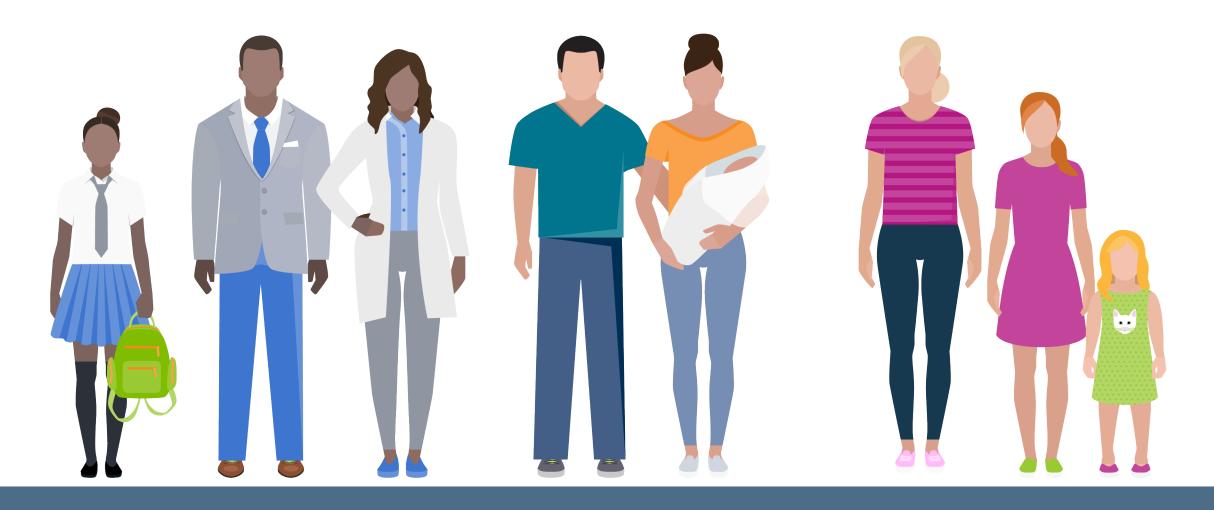
# FOLIO Insights: Evolving Open Source SaaS Services Mike MacKinnon | mmackinnon@ebsco.com



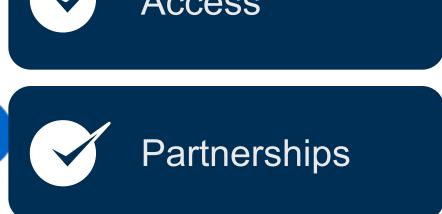
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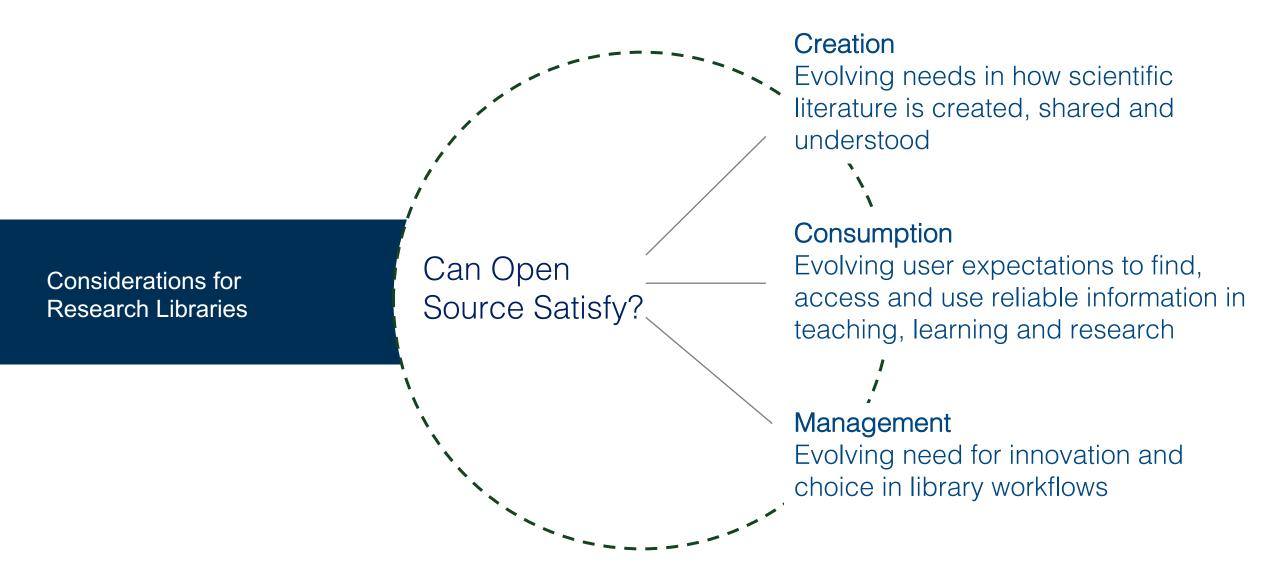
# Modern Software Landscape is Exceedingly More Open

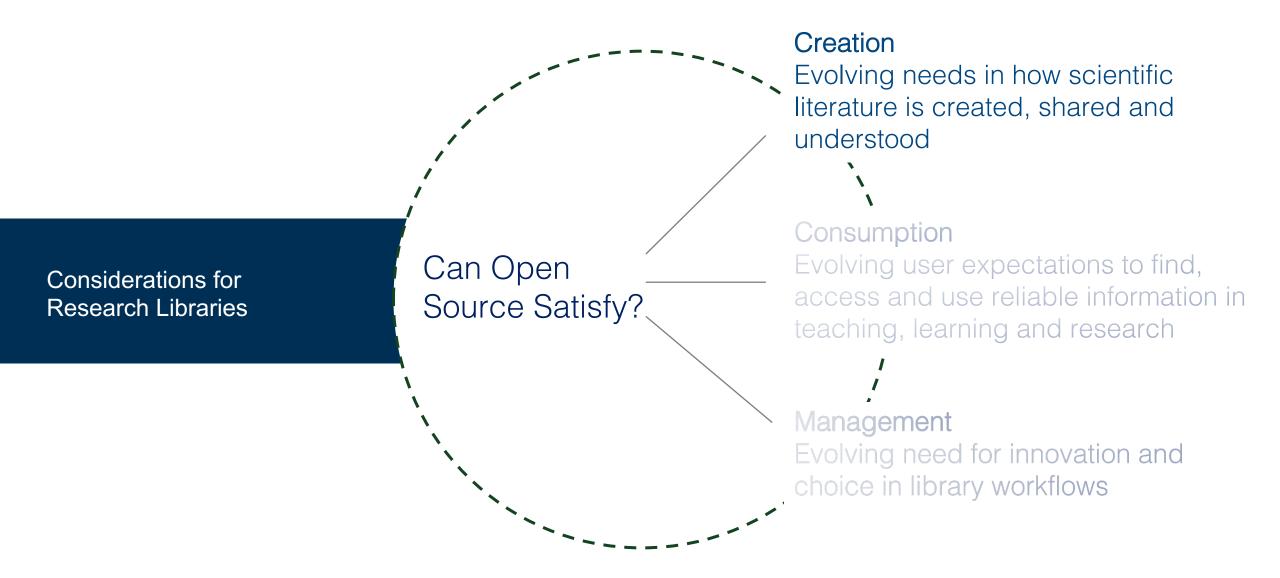












# Challenges with research today: beyond the article

Data, computational code, methods

- Efficiency
- Findability
- Re-use and reproducibility
- Collaboration
- Publishing
- 'Compliance'





- Dissemination
- Discovery
- Preservation
- Insights

Where is the underlying code, data and methods?

How best to publish, share, collect and preserve the underlying output?

values (computed, using Cuttlinks '', based on the read alignments to the genome). This analysis was done within R environment v 3.1.3 GUI 1.65 Snow Leopard build (6912)<sup>12</sup>. See Supplementary Text 1 for detailed commands, and a supplement zip file for the R input (available in Zenodo: http://dx.doi.org/10.5281/zenodo.17606).

We  $\log_2$ -transformed the FPKM matrix (after adding 1 to avoid undefined values). To visualize the data, we used an approach that is similar in principle to that used by the ENCODE mouse consortium and Lin et al. Specifically, we used the function 'prcomp' (with the 'scale' and 'center' options set to TRUE) to perform principal component analysis (PCA) of the transposed FPKM matrix (so that samples were now in rows and genes in columns), after removal of invariant columns (genes). Scatter plots of the PCA results were generated using the ggplot2 package<sup>13</sup>. In agreement with the findings of Lin et al. <sup>2</sup> the samples cluster mostly by species (Figures 2a, Figure S1 and Figure S2). We also plotted the heatmap of the matrix of Pearson correlations between the 26 samples, using the pheatmap function from the pheatmap package v1.0.214 with default settings (i.e. complete linkage hierarchical clustering using the Euclidean distances). Again, samples from the same species tend to cluster together (Figure 2b).



Figure 2. Recapitulating the patterns reported by the mouse ENCODE papers.

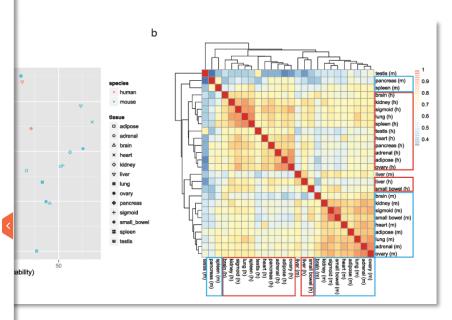
a. Two-dimensional plots of principal components calculated by performing PCA of the transposed log-transformed FPKM values (from 14,744 orthologous gene pairs) for the 26 samples, after removal of invariant columns (genes). b. Heatmap based on pairwise Pearson correlation of expression data used in panel a. We used

Euclidean distance and complete linkage as distance measure and clustering method, respectively.

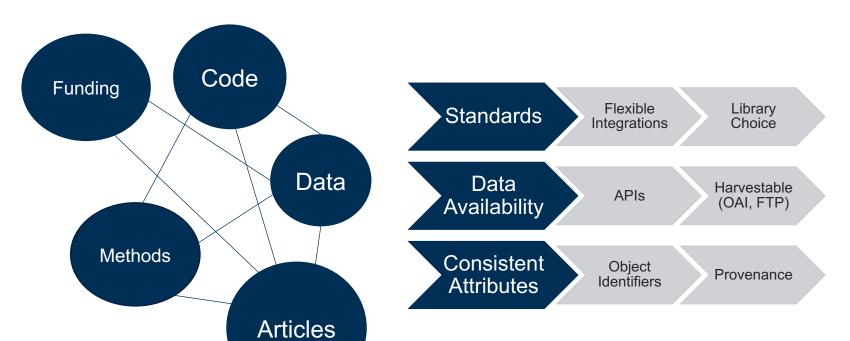
#### Analysis of normalized data after accounting for batch effects yields clustering by tissue

A previous evaluation of normalization methods for RNA-Seq data<sup>15</sup> suggested that FPKM values were not optimal for clustering analysis. Therefore, as a basis for our reanalysis, we used the matrix of per-gene raw fragment counts. The entire analysis was done within R environment v 3.1.3 GUI 1.65 Snow Leopard build (6912)<sup>12</sup>. See Supplementary Text 2 for detailed commands, and a supplement zip file for the R input (available in Zenodo: <a href="http://dx.doi.org/10.5281/zenodo.17606">http://dx.doi.org/10.5281/zenodo.17606</a>).

Following Li et al. <sup>16</sup>, we removed the 30% of genes with the lowest expression as determined by the sum of fragment counts across all samples. Next, due to the presence of mitochondrial genes among the overrepresented sequences in the data, we also removed reads that map to the 12 mitochondrial genes. This left us with expression data from 10,309 genes for analysis. We note that merely limiting the analysis to this subset of genes does not have a marked effect on the patterns reported by Lin et al. (Figure S3; detailed commands in Supplementary Text 3, and a supplement zip file for the R input (available in Zenodo: http://dx.doi.org/10.5281/zenodo.17606)). We performed within-column normalization to remove the GC bias in the data, indicated by the initial quality assessment. To this end, we applied the 'withinLaneNormalization' function from the EDASeq package v2.0.017 to each column in the matrix, using the gene GC



# Desirable Open Infrastructure





Discovery, analytics, IR, LSP

Disseminate, collect, understand and manage

# Research output



Researchers
Work more efficiently, find,
re-use and reproduce research

Library
Support researchers, collect and disseminate research

PUBLISH

ABOUT

**BROWSE** 

SEARCH

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advanced search





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RESEARCH ARTICLE

# Validation of functional calibration and strap-down joint drift correction for computing 3D joint angles of knee, hip, and trunk in alpine skiing

Benedikt Fasel, Jörg Spörri, Pascal Schütz, Silvio Lorenzetti, Kamiar Aminian 🖪

Published: July 26, 2017 https://doi.org/10.1371/journal.pone.0181446

Article	Authors	Metrics	Comments	Media Coverage
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#### Abstract

Introduction

Methods

Results

Discussion

Conclusion

Supporting information

Acknowledgments

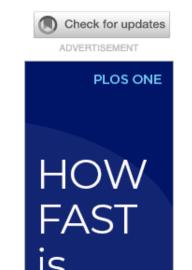
References

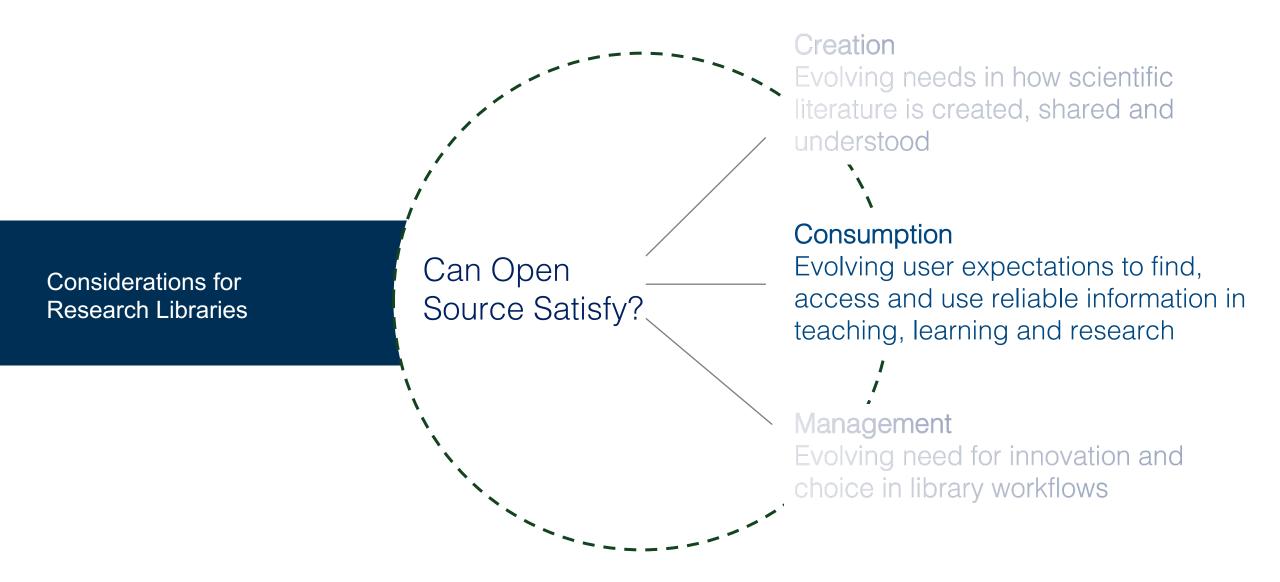
#### Abstract

To obtain valid 3D joint angles with inertial sensors careful sensor-to-segment calibration (i.e. functional or anatomical calibration) is required and measured angular velocity at each sensor needs to be integrated to obtain segment and joint orientation (i.e. joint angles). Existing functional and anatomical calibration procedures were optimized for gait analysis and calibration movements were impractical to perform in outdoor settings. Thus, the aims of this study were 1) to propose and validate a set of calibration movements that were optimized for alpine skiing and could be performed outdoors and 2) to validate the 3D joint angles of the knee, hip, and trunk during alpine skiing. The proposed functional calibration movements consisted of squats, trunk rotations, hip ad/abductions, and upright standing. The joint drift correction previously proposed for alpine ski racing was improved by adding a second step to reduce separately azimuth drift. The system was validated indoors on a skiing carpet at the maximum belt speed of 21 km/h and for measurement durations of 120 seconds. Calibration repeatability was on average <2.7° (i.e. 3D joint angles changed on average <2.7° for two







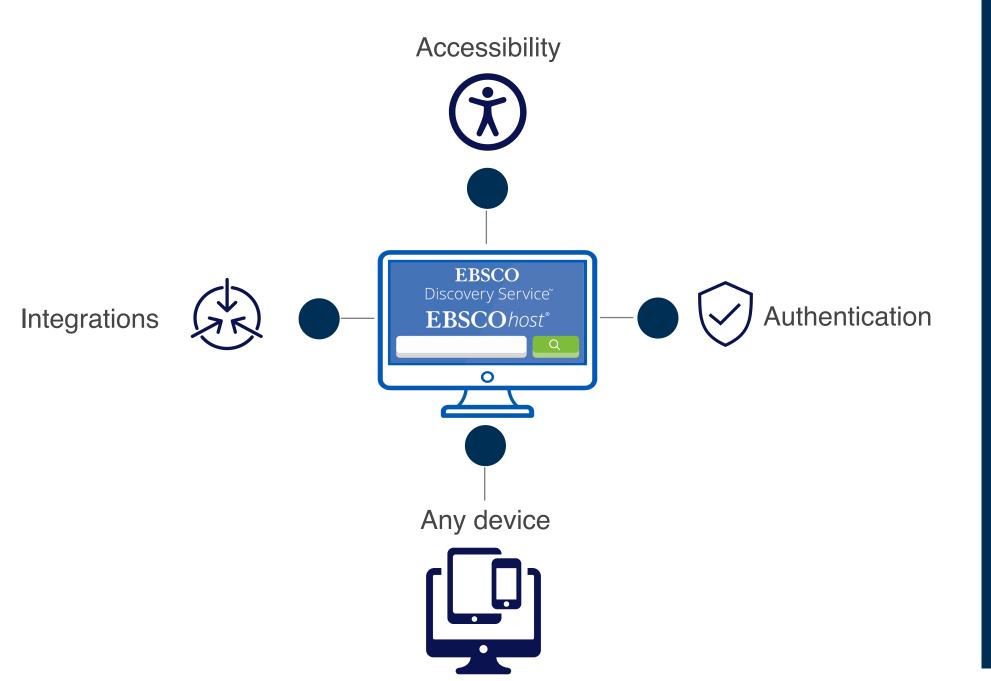


# User experience: what people expect



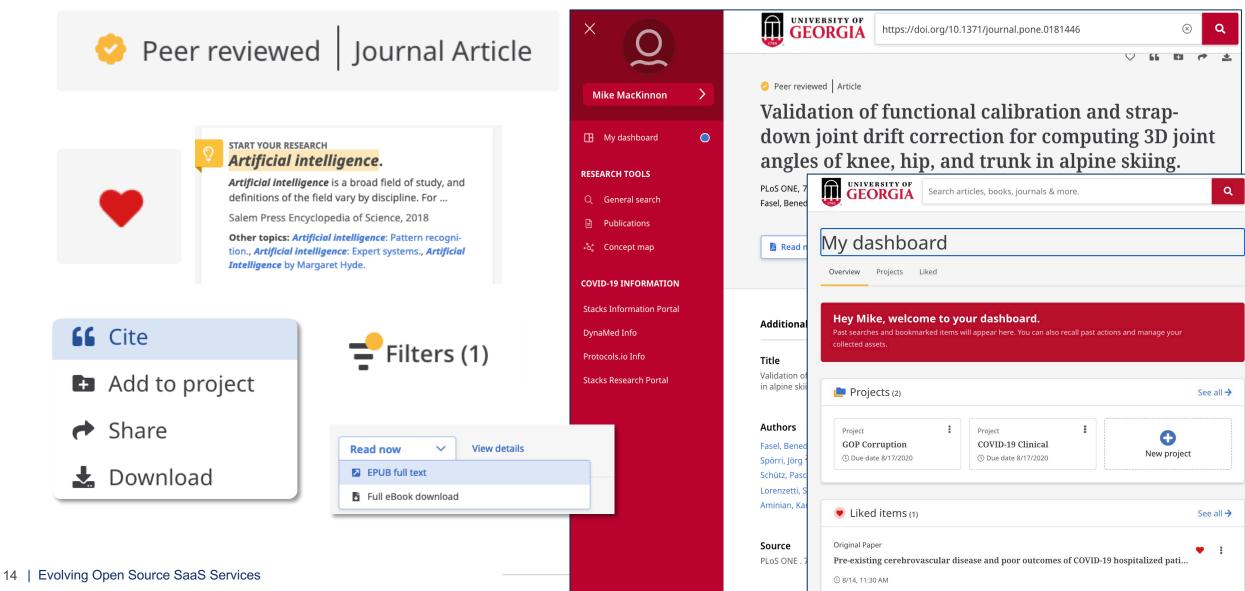
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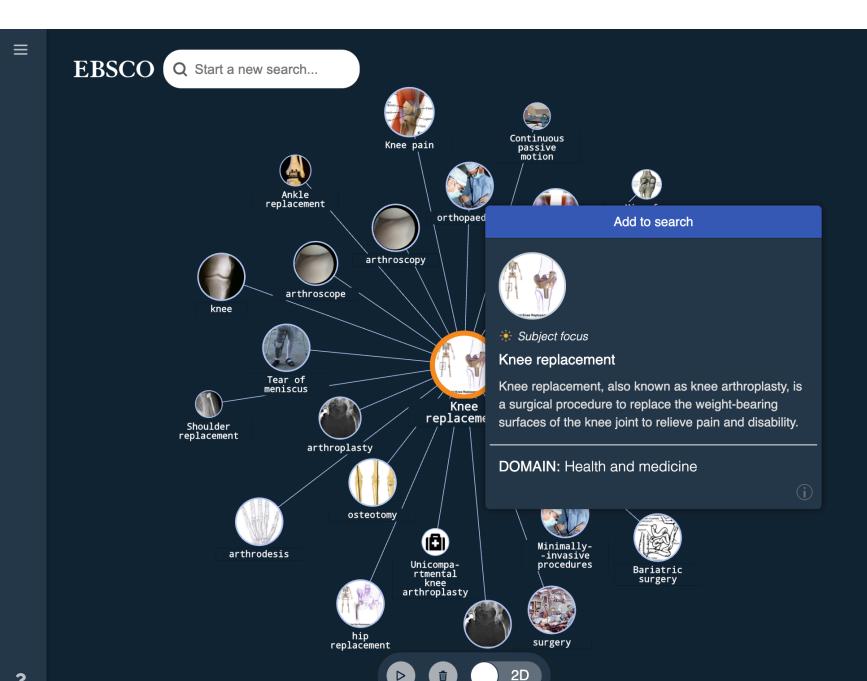
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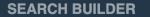


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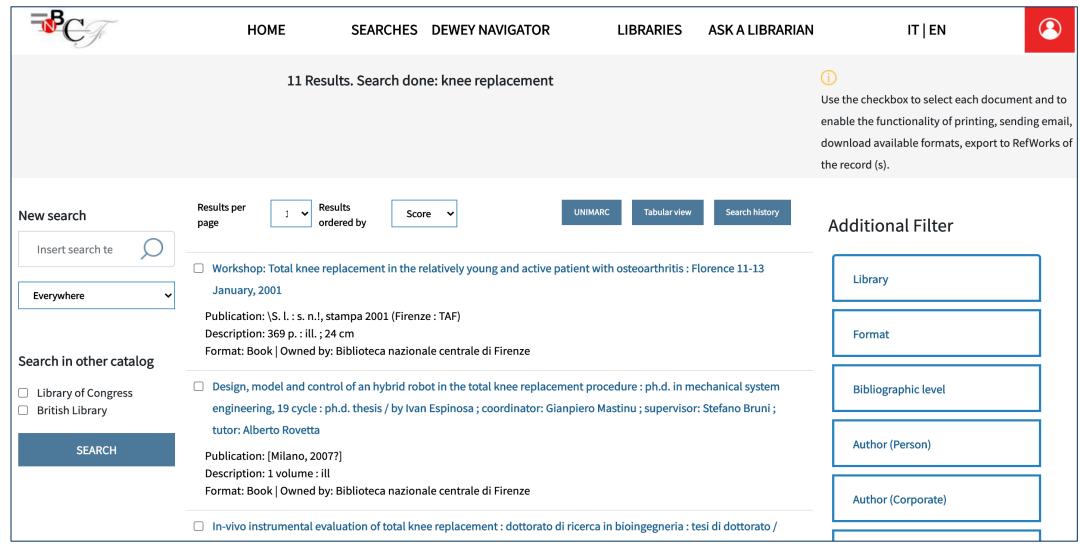
osteoarthritis × AND

Continuous passive motion ×

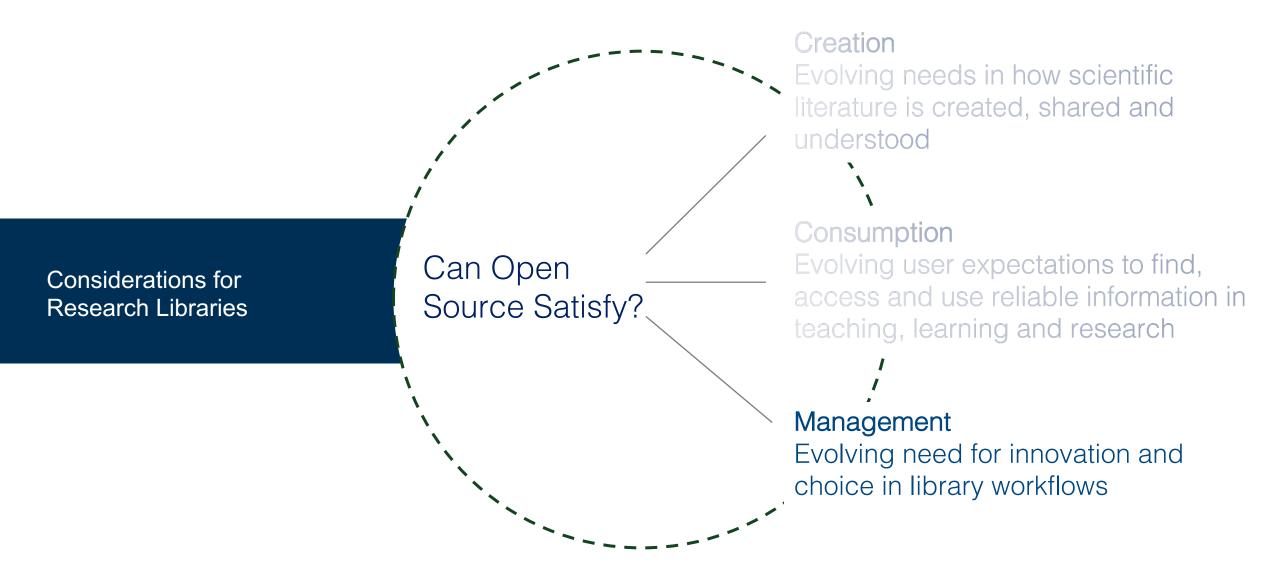
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**Content Preview** 

# **Evolving Open Source UX too!**



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core functionality (circulation, acquisitions, cataloging, ERM, etc.)

