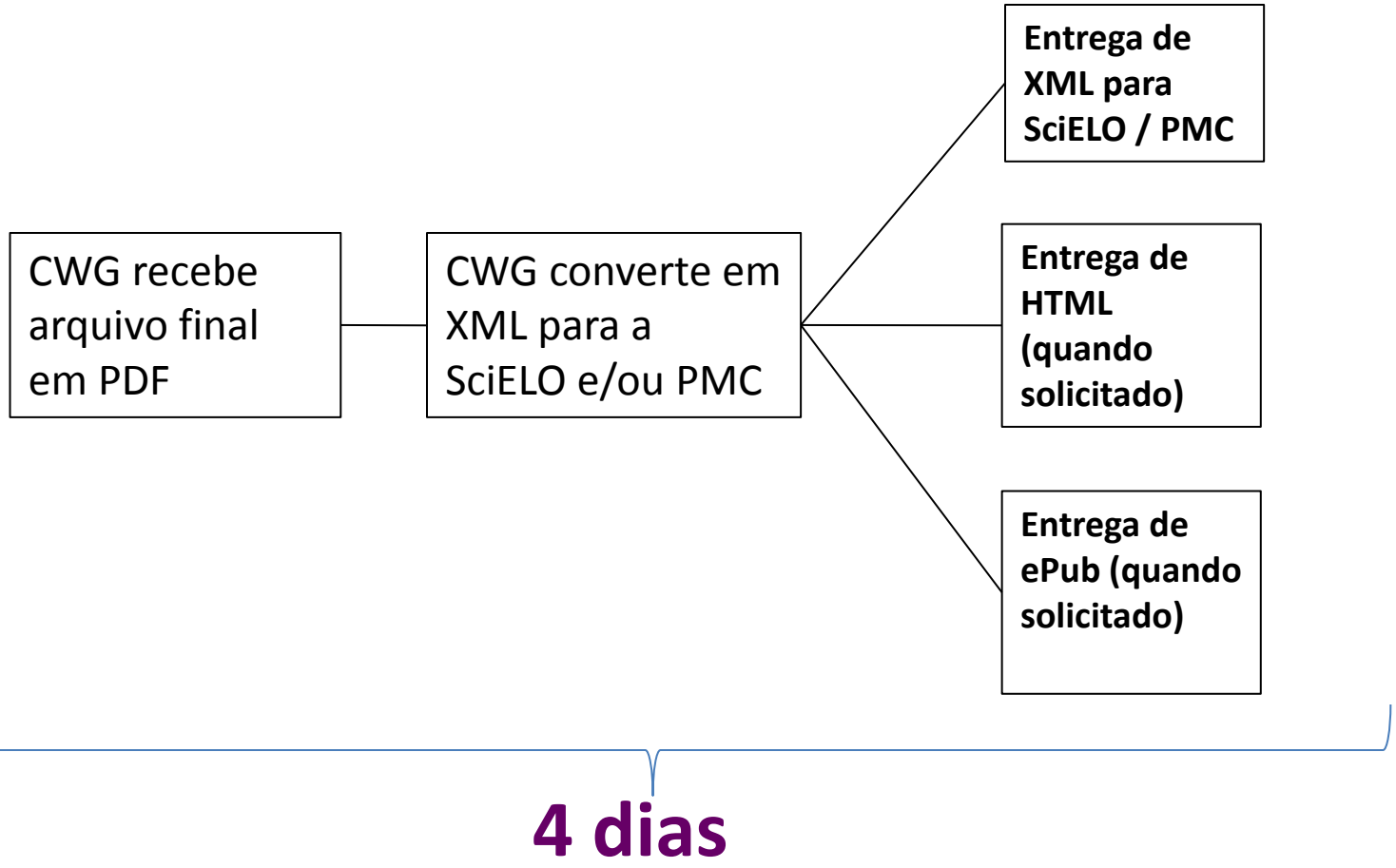
Processo de conversão de PDF para XML



O que mais podemos oferecer?

- **Revisão de idioma** – para autores não nativos no idioma Inglês.
- **Tradução**
- **Gerenciamento de projeto**

Para Autores e Editores

Serviços de revisão de idioma

- Nosso serviço de revisão de idioma inclui uma revisão **especializada** do artigo – gramatical, ortográfica, estrutura da frase e fluência. Nossos editores também podem sugerir alterações para tornar o conteúdo mais **coerente**, **compreensível** e **preciso**.
- Apenas editores **nativos do idioma inglês** dos Estados Unidos e Inglaterra.
- Todos editores têm **conhecimento da área do artigo que está sendo revisado**.
- O tempo de entrega das revisões é de **3 ou 6 dias**.

Em resumo:

1. **Conhecimento técnico e experiência**
   a. 500,000 XML pages
   b. Quase 20 anos de experiência em XML, 80 anos em serviços editoriais
   c. Parcerias com a SciELO e PMC – sabemos o que eles querem e precisam em termos de XML
2. **Processos flexíveis para atender demandas específicas**
   a. Oferecemos o processo completo ou apenas a conversão do PDF para o XML
3. **Conjunto completo de serviços de edição – revisão de idiomas e tradução**
4. **Espaço para crescer com uma única empresa – tudo o que você precisa para ter uma revista de qualidade e com alto fator de impacto. Sem arrependimentos.**
5. **Parceria com a Caboverde – serviços e apoio locais excepcionais aliados aos serviços de edição de uma empresa reconhecida internacionalmente.**

Obrigada!

Dr. M
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Teste comparativo entre o resultado de revisão de um artigo da REEUSP, entre Charlesworth e American Journal Experts

"Encaminhei os textos para comparar sem que conseguissem identificar as empresas a quatro pessoas, sendo parte delas autores do manuscrito. Exceto uma, todas acharam que o trabalho da Charlesworth é melhor do que o outro (AJE). Conclusão: nesta experiência, a Charlesworth se saiu melhor, no entender da maioria de nós."

Profa. Dra Emiko Yoshikawa Egry, Editora chefe da Revista de Enfermagem da Escola de Enfermagem da USP

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