Resources for training trainers

Using the
Mastery Rubric for Bioinformatics

PROFESSIONAL GUIDE

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Overview

This Professional Guide outlines how the Mastery Rubric for Bioinformatics (MR-Bi) can be used as a practical tool both to inform course design, and to support professional development. The specific focus here is on understanding *how* the MR-BI's key elements may be used to identify an individual's training needs, and to shape course design around target skills and developmental stages.

Teaching Goals & Learning Outcomes

This Guide illustrates how the MR-Bi can help to pinpoint training requirements, and to target courses to specific learning outcomes at appropriate levels of cognitive development. On reading the Guide, and engaging with the exercises, you will be able to:

- *list* the principal components of the MR-Bi;
- *describe* how the MR-Bi's developmental stages relate to Bloom's-levels of cognitive complexity;
- *pinpoint* your own/your mentees' stage(s) of development within the MR-Bi, and hence your/their potential training needs;
- *identify* the developmental stages appropriate for a training course;
- *identify* the knowledge, skills and abilities that are the target of that course;
- *use* the MR-Bi in conjunction with Bloom's verbs to articulate learning outcomes for that course; and
- *explain* how the MR-Bi could be used to adapt your training to the needs of individual learners participating in a course.

1 Introduction

Bioinformatics education and training programmes require purposeful integration of fundamentally different discipline-specific perspectives, habits of mind and basic knowledge (from the life and computational sciences) often in limited time-frames[1,2]. Blending life-science and computational skills, and ways of thinking, systematically and formally into coherent bioinformatics programmes can therefore be difficult.

Attempting to meet some of the challenges, various **curriculum** guidelines, defining core bioinformatics **competencies**, have been developed[3-6]. However, often missing from such approaches are i) community consensus on definitions of competence and/or which competencies should be considered core; and ii) the route[7] and requisite time-frame for achieving them. This has made competency-based approaches hard to apply in practice[8-10].

A rather different approach was taken in the creation of Mastery Rubrics (MRs)[7]. Unlike conventional **rubrics**, MRs aim to develop specific Knowledge, Skills and Abilities (KSAs) along stages in a developmental trajectory (from uninitiated student to independent practitioner) by describing the performance or behaviours typical of learners at each stage. MRs thus span the full curriculum rather than individual assignments[7,11].

The Mastery Rubric for Bioinformatics (MR-Bi) was created specifically to provide a framework to facilitate self-directed learning and to help build bioinformatics curricula and courses. It prioritises the development of independence and scientific reasoning, and is structured to allow individuals (regardless of career stage, disciplinary background, or skill level) to locate themselves within the framework.

This Guide outlines some practical applications of the MR-Bi to bioinformatics course design, and to individual professional development; its companion resource, *Introducing the Mastery Rubric for Bioinformatics – a Professional Guide*[12], presents – and describes in greater detail – the MR-Bi's key features. The two Guides build on *The Mastery Rubric for Bioinformatics: a tool to support design and evaluation of career-spanning education and training* by Tractenberg *et al.*[11], and form part of the GOBLET-ELIXIR resources for training trainers.

2 About this Guide

This Guide gives a brief overview of the principal features of the MR-Bi; it follows with suggestions on how to use the tool in practical bioinformatics education or training settings. Exercises and Reflections are provided to help readers to consider i) how the MR-Bi can be used to gauge learners' (and indeed their own) levels of performance and to highlight their requisite training needs; and ii) how the MR-Bi framework may be used to inform a structured approach to the design of bioinformatics education programmes or training courses. Throughout the text, key terms – rendered in **bold** type – are defined in boxes. Additional information is provided in supplementary boxes and figures, and the appended Supplementary Materials.

KEY TERMS

Competencies: multi-dimensional, complex, task-specific behaviours that represent what individuals can do when they bring their knowledge, skills & abilities together appropriately, at the right level(s) for the right application, to achieve a given task

Curriculum: the inventory of tasks involving the design, organisation & planning of an education or training enterprise, including specification of learning outcomes, content, materials & assessments, & arrangements for training teachers & trainers

Rubric: in education, a tool used to evaluate & grade student work; often presented in tabular form, rubrics generally contain evaluative criteria, qualitative performance descriptions for those criteria at specific achievement levels & an associated scoring system

3 What is the MR-Bi?

The MR-Bi is basically a table that provides qualitative criteria to help instructors evaluate learner performance at defined levels of achievement. Performance is characterised across stages of the full academic spectrum, from a student, new to the field, to an experienced, fully independent scientist. This has ramifications for individuals engaging in professional development (whether they're seeking to augment existing skills or to acquire new ones), for supervisors aiming to upskill their students, and for instructors aiming to develop bioinformatics courses or programmes.

3.1 What does the MR-Bi 'table' look like?

The table's axes list i) the KSAs that underpin bioinformatics as a scientific discipline; and ii) five stages of a developmental trajectory, from less to more expert. For each KSA, the cells contain descriptions (so-called Performance Level Descriptors (PLDs)) of how a learner might be expected to perform at each stage and thence to change over time. Figure 1 summarises the overall structure.

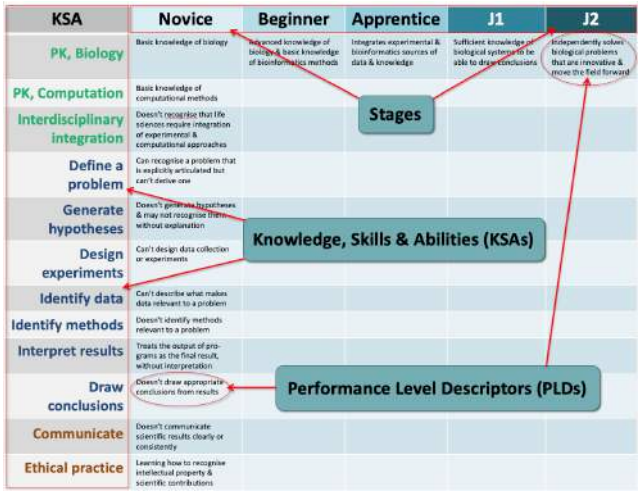

Figure 1 *Structure of the MR-Bi. The x-axis depicts the stages of a developmental trajectory, from Novice to Journeyman; the y-axis lists the KSAs to be delivered by a course or programme; the cells (the PLDs) describe how a learner might typically perform, & change over time, when traversing the trajectory (only PLD excerpts are shown here – the complete set of PLDs is provided in Tractenberg et al.[11] & Via et al.[12]).*

3.2 The MR-Bi's KSAs, stages & PLDs

The KSAs, stages and PLDs of the MR-Bi are described in detail in the companion to this resource, *Introducing the Mastery Rubric for Bioinformatics – a Professional Guide*[12]. Here, we give just a brief overview of its key components.

As illustrated in Figure 1, the MR-Bi encompasses 12 KSAs:

1. *Prerequisite knowledge, biology*
2. *Prerequisite knowledge, computational methods*
3. *Interdisciplinary integration*
4. *Define a problem based on a critical review of the literature*
5. *Hypothesis generation*
6. *Experimental design*
7. *Identify data that are relevant to the problem*
8. *Identify & use appropriate analytical methods*
9. *Interpretation of results/output*
10. *Draw & contextualise conclusions*
11. *Communication*
12. *Ethical Practice*

The first two KSAs are discipline-specific – the fundamental elements of bioinformatics: *Prerequisite knowledge, biology* and *Prerequisite knowledge, computational methods*. *Interdisciplinary integration* is included because bioinformatics is an interdisciplinary field that brings together radically different approaches, perspectives and professional practices. The remaining KSAs are based on core elements of the scientific method. *Communication* and *Ethical practice* are included owing to the importance both of being able to describe and disseminate scientific results to a range of different audiences, and of the necessity for sound ethics to underpin all aspects of the scientific enterprise.

The stages of the MR-Bi explicitly outline an evidence-based developmental trajectory of increasing cognitive complexity: learners' performance, behaviours, habits of mind and required level of supervision at each stage are observably different on the road to independence. As such, it's relatively straightforward to relate these stages to levels of **Bloom's taxonomy**[13,14]; moreover, as Bloom's is widely used in the development of education programmes, we can further consider how the stages of the MR-Bi, in tandem with Bloom's levels, might relate to traditional stages of academic progression – see Table 1. This broad mapping allows instructors to target their courses to specific developmental stages, and ultimately to ensure that their **Teaching Goals (TGs)** are congruent with the cognitive complexity of their intended **Learning Outcomes (LOs)**.

Table 1 ***MR-Bi stages, Bloom's cognitive levels & academic stages.*** *The exact mapping of levels & stages isn't set in stone, but gives a rough idea of the expected level of cognitive skills for learners at each MR-Bi stage.*

MR-Bi stage	Bloom's level		Academic stage
Journeyman J2	late 6	evaluate	career postdoc, PI
Journeyman J1	early 6, 5	evaluate, synthesise	early postdoc, late PhD student
Apprentice	early 5, 3-4	synthesise, analyse apply	early PhD student, late Master's
Beginner	2-3	apply, understand	early Master's, late undergraduate
Novice	1-2	understand, remember	early undergraduate

For each KSA, at each developmental stage, the PLDs describe performance and map progression as learners traverse the trajectory from Novice to Journeyman, gaining greater expertise, and independence, at each level. The PLDs are intended to be high-level guides, to illustrate the types of learner performance, behaviour or habits of mind that are characteristic at each stage. They're not intended to be definitive: rather, they should be familiar as *general* learner traits, showing instructors how the performance of learners typically changes as their cognitive skills develop over time.

KEY TERMS

Bloom's taxonomy: a popular classification of cognitive skills that features a six-level hierarchy of increasing complexity, from the basic skill of *remembering* (able to recall facts & basic concepts) to the advanced skill of *evaluating* (able to defend opinions or decisions)

Learning Outcome (LO): the KSAs that learners should be able to demonstrate after instruction, the tangible evidence that the teaching goals have been achieved; LOs are *learner-centric*

Teaching Goal (TG): the intentions of an instructor regarding the purpose of a curriculum/course/lesson/activity/set of materials; TGs are *instructor-centric* (also termed instructional objectives)

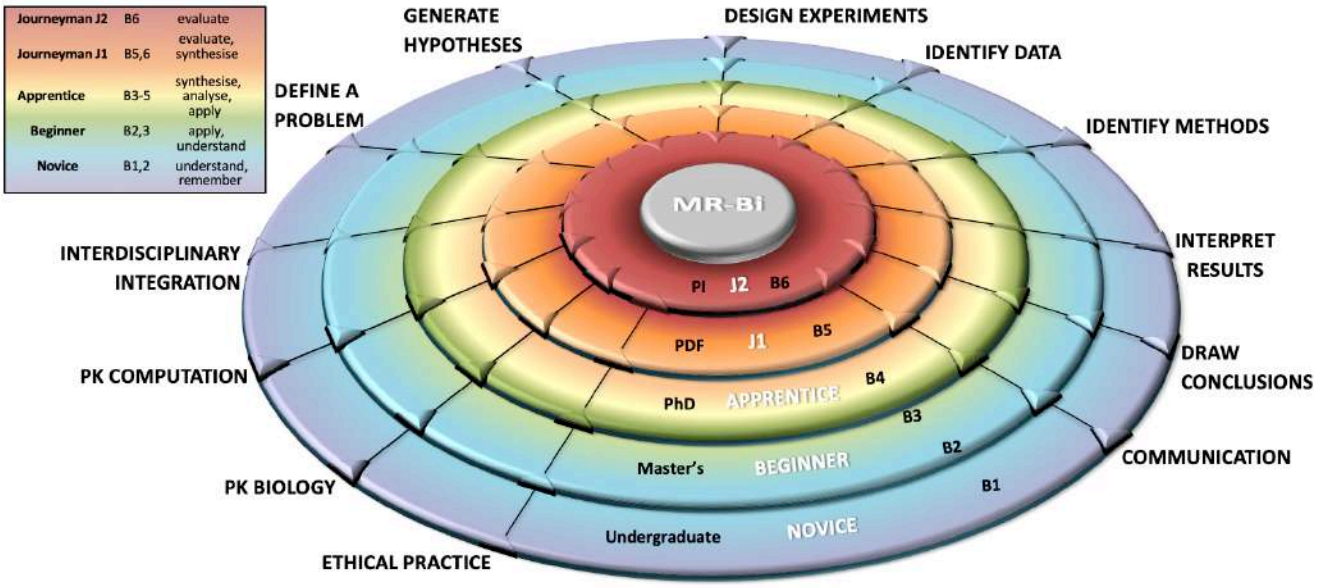

Figure 2 ***Overview of the structure of the MR-Bi.*** *12 KSAs (outermost labels) are encapsulated, together with a developmental trajectory, from Novice (outer circle) to late Journeyman (inner circle). The stages broadly map to the continuum of Bloom's levels, B1-B6 (denoted by the blending of each spectral colour into the next) & to familiar stages of academic progression, from undergraduate, Master's & PhD (which require considerable supervision) to the increasingly independent Post Doctoral Fellow (PDF), & thereafter to Principal Investigator (PI) & subject mastery. The structure is highly adaptable to other disciplines because only two of its KSAs are discipline-specific, so these alone would need altering to focus the Rubric on closely related subjects.*

The overall structure of the MR-Bi is summarised in **Figure 2**. The Figure illustrates how, in a stepwise fashion, each developmental stage builds upon the next in terms of cognitive complexity (advancing from Bloom's level 1 to level 6) as an individual progresses from less to more expert, from Novice (outermost layer) to J2 Journeyman (innermost layer). The figure also shows how the stages may be broadly aligned with typical stages of academic progression, from undergraduate, Master's and PhD student, through postdoc to fully independent scientist. Beneath each layer (not shown, but see **Figure 3**) are the PLDs that describe learner performance at each stage. Suffice it to say, here, that the PLDs evolve between stages, reflecting both a growing sense of self-awareness and a diminishing need for guidance along the route to independence: Novices generally lack awareness of gaps in their knowledge, while Beginners are starting to recognise that gaps exist – both need guidance; Apprentices do recognise limits to their knowledge, and will actively seek guidance, while J1 Journeymen tend to work collaboratively with supervisors prior to becoming fully independent – J2 – thinkers.

An insight into this complexity is given in **Figure 3**, which separates the layers from one another to reveal some of the PLDs associated with each of the KSAs at each stage. The corresponding Bloom's level is shown in the bottom right-hand quadrant (for the J2 Journeyman stage depicted in the foreground, this is Bloom's level 6 – *evaluate*); this is also reflected in the coloured triangles flagging each of the KSAs, allowing us to see, at a glance, the progression in cognitive complexity between stages (for consistency, the same colour scheme is used in **Table 1** and **Figure 2**). Also shown (although not visible for each stage depicted in the figure) is a general description of a bioinformatics practitioner: here, for example, it's suggested that the J2 Journeyman is, *"an independent scientist who expertly integrates bioinformatics & other methodologies, as needed, to achieve desired objectives…" etc.* These general descriptions allow individuals rapidly to identify their own stage(s); they also allow supervisors and instructors to identify (and target) those of their mentees and learners.

As mentioned earlier, the complete MR-Bi, including all the PLDs, is available for reference in both the companion Guide[12] and the original article by Tractenberg *et al.*[11]. It isn't in scope to examine all of the PLDs in detail at this point; nevertheless, it's instructive to dig a little deeper, to examine how, in conjunction with the KSAs and stages, they may be used to inform decision-making in areas such as individual professional development and course design.

REFLECTIONS

1 Consider your current level of bioinformatics training.
2 Thinking about **Figure 2**, for each KSA, do you recognise your own stage of development? Would you consider yourself to be at the same stage of achievement for each?

EXERCISES

1 Review section 3 (see also the introductory guide[12]), then write down and explain the three principal components of the MR-Bi.
2 Write down the five developmental stages of the MR-Bi.
3 Write down the levels of Bloom's taxonomy of cognitive complexity. How many are there?
4 To which level(s) of Bloom's taxonomy does the MR-Bi's Apprentice stage most closely relate?

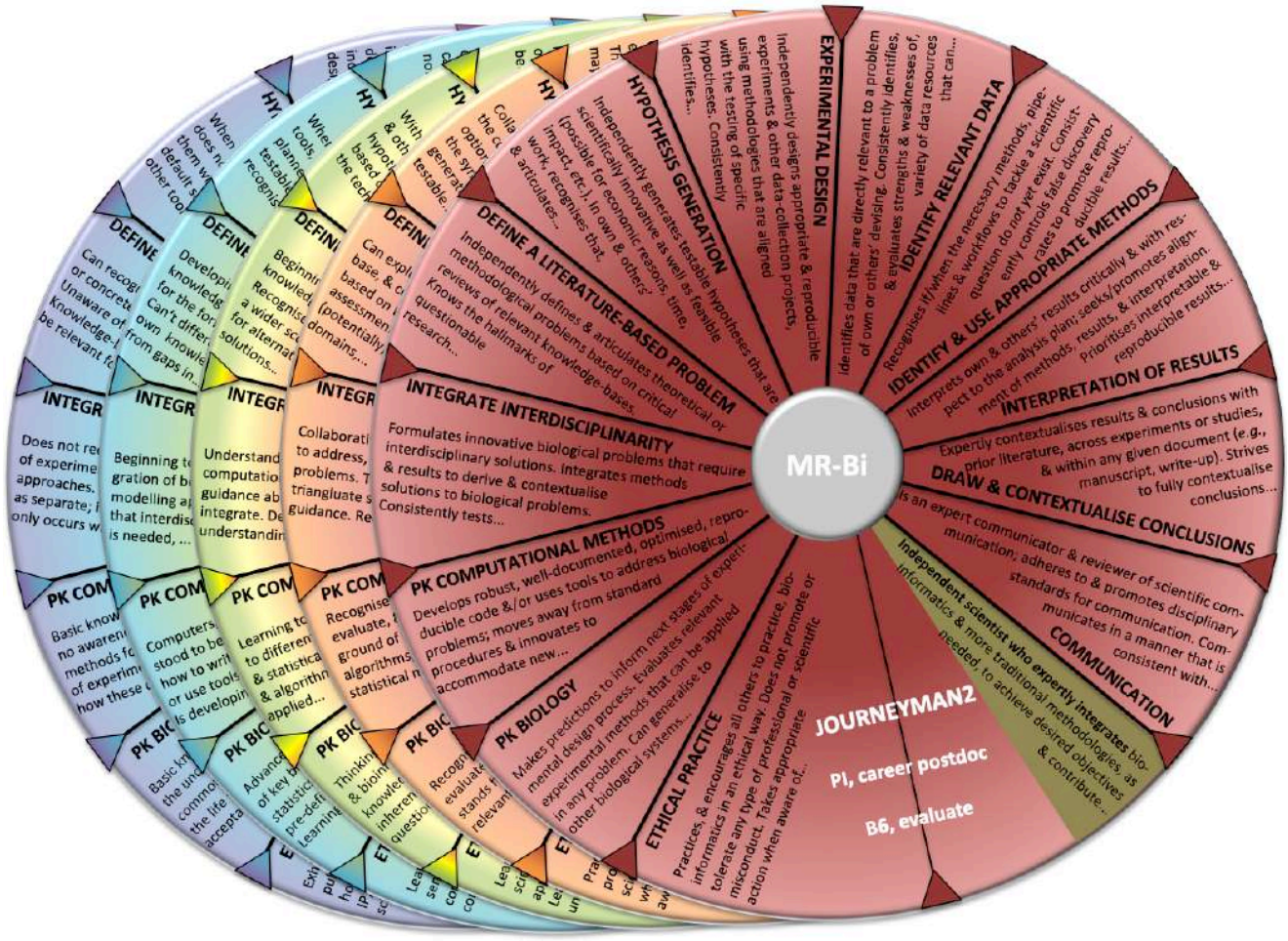

Figure 3 ***Expanded view of the MR-Bi's structure.*** *The disks denote the developmental stages, with the J2 Journeyman in the foreground & Novice in the far background. For each KSA, excerpts from the full set of PLDs are depicted. The colours denote, for each KSA at each stage, the requisite Bloom's level(s), B1-B6 (as per* ***Table 1*** *&* ***Figure 2****); the Bloom's level is also explicitly noted in the bottom right-hand quadrant: for the J2 Journeyman, this is B6, evaluate. Also shown in this quadrant is the relevant academic stage, alongside a general description of a bioinformatics practitioner at this stage.*

4 Applications of the MR-Bi

As a decision-support tool, the MR-Bi has applications in various education and training scenarios: these include (but aren't limited to) professional development (*e.g.*, helping to guide individuals who're seeking to expand their own skill-sets); mentorship of PhD students or postdocs (*e.g.*, helping supervisors to identify the specific training needs of their students/mentees); and curriculum or course design (*e.g.*, helping instructors to better structure and/or target their teaching). Let's take a closer look at some of these scenarios.

4.1 Professional development

Let's first consider using the MR-Bi as a tool for self-reflection. We imagine a life-science PI who wishes to become self-sufficient in basic bioinformatics techniques, rather than having to ask his or her colleagues (or students!) for help. This individual recognises him or herself as a J2 life scientist (and, within the life sciences, as a J2 reviewer of the scientific literature, generator of hypotheses, experimental designer, communicator, and so on.), while at the same time acknowledging being a Beginner both in computational methods in general and in applying appropriate bioinformatics methods in particular – see **Figure 4**. This is someone who wants to *understand* the rudiments of how to code or script, and how to *apply* relevant bioinformatics tools and methods in his/her work. The detailed Beginner-level PLDs for the *Prerequisite knowledge, computational methods* KSA are congruent with those aspirations:

> *"Learning how to write... code, run software, or use tools… Developing awareness of bioinformatics tools… & resources, but isn't able to choose or apply the most appropriate…. Developing awareness that tools require input parameters, but uses defaults. Learning to read … & make minor modifications to existing code/scripts."*

Similarly for *KSA Identify & use appropriate analytical methods*:

> *"Learning to recognise pros & cons of methods/software... Becoming aware of default settings… & their effects on results; & beginning to explore... tailored settings. Understands that more than one method/tool may be available… but can't choose effectively. Learning*

about similarities & differences across methods, & that choices… should leverage independence… to support reproducible results."

Identifying with the Beginner-level descriptions for these specific KSAs highlights the level of training needed by this particular individual – Bloom's 2-3 (*understand*, *apply*) – which is the kind of level typically delivered in modules of late undergraduate or early Master's programmes, or in basic/introductory training courses. Potentially, additional bioinformatics training might also be required in other areas, at different levels: *e.g.*, in identifying relevant data-resources, and evaluating their relative strengths and weaknesses; in being fully able to interpret various bioinformatics program outputs; or in applying bioinformatics-relevant ethical practices, *etc.* In this case, the PLDs for the relevant KSAs may again be used to pinpoint the current developmental stage for each, and hence the most appropriate levels of training, thereby outlining a kind of 'learning path' for this individual, as summarised in **Figure 5**.

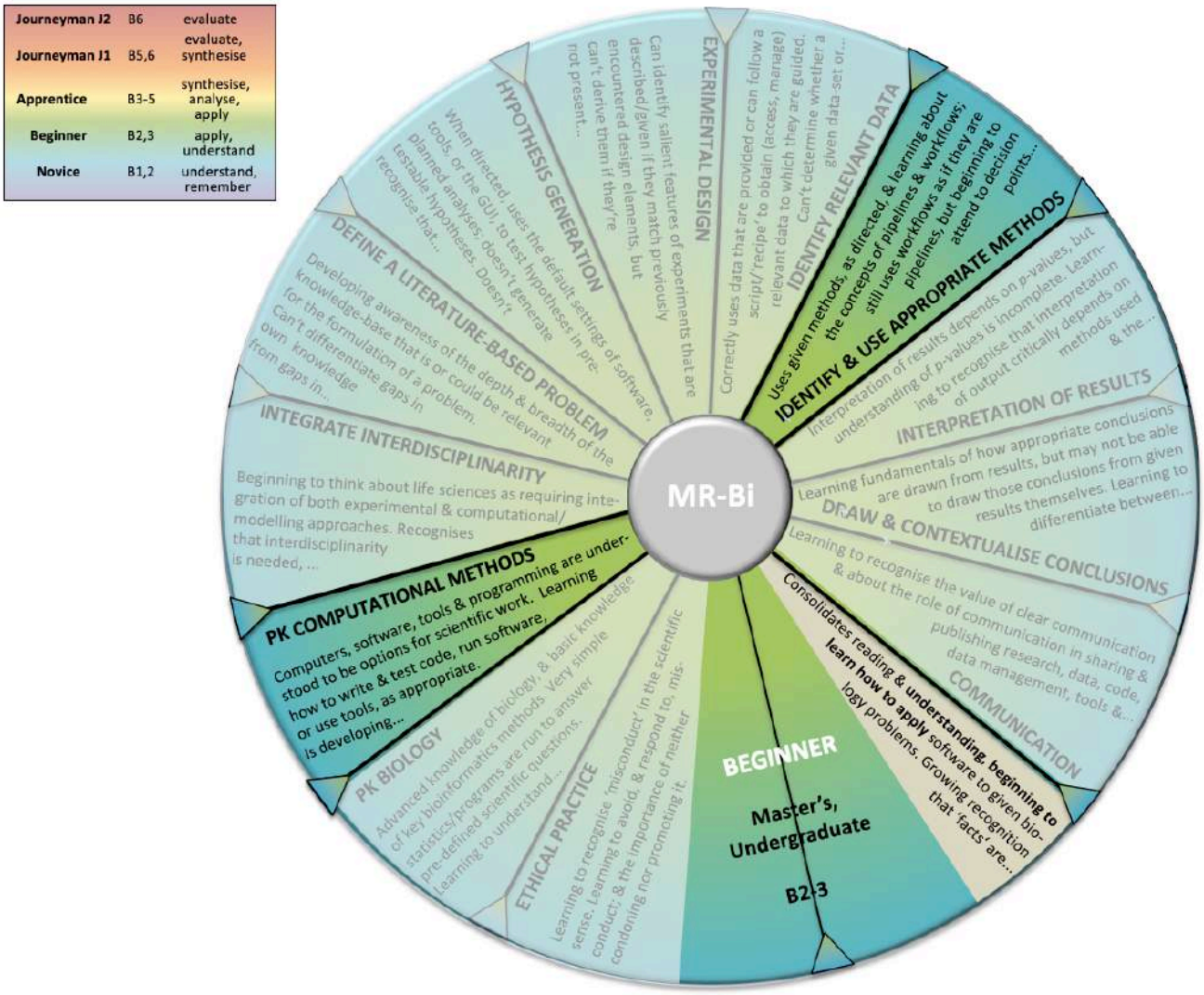

Figure 4 ***Beginner-level PLDs for KSAs, PK Computational methods and Identify & use appropriate methods.*** *Excerpts from the PLDs for the two highlighted KSAs are shown; the colours denote the requisite Bloom's levels; the Bloom's levels are also explicitly noted in the bottom right-hand quadrant – for the Beginner, these are B2-3: understand, apply. Also shown in this quadrant is the relevant academic stage(s) (here, the Beginner stage is consistent with late undergraduate-, early Master's-level thinking), alongside a general description of a bioinformatics practitioner at this stage.*

As mentioned previously, the process outlined here for helping individuals to assess their own training needs, as part of their ongoing development, may equally be used by supervisors, jointly with their students or mentees, to identify any specific training that may be required to expedite their particular research programmes. Here, the approach benefits from being collaborative: together, supervisor and student/mentee identify the relevant KSAs in which training is required, and broadly use the PLDs to pinpoint the student/mentee's current developmental stage: *e.g.*, to complete a particular research project effectively, upskilling in a particular programming language or statistical package (say from Beginner to Apprentice, or from Apprentice to J1 level) might be required. Working together in this way yields a common understanding of the level of skills required to satisfy the desired training needs, to enhance both the individual's abilities and the outcome of the research project. The result of such an analysis would look similar to that depicted in **Figure 5** (which shows the KSAs and stages selected by a fictional J2 life scientist), but likely with few or no KSAs at the J2 Journeyman stage, and more selected at Beginner or Apprentice levels. Together, depending on the time available, the chosen levels and their PLDs then suggest whether a short training course might be the best way to close the identified skills gaps or, say, a full module of an academic Master's programme.

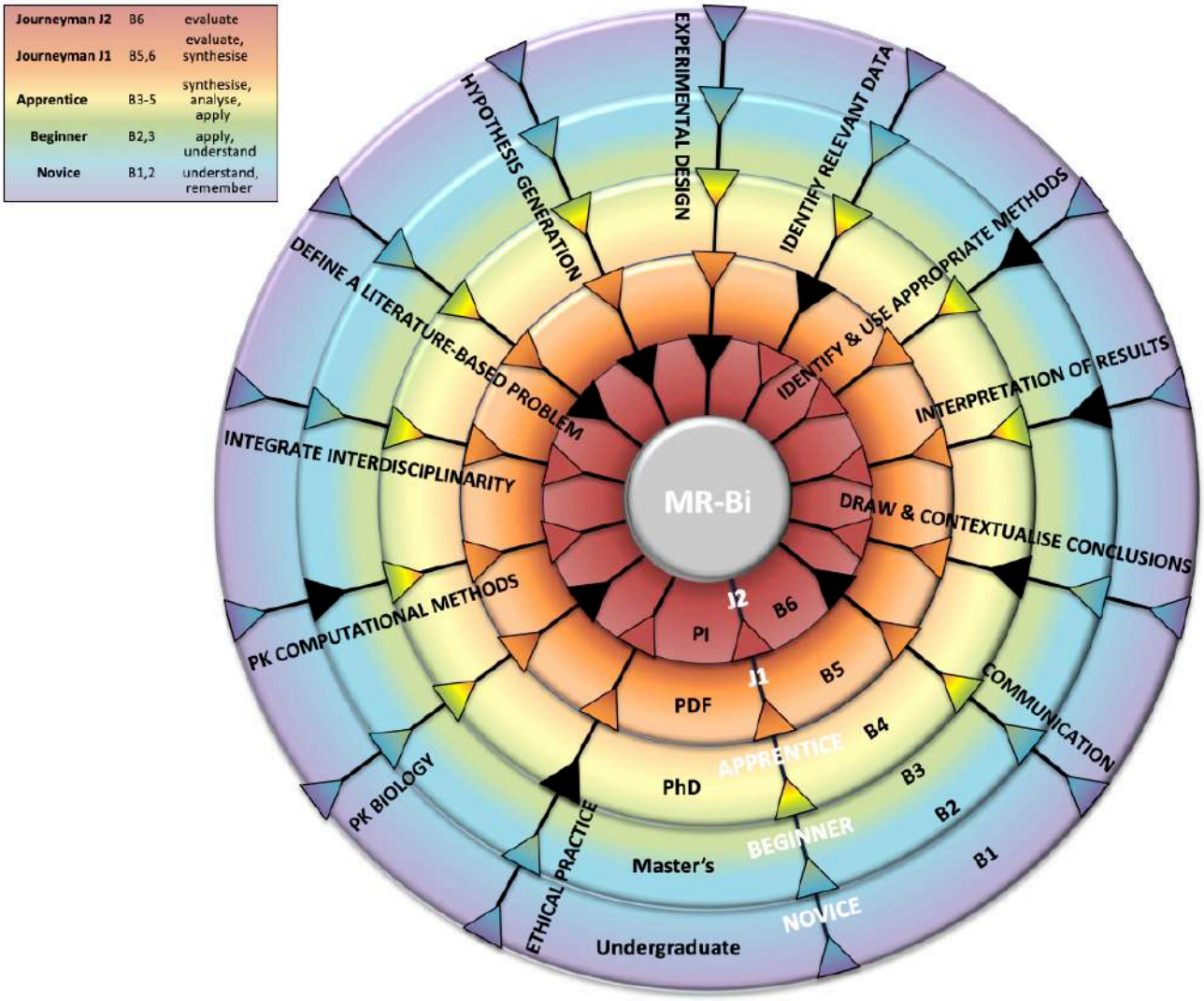

Figure 5 ***Professional development – using the MR-Bi to define an individual learning path.*** *The illustrated structure echoes that shown in* ***Figure 2****. Here, an individual identifies him or herself as a J2 life scientist, J2 reviewer of the scientific literature, etc., but as a Beginner or Apprentice in other KSAs (denoted by black triangles). Pinpointing the particular developmental stage for given KSAs highlights the areas where specific training is needed, at the requisite Bloom's &/or academic level (undergraduate, Master's, etc.), to close the known skills gaps. Together, the identified KSAs & stages highlight targeted training opportunities, allowing individuals to track their professional development from their current to higher levels of performance.*

EXERCISES

1 Examine **Figure 5 –** it might also be helpful to review the PLDs in **Table 2** of the companion introductory guide to the MR-Bi[12]. For each KSA, think again about your own stage of development.

2 Refer to the template *Professional Development* figure in the Supplementary Materials, **SM1**, at the **end of this Guide** (page 14).

3 For each KSA, fill in or tick the stage with which you most identify.

4 Are you at the same stage of achievement for each? If not, write down the area(s) in which you consider yourself less proficient?

5 With this in mind, are you able to pinpoint the type &/or level of training or professional practice that might help you progress to a higher level of accomplishment for that, or those, KSA(s)?

REFLECTIONS

1 If you supervise individual Master's &/or PhD students, think now about *their* levels of bioinformatics training.

2 For one or two such students, consider their stages of development. Can you identify KSAs in which they're least proficient?

3 For those KSAs, can you identify additional training, at a specific level, that might help to close their current skills gaps?

4 Consider classes in which you teach groups of students (who're typically at different stages of development). How might this approach help you to support weaker/stronger students in the class?

5 Consider how this approach could be used by students themselves to identify their *own* training needs.

4.2 Course design

As we've just seen, with its explicit developmental trajectory, the MR-Bi can be used to facilitate individuals' professional development by helping them to recognise their training needs, and thence to identify targeted training opportunities. It can also be used to support the design of short courses, by helping instructors to focus on teaching goals (and requisite LOs) that are time-limited.

To consider how this might work in practice, let's imagine being an instructor who wishes to develop a basic bioinformatics module or course: this could be a component of, say, a summer school or a wider Master's programme. The first step would be to identify the KSAs relevant to the course, and the appropriate developmental stages.

Suppose we want the module to confer foundational – Beginner-level – KSAs in *Biology* and *Computational methods*, and to build up to Apprentice-level KSAs in *Identifying & using appropriate methods*, *Interpretation of results*, *Drawing & contextualising conclusions*, and *Communication*. This means focusing on these stages and these KSAs alone, ignoring the rest, as shown in **Figure 6**.

To build a course around these (or indeed any course focusing on any KSAs), we recommend following a structured paradigm. Further details are given in the companion resource, *Course design: considerations for trainers – a Professional Guide*[15], and in its parent preprint[16]. These papers use Nicholl's 5-phase paradigm for curriculum/course design[17] as an exemplar – see **Figure 7**.

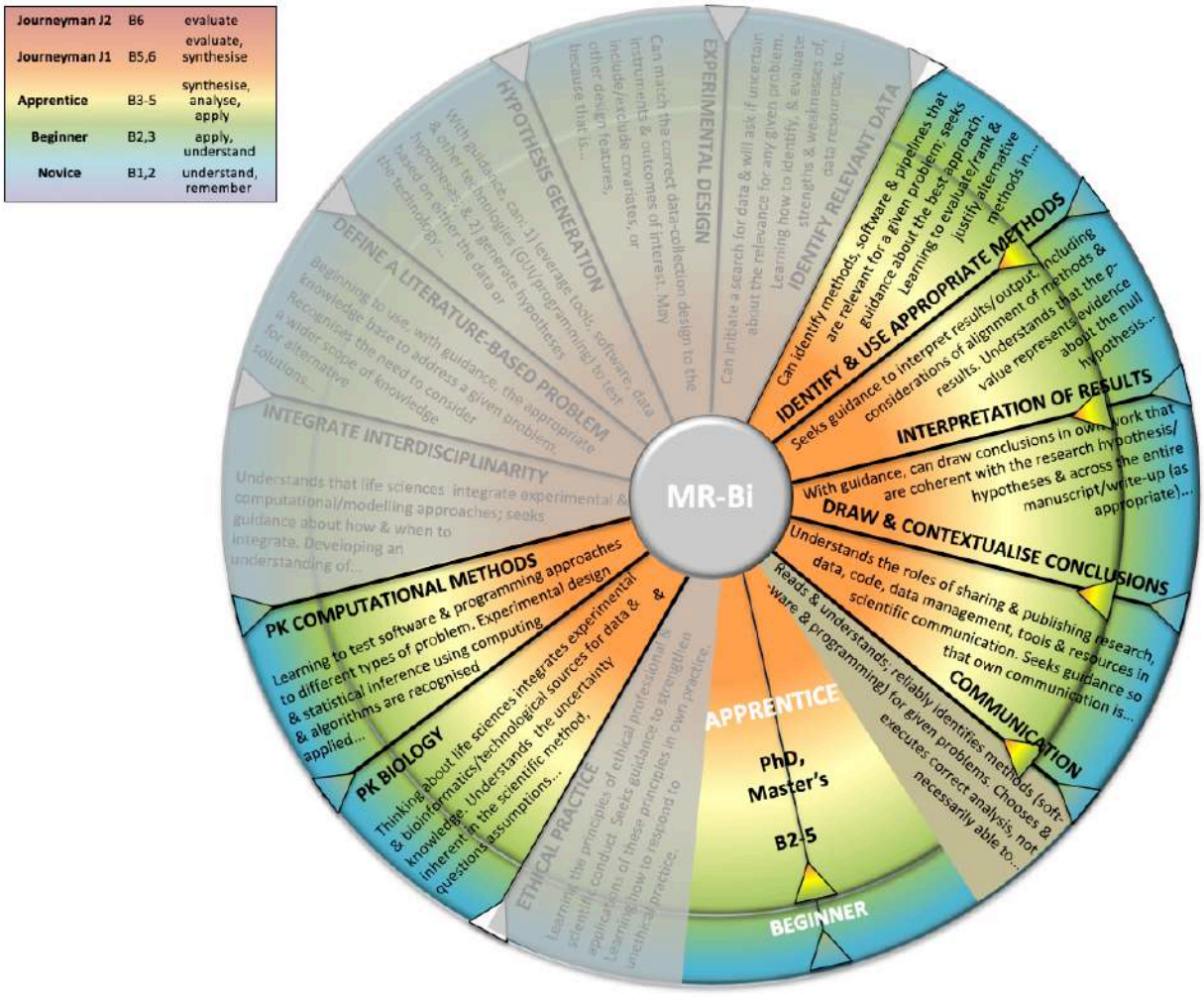

Figure 6 ***Course design with the MR-Bi.*** *To build a basic course in bioinformatics, an instructor selects seven target KSAs, ignoring the rest (greyed-out KSAs). The course aims to confer Beginner-level knowledge of Biology & Computational methods (bottom left-hand quadrant) & build to Apprentice-level skills in four other KSAs (right-hand side). The stages map to appropriate cognitive levels for Masters & early PhD students, Bloom's B2-B5.*

REFLECTIONS

1 Consider the stages in the example course in **Figure 6.** How might the MR-B's PLDs & KSAs help to write the course prerequisites?

2 How might the PLDs help to write the course description?

3 Think of a course you teach. Can you identify the developmental stages & KSAs it targets or spans?

4 Which Bloom's level(s) do you think your course aims to support? Is this consistent with the stages it targets or spans? If not, can you think of ways in which the MR-Bi might help to revise your course?

Nicholl's five phases of curriculum or course design

Nicholls' paradigm[17] for curriculum/course development comprises five key phases, as illustrated in Figure 7. The process involves i) defining intended Learning Outcomes (LOs), ii) selecting **Learning Experiences** (LEs) to help learners achieve those outcomes, iii) developing content relevant to the LOs, iv) devising assessments to ensure learner progression towards them, and finally, v) evaluating the effectiveness of the LEs for leading learners to the LOs.

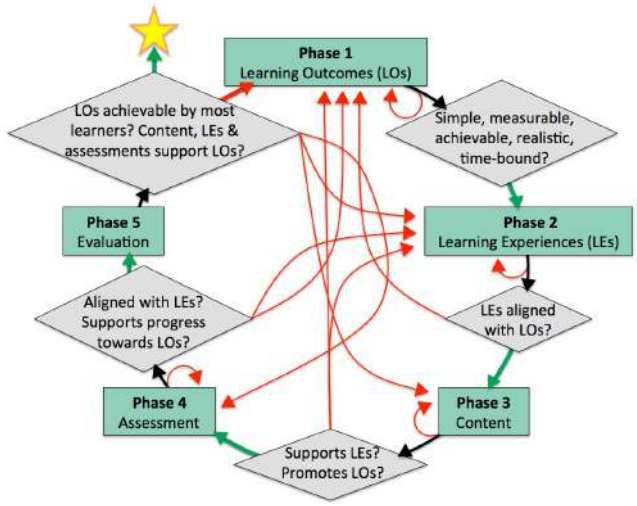

Figure 7 ***Nicholls' phases of course design & their dependencies.*** *At each phase, decision-points (grey diamonds) must be satisfied, otherwise that or the previous phase(s) must be revisited (red arrows), before moving on to the next phase (green arrows). The course-design process is considered complete (star) when all the criteria have been met.*

As Figure 7 shows, at each phase, decision-points test whether specific criteria have been met: *e.g.*, at Phase 1, are the intended LOs SMART – Specific, Measurable, Achievable, Realistic and Time-bound[15,16]? At Phase 2, are the LEs aligned with the LOs? At Phase 3, does the content support the LEs and promote the LOs? And so on. If the criteria at any decision-point haven't been met, either that or the previous phase requires revision, or Phase 1 needs revision. Only at the end of this iterative cycle of refinement can the process be regarded as complete. The crucial take-away here is that Phase 1 is the first-class citizen of the design process, because each phase must be congruent with it – and Phase 1 is articulating LOs. The role of LOs is thus pivotal: they must have specific characteristics to function, and support each of the other phases as they do.

Why LOs are important

The course-design process begins, then, by stating the intended LOs: as noted earlier, LOs are explicit statements of the KSAs (at the requisite level of cognitive complexity) that learners are expected to achieve, and be able to demonstrate, on completion of a period of instruction. To help formulate LOs, it's important to reflect on your TGs, the KSAs you intend to be achieved, how you propose to get there, and how you'll know whether you succeeded. Messick[18] encapsulated this process in the form of three succinct questions:

1. What KSAs are the targets of instruction (and assessment)?
2. What learner actions/behaviours will reveal these KSAs?
3. What tasks will elicit these specific actions or behaviours?

These questions support all phases of course development, guiding not only the creation of relevant tasks (to reveal the target KSAs) but also the rational development of suitable assessments (*i.e.*, clarifying *what to assess*), commencing with stating intended LOs. Ultimately, LOs provide structure and context for decision-making (by instructors and learners), hence their primary role in course design.

EXERCISES

1 Consider again a course you teach & the LOs it aims to deliver. Do the content, LEs & assessments support delivery of your intended LOs at the appropriate Bloom's levels?

2 For one (or all) of your LOs, create a lesson plan, as explained in detail in Supplementary Materials, **SM2** (page 15).

3 Did this process suggest that any adjustments might be needed to your course or are all of its components fully aligned with your LOs?

Using the MR-Bi to help define LOs

Writing coherent LOs is challenging: they must contain appropriate (Bloom's) verbs that express measurable, observable and assessable actions, describing what successful learners will be able to do – *and at what level of cognitive complexity* – after instruction[16] (further information on Bloom's verbs, and guidance on how to write effective LOs is available in the companion Guide[15] and elsewhere[19]). Broadly, this means making statements such as, "*by the end of this course, students will be able to X...*", where *X* is a verb at the requisite Bloom's level: *e.g.*, *define* (B1), *explain* (B2), *use* (B3), *infer* (B4), *generate* (B5), *justify* (B6). A small selection of such verbs is given in the box below.

Sample verbs at different Bloom's levels

Judicious choice of active verbs can inform the articulation of LOs, pitched at the relevant level of cognitive complexity. Briefly, these levels relate to 1) recalling information; 2) demonstrating an understanding of facts; 3) applying knowledge to real situations; 4) resolving complex ideas into simpler elements, and identifying patterns; 5) gathering ideas into a coherent whole, and creating new ideas; and 6) the ability to assess theories and outcomes, and make and defend judgements.

Bloom's level		Sample verbs
6	evaluate	justify, compare, contrast, critique, determine, appraise, rate
5	synthesise	combine, generate, integrate, devise, formulate, compose, illustrate
4	analyse	examine, infer, calculate, resolve, relate, test, solve
3	apply	perform, use, demonstrate, implement, manipulate, select, modify
2	understand	explain, discuss, exemplify, classify, distinguish, summarise, review
1	remember	define, describe, outline, identify, list, label, name

Recall that our example course aimed to grow in cognitive complexity, building from Beginner-level KSAs in *Prerequisite knowledge, biology* and *computational methods*. Looking at the PLDs for *PK, biology*, Beginner characteristics are described as follows:

"Advanced knowledge of biology, & basic knowledge of key bioinformatics methods... Learning to understand the uncertainty inherent in the scientific method, questions assumptions in the data..."

KEY TERMS

Learning Experience (LE): any setting or interaction in or via which learning takes place: *e.g.*, a lecture, game, exercise, role-play, *etc.*

As summarised in **Figure 8**, depending on the precise content of the course, appropriate Beginner LOs (Bloom's levels 2-3: *understand*, *apply*) for *Prerequsite knowledge, biology* might therefore be,

"*by the end of the course, students will be able to explain the natural processes of transcription & translation*" or

"*summarise the challenges of in silico gene prediction in terms of gene structure*".

Here, the verbs *explain* and *summarise* are at Bloom's level 2 (see box on previous page), reflecting learners' understanding of the specified biological concepts presented in the course, and their grasp of the uncertainty inherent in gene-prediction tools.

Moving on to the PLDs for *Prerequisite knowledge, computational methods*, as we saw earlier, the characteristics of the Beginner are described as:

"Learning how to write... code, run software, or use tools… Developing awareness of bioinformatics tools… & resources, but isn't able to choose or apply the most appropriate…. Developing awareness that tools require input parameters, but uses defaults. Learning to read … & make minor modifications to existing code/scripts."

Again, depending on the course content, suitable Beginner LOs for *Prerequisite knowledge, computational methods* might be,

"*by the end of the course, students will be able to classify popular bioinformatics databases*" or

"*perform BLAST searches online using default parameters*".

Here, the verbs *classify* and *perform* are at Bloom's level 2 and 3 (respectively), reflecting learners' understanding of the range of available bioinformatics resources, and their ability to use the default version of a commonly used search tool via the Web.

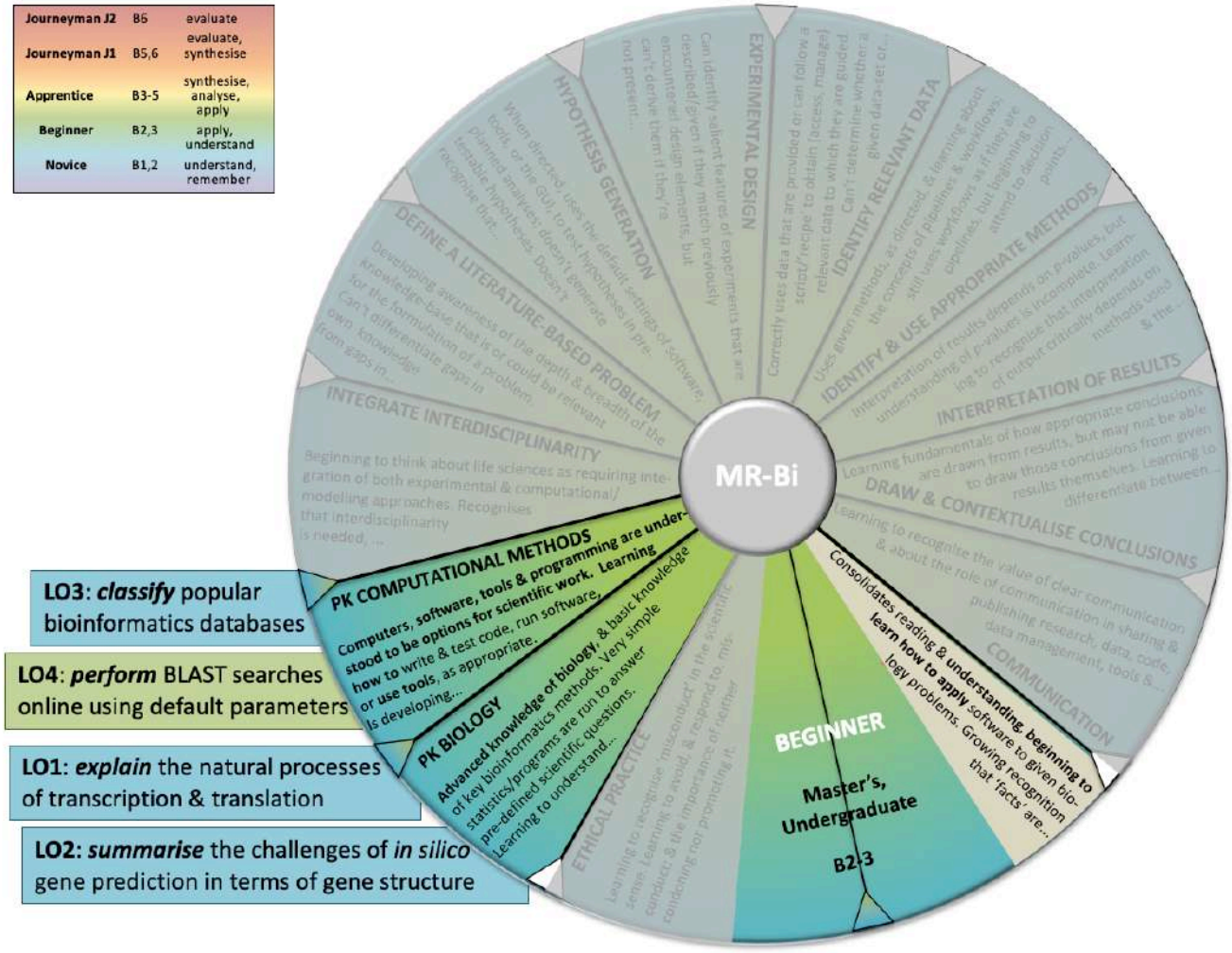

Figure 8 ***Devising Beginner-level Learning Outcomes (LOs) for Prerequisite knowledge, biology & Prerequisite knowledge, computational methods.***
Excerpts from the PLDs for the two highlighted KSAs are shown, alongside possible LOs for a Beginner-level course, at the appropriate Bloom's levels: B2-3 (understand, apply).

The course further aimed to develop learners to Apprentice-level in *Identifying & using appropriate methods*, *Interpretation of results*, *Drawing & contextualising conclusions*, and *Communication*. Looking, first, at the PLDs for *Identifying & using appropriate methods*, the characteristics of the Apprentice are described as follows:

"Can identify methods, software & pipelines relevant for a given problem; seeks guidance about the best approach. Learning to rank & justify alternative methods in terms of… their efficiency & relevance... Learning how reproducibility can be affected by the choice & implementation of methods, including independent replication of the same method vs. using diverse methods."

As summarised in **Figure 9**, depending on the specific course content, an appropriate Apprentice-level LO (Bloom's levels 3-5: *apply*, *analyse*, *synthesise*) for *Identifying & using appropriate methods* might therefore be,

"*by the end of the course, students will be able to use pattern-recognition tools to identify the families to which protein sequences belong.*"

Here, the verb *use* is at Bloom's level 3, reflecting learners' ability to apply different analysis tools to determine the likely functions of uncharacterised protein sequences.

Moving on to the PLDs for *Interpretation of results*, the characteristics of the Apprentice are described as:

"*Seeks guidance to interpret results/output… Recognises that, but doesn't always act as if, very small p-values are not 'highly significant results'... Recognises when the interpretation of immediate results is an interim step in an overall problem-solving context.*"

Again, depending on the course content, a suitable Apprentice-level LOs for *Interpretation of results,* might be,

"*by the end of the course, students will be able to examine search outputs to determine the biological significance of results*".

Here, the verb *examine* is at Bloom's level 4, reflecting learners' ability to analyse program outputs and infer their significance.

Looking at the PLDs for *Drawing & contextualising conclusions*, the Apprentice is described as follows:

"*With guidance, can draw conclusions… coherent with the research hypothesis... Learning to critically contextualise results; draws the most obvious conclusions, but struggles to see patterns... Learning to recognise how independence of multiple methods applied to similar data/problems supports reproducible conclusions.*"

Here, a feasible Apprentice-level LO for *Drawing & contextualising conclusions,* might be,

"*by the end of the course, students will be able to combine results of multiple search outputs to draw functional conclusions about novel protein sequences*".

Here, the verb *combine* is at Bloom's level 5, reflecting learners' ability to synthesise diverse program outputs in order to draw meaningful conclusions.

Finally, in the PLDs for *Communication*, the characteristics of the Apprentice are described as:

"*Understands the roles of sharing & publishing… in scientific communication... Learning to document code, annotate data & add metadata – & the importance of these…. Learning the importance of adapting communication to fit the receiver... Learning that transparency in all communication represents ethical practice...".*

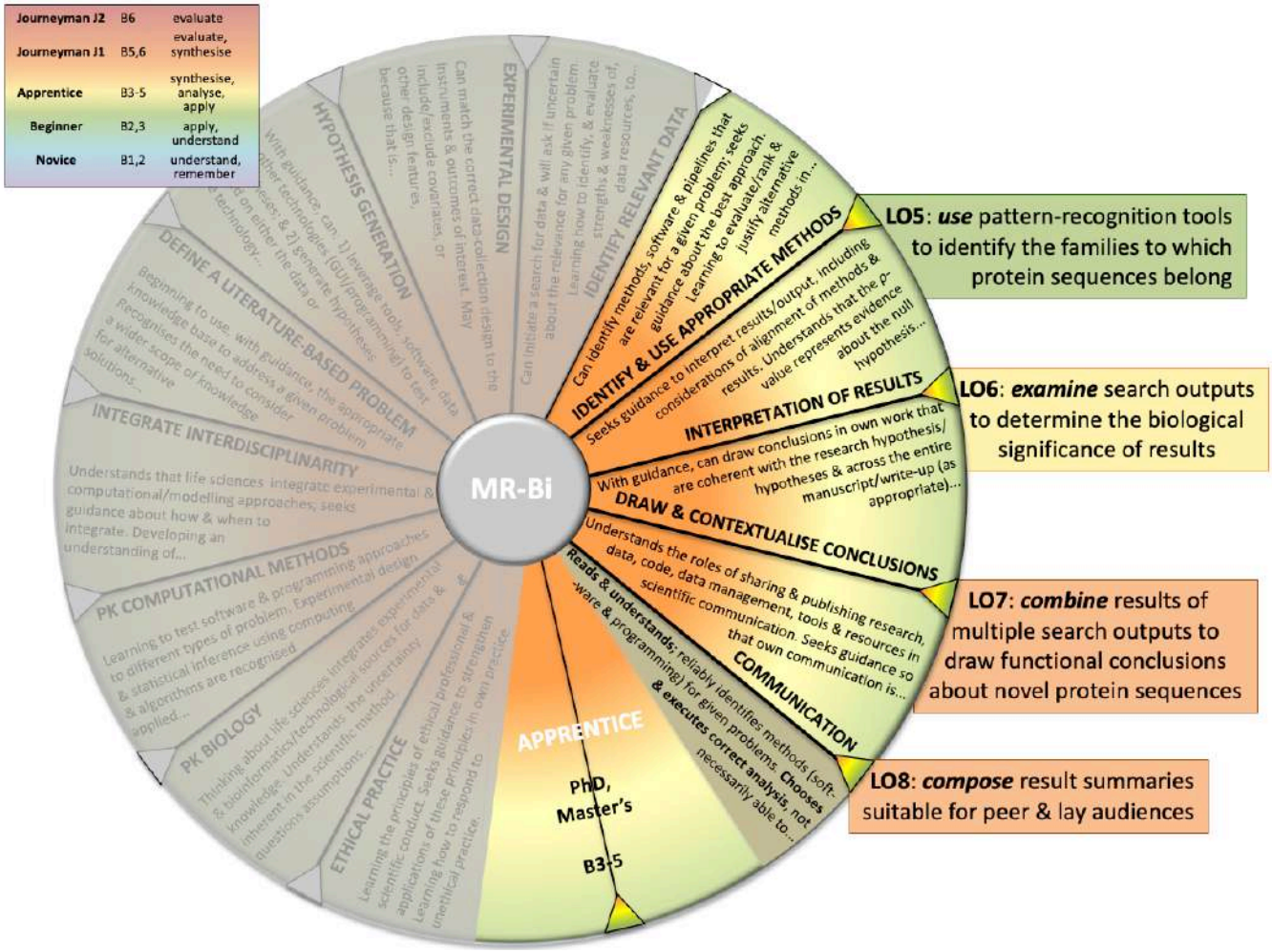

Figure 9 ***Devising Apprentice-level learning outcomes for Identify & use appropriate methods, Interpretation of results, Draw & contextualise conclusions, & Communication.*** *Excerpts from the PLDs for the four highlighted KSAs are shown, alongside possible LOs for an Apprentice-level course, at the appropriate Bloom's levels: B3-5: apply, analyse, synthesise.*

A reasonable Apprentice-level LO for *Communication* might thus be,

"by the end of the course, students will be able to compose result summaries suitable for peer & lay audiences".

Here, the verb *compose* is at Bloom's level 5, reflecting learners' ability to integrate a range of disparate results, and to formulate them appropriately for reception by different audiences.

The above LOs are obviously just exemplars – any other set could equally have been created, depending on the content of our imaginary course. What's important is the process we went through to devise them: the selected course KSAs, coupled with the PLDs at the requisite stages (Beginner, Apprentice), constrained the scope of the target outcomes, while judicious choice of the relevant Bloom's verbs helped to produce outcomes broadly consistent with SMART criteria.

EXERCISES

1 Consider the table you created in the previous exercise for some (or all) of the LOs of a course you teach. This table provides a mechanism for aligning your TGs with your LOs, LEs & content (including assessments), offering a virtuous cycle for course revision until its components are congruent with the targeted Bloom's levels.

2 Let's now extend this table to include key elements of the MR-Bi.

3 Add two columns to the left of the table, labelling them KSA & PLD (if the table gets too big, consider removing the '*Content*' column). To get the idea, refer to the example table, which combines all of these elements, in Supplementary Materials, **SM3** (page 16).

4 For each LO, in the KSA column, write down which KSA is targeted by that LO; in the PLD column, write the relevant descriptions, at the appropriate Bloom's level, that apply to each LO.

5 Having completed the table, were any further adjustments needed, or did all the course components (including the allocated time) remain fully aligned &/or appropriate? For reference, compare your final result with the table in Supplementary Materials, **SM3.**

5 Discussion

At first sight, the MR-Bi may seem daunting, and its possible roles in professional development and course design not obvious. Nevertheless, when broken down to focus only on the components relevant to a specific application, it can be a useful assistive tool.

In the context of course design, for example, it allows instructors to fix on just the KSAs encapsulated in the training session(s), and only at the target developmental stage(s) – thus, for the purposes of developing a short course, most of the rest of the MR-Bi can be ignored. The PLDs for the selected KSAs can then help to inform the articulation of LOs, ensuring that they're specific to the scope of those KSAs, and providing context for typical learner behaviours and cognitive abilities at those stages. In turn, in concert with the particular course content, this facilitates choice of relevant Bloom's verbs to accurately depict what learners will be able to do by the end of the course.

Of course, choosing Bloom's verbs to draft LOs for any course can be done without reference to the MR-Bi. However, using the MR-Bi as an organising framework helps to keep LOs in scope, not just in terms of the KSAs targeted, but also in terms of *the cognitive abilities and behaviours made explicit in the PLDs*. A key contribution the MR-Bi brings here is that it's broadly content agnostic – its primary focus is on developing behaviours and habits of mind consistent with the rigours of the scientific method: *e.g.*, for a basic course on protein sequence analysis (aiming, say, to progress a Beginner to Apprentice level), reference to Bloom's might yield a simple LO as follows,

"by the end of the course, learners will be able to infer the functions of novel protein sequences".

Using the MR-Bi, however, allows us to go a step further. For example, the PLDs for *Drawing & contextualising conclusions* suggest that an Apprentice is,

"Learning to critically contextualise results... Learning that 'full' contextualisation of conclusions requires consideration of limitations deriving from methods & their applications, & their effects on results & conclusions. Learning to recognise how independence of multiple methods applied to similar data supports reproducible conclusions."

With this in mind, as we saw earlier, a more specific LO could be,

"by the end of the course, learners will be able to combine results of multiple search outputs to draw functional conclusions about novel protein sequences."

This LO, then, informed by the relevant PLDs for this KSA, makes clear the *behaviour* (combining multiple methods) that will lead learners to be able to make appropriate functional conclusions. Note also the progression in the PLDs above from those at Beginner level:

*"Learning fundamentals of how appropriate conclusions are drawn from results, but may not be able to draw those conclusions from given results themselves… Conclusions are generally aligned with given results, but when multiple methods are used, **doesn't recognise the dependencies among methods that appear to reinforce, but actually replicate, results**..."*

Overall, then, using the MR-Bi allows instructors to structure their courses around specific KSAs at particular developmental stages; its PLDs then help them to formulate very focused LOs, by explicitly describing and *staging* performance levels such that they can be achieved progressively along a path of increasing cognitive complexity. The PLDs thereby also facilitate consistent evaluation of learner performance within each of the selected KSAs.

Another important aspect the MR-Bi is that it recognises that individuals may be at different levels in different KSAs, and may progress through them at different speeds. Reference to the PLDs allows individuals wishing to acquire bioinformatics skills to locate themselves within the table, regardless of their current skill level or disciplinary background: *e.g.*, a person may consider him/herself a *J2 Journeyman in the life sciences*, yet a *Novice in computational methods*. The MR-Bi can thus pinpoint a learner's stage (hence current level of performance of any KSA), highlight potential training gaps, and thereby a route(s) – or 'learning path(s)' – for self-directed learning, from lower-level to higher-level skills. This feature can also be exploited by instructors, who may have a mix of students within their class with different aptitudes, some at Novice and some at Beginner levels of cognitive complexity, with others perhaps even at Apprentice or higher levels. Such understanding can help instructors to pitch, and if necessary to adjust, their teaching accordingly (*e.g.*, by setting additional LOs targeting more advanced levels of critical-thinking skills and cognitive behaviour just for those individuals).

In this Guide, we've seen that the MR-Bi is a versatile tool, with applications ranging from the structured development of training

courses to the elucidation of potential individual learning paths. If you need more details about the MR-Bi's key features, we recommend reading the introductory companion resource[12].

TAKE HOMES

1. The MR-Bi is a comprehensive tool that can facilitate professional development & course design;
2. Its principal components are i) five developmental stages (from Novice to late Journeyman), ii) 12 (primarily scientific-method focused) KSAs, & iii) a set of associated PLDs;
3. The PLDs describe how performance & critical thinking typically change as learners progress through the developmental trajectory;
4. The developmental stages can be mapped both to specific Bloom's-levels of cognitive complexity & to broad academic levels;
5. The interplay between these elements allows i) learners to pinpoint their current skill levels & hence to gauge their training needs; & ii) instructors to design courses in a structured way;
6. Specifically, instructors may identify, & focus on, the subset of KSAs & stages directly relevant to their course, & then use the associated PLDs, alongside appropriate Bloom's verbs, to articulate LOs;
7. This structured approach helps to constrain the scope of the intended LOs, ensuring that they target the relevant levels of cognitive development, & that they're specific & realistically achievable within the time-frame of the course.

6 References & further reading

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13 Bloom BS. (1956) ***Taxonomy of educational objectives: the classification of educational goals. Handbook 1: The cognitive domain.*** David McKay, New York, USA.

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18 Messick S. (1994) **The interplay of evidence and consequences in the validation of performance assessments.** *Educational Researcher,* **23**(2), 13-23.

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GOBLET Professional Guides build on GOBLET's Critical Guide concept, using layout ideas from the Higher Apprenticeship specification for college-level students in England. The contents herein build on *The Mastery Rubric for Bioinformatics: a tool to support design and evaluation of career-spanning education and training* by Tractenberg *et al.*, 2019[11].

8 Licensing & availability

The Guide is freely available for download via the GOBLET portal (**www.mygoblet.org**) and the F1000Research Bioinformatics Education and Training Collection (**f1000research.com/collections/bioinformaticsedu?selectedDomain=documents**).

9 Disclaimer

Every effort has been made to ensure the accuracy of this Guide; GOBLET cannot be held responsible for any errors/omissions it may contain, and cannot accept liability arising from reliance placed on the information herein.

Introduction

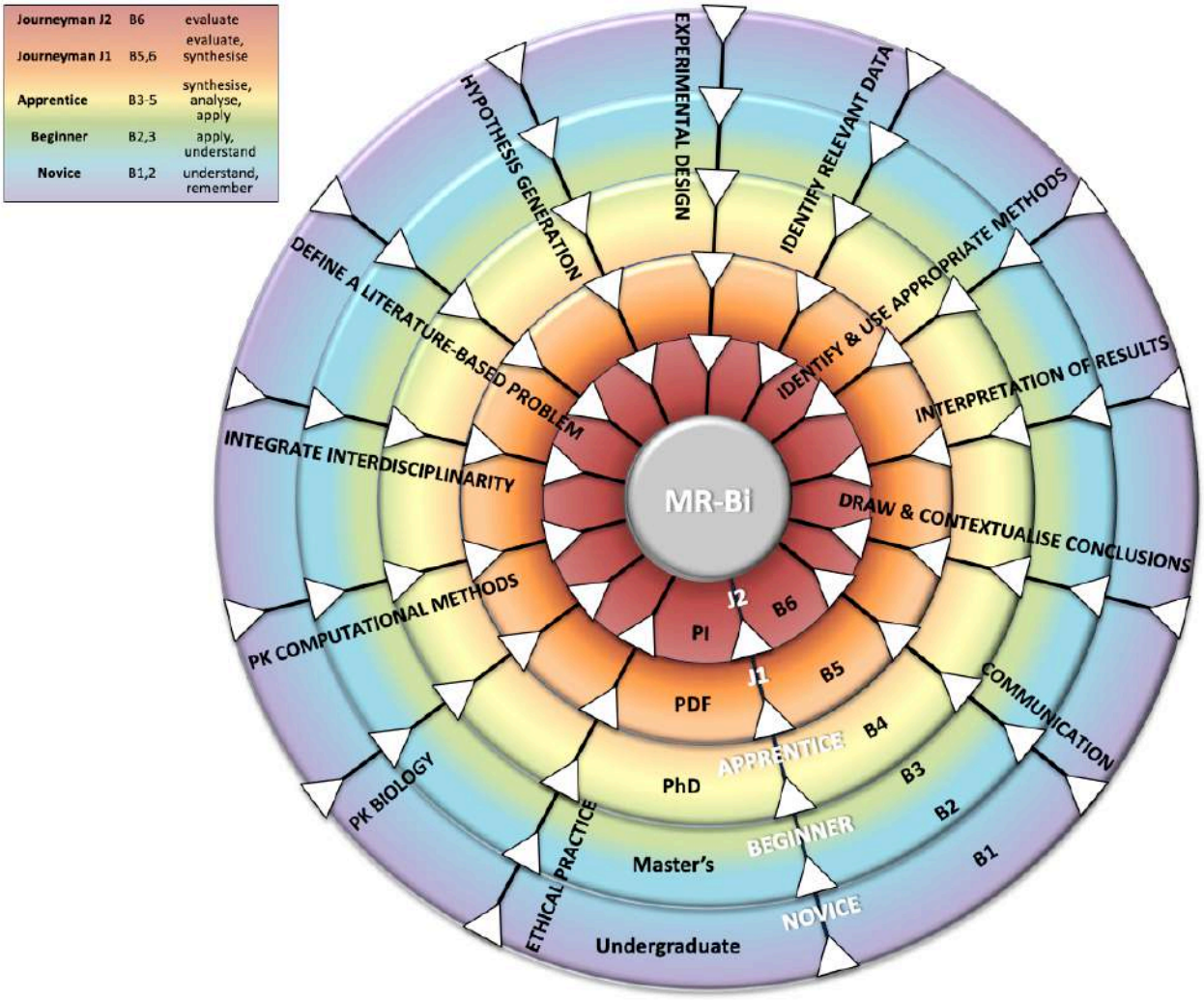
The following Supplementary Materials (SMs) have been developed to support *Using the Mastery Rubric for Bioinformatics – a Professional Guide* (pages 1-13 above), with some practical applications of the MR-Bi to professional development, lesson planning and course design.

SM1 Professional development – using the MR-Bi to define an individual learning path

The structure illustrated below shows the layers of the MR-Bi building from Novice to J2 Journeyman, with corresponding changes in Bloom's levels of cognitive complexity. The KSAs (elaborated in more detail in the companion Guide, *Introducing the Mastery Rubric for Bioinformatics*[1]) are shown as radial 'spokes'. This structure can be used as a template to facilitate professional development, both for yourself and/or for any individuals you supervise.

To identify your own stage of development for each KSA, you can tick the triangles at the requisite stage along each spoke. This may highlight areas where specific training could be useful, and the level of training needed (beginner, advanced, *etc*.) to close the identified skills gaps, allowing you to track your development from your current to higher levels of performance: *e.g.*, you may consider yourself a life science J2 Journeyman, but tick Beginner-level KSAs *Prerequisite knowledge, computational methods* and *Identify & use appropriate analytical methods*, because you wish to learn how to write code, and want to know what bioinformatics methods are available for characterising protein sequences, and how to use them. The descriptions for these KSAs embody the Bloom's levels (2-3: *understand, apply*) typically delivered in modules of late undergraduate or early Master's programmes, or in introductory training courses. This allows you to choose a 'learning path' for these KSAs that best suits your needs, whether full modules within degree courses or, say, specific short training courses online, depending on the time you have available.

You can use the same approach with individuals you supervise. For each KSA, you can help them to pinpoint their stage of development, then (looking at the general descriptions and PLDs) jointly identify the training required to take them to the next level(s) of performance.



SM2 Instruction design in practice: creating & using a lesson plan to implement Nicholls' five steps

In SM2, we offer a pragmatic approach to implementing Nicholls' five steps[2,3] in your everyday lesson-planning practice. The example here is based on the 'basic bioinformatics module' described in section 4.2 (pages 8-12), centring on a 1.5-hour lesson aiming to achieve **LO4:** ***Perform*** *BLAST searches online using default parameters*.

As an instructor, you must first decide whether, based on your experience and your learners' prior knowledge, this LO is achievable in the allotted time. If not, then you'll either need to allocate more time to your in-class LEs, or give additional learning opportunities and/or materials ahead of the lesson. It may be helpful, both for you and for your learners, if you write down the knowledge you'll need to impart in order for them to be able to achieve the LOs. You can write this in the same style generally used for articulating LOs. For example:

To achieve LO4, learners should be able to describe the main features of the BLAST algorithm, to explain its purpose & limitations, & to explain the main features of its Web interface.

Now, create an empty table with the following column headers:

1.TG	2.Bloom's & LO	3.Time	4.LE	5.Description	6.Content

1. TG (Teaching Goals)
2. Bloom's & LO (Bloom's level & Learning Outcomes)
3. Time (time available or needed for instruction/learning activity)
4. LE (Learning Experience type, including formative assessment)
5. Description (may also describe the type of assessment)
6. Content/materials (may also include assessment materials)

SM 2.1 Creating the lesson plan

To elaborate the lesson plan, complete the above empty table by performing the following steps:

Step 1 Insert LO4 in column 2. At this point, consider the Bloom's level of cognitive complexity the LO targets: here, ***perform*** suggests Bloom's level 3 – ***apply*** (relevant verbs: *perform*, *use*, *demonstrate*, *implement*, *etc.*). It may help if you colour column 2 according to the targeted Bloom's level (for a reminder of the Bloom's levels/colours, refer to the figure on page 14 above in SM1), which will help to ground your instruction, and intended LOs, in the same expected level of achievement.

Step 2 Focus on the verb – ***perform*** – and on the action/task learners will be able to do by completing a sequence of LEs: *i.e.*, to ***Perform*** *BLAST searches online using default parameters*. To be able to do this, learners will need to:

1. Gain knowledge of the BLAST Web interface, understand its main features, and how to use them (including changing its parameters) to perform searches;
2. Practice the activity of ***performing*** BLAST searches.

Consider your TGs ***and*** the LEs you'll use to deliver them. In column 1, write your LO4 TGs; in column 4, enter the LEs that will lead learners to achieve LO4, estimating the time available/needed for each LE in column 3; insert specific descriptions of the LEs in column 5.

Step 3 In column 6, for each LE, specify the materials (which, taken together, represent the content needed to lead learners to achieve LO4). In this column, it might also be useful to provide links and/or references to the materials.

The final result may resemble the completed table illustrated below. Adopting the process of compiling such a table in your teaching practice can help you to concentrate on the Bloom's level appropriate for your intended LO(s), and to iteratively refine i) the LO(s), ii) the time allocated to achieving them, and iii) your TGs, so that all are ultimately congruent. This can help you both to keep to the topic and to temper your expectations of what learners will be able to achieve; if shared with learners, it can also clarify what they can expect from any given teaching session and, also, what will be expected of them.

Note that the table could also contain rows for course evaluation steps; however, for simplicity, course evaluation isn't dealt with further here. A more extensive table, for a much larger course in which LO4 is one of four LOs, is elaborated in SM3, showing how TGs and LOs are further informed by the cognate KSAs and PLDs of the MR-Bi.

TG	Bloom's & LO	Time	LE	Description	Content/materials
To introduce the BLAST Web interface, to explain how it works & show how to **perform** searches	**B3: apply** LO4: **Perform** BLAST searches online using default parameters	30 min	Participative lecture & demo; learners follow on their own computers	Describe BLAST, its purpose & limitations, explain how it works, including the meaning of input parameters & how those affect results. Show how to run Web-based searches of protein *sequence* databases	BLAST Web interface.
To show how to **use** BLAST with different parameters & how this affects outputs		20 min	Hands-on tutorial	Ask learners to perform a BLAST tutorial where they'll apply both default & custom parameters to search sequence databases. The tutorial will reveal differences in the results	Tutorial on BLAST Web interface & different types of search
To give practice at **performing** searches & reinforce learning		25 min	Work in pairs	Ask learners to run further BLAST searches with another set of sequences, & to describe their results in a shared document, noting their search parameters	Input sequences & databases; shared document
To give feedback, & ensure learners know how to **apply** different BLAST parameters		15 min	Formative feedback/ Q&A session	Discuss the shared document, comment on the results described by the pairs	Shared document

SM 3 Using the MR-Bi in conjunction with Nicholls' phases of course design to inform lesson planning

This table shows an exemplar course on using bioinformatics databases & BLAST for protein sequence analyses. The course addresses three KSAs & targets four LOs, each at a different Bloom's level. The table shows how, for each KSA, the respective PLDs inform both the TGs & LOs. It further shows how to organise appropriate LEs for delivering the intended LOs & the time available or required for each, including time set aside for formative assessment. The final column describes in more detail what each LE entails.

KSA	PLD	TG	Bloom's level, LO	Time	LE	Description
Prerequisite knowledge, computational methods	*Learning how to write... code, run software, or use tools... **Developing awareness of bioinformatics tools... & resources**, but isn't able to choose or apply the most appropriate.... Developing awareness that tools require input parameters, but uses defaults. Learning to read ... & make minor modifications to existing code/scripts.*	To provide context, describe popular bioinformatics databases, & to explain their differences & similarities	**B2: understand** LO3: **Classify** popular bioinformatics databases	30 mins	Participative lecture (slides & demo)	Describe some popular bioinformatics databases (protein/DNA sequence, protein family, protein structure), the data they contain & how the data were generated (how similar/different the underlying methods are). Show where to find the resources & how to navigate them; learners follow on their computers
		To give learners practice at exploring databases & **understanding** their contents		35 mins	Work in pairs	Give learners further examples of named databases. In pairs, ask them to locate the resources, explore their contents & write their classifications to a shared file
		To provide feedback, & ensure learners know how to **classify** resources		10 mins	Formative feedback/ Q&A session	Discuss the shared document, comment on the classifications made by the pairs
		Establish whether learners have remembered & **understood** the differences between databases		15 mins	MCQ	Ask learners to complete a short MCQ in which they must classify given bioinformatics databases according to the type of data they contain (protein/DNA sequence, protein family, protein structure...)
Prerequisite knowledge, computational methods	*Learning how to write... code, run software, or use tools... Developing awareness of bioinformatics tools... & resources, but isn't able to choose or apply the most appropriate.... **Developing awareness that tools require input parameters, but uses defaults.** Learning to read ... & make minor modifications to existing code/scripts.*	To introduce the BLAST Web interface, to explain how it works & show how to **perform** searches	**B3: apply** LO4: **Perform** BLAST searches online using default parameters	30 mins	Participative lecture & demo; learners follow on their own computers	Describe BLAST & its purpose, explain how it works, including the meaning of input parameters & how those affect search results. Show how to run Web-based searches of protein *sequence* databases
		To show how to **use** BLAST with different parameters & how this affects outputs		20 mins	Hands-on tutorial	Ask learners to perform a BLAST tutorial in which they will apply both default & custom parameters to search sequence databases. The tutorial will reveal differences in the results
		To give practice at **performing** searches & reinforce learning		25 mins	Work in pairs	Ask learners to run further BLAST searches with another set of sequences, & to describe their results in a shared document, noting their search parameters
		To give feedback, & ensure learners know how to **apply** different BLAST parameters		15 mins	Formative feedback/ Q&A session	Discuss the shared document, comment on the results described by the pairs
Interpretation of results	*Seeks guidance to interpret results/output... **Recognises that, but doesn't always act as if, very small p-values are not 'highly significant results'**... Recognises when the interpretation of immediate results is an interim step in an overall problem-solving context.*	To show how to **examine** & interpret different database search outputs, & how to infer biological significance from search results	**B4: analyse** LO6: **Examine** search outputs to determine the biological significance of results	30 mins	Demo	Show how to search a range of protein family databases, explain how to interpret the outputs, & how to infer biological significance from the results. Explain, with examples, the difference between statistical & biological significance (*e.g.*, by showing a statistically significant result that is not biologically significant)
		To give learners practice running different searches, **analysing** outputs & determining the significance of results		40 mins	Hands-on practical	Ask learners to follow a tutorial, using both characterised & uncharacterised sequences to search various protein sequence & protein family databases. Ask them to examine the results, to determine their biological significance & to write their results to a shared document
		To give feedback, ensure learners can **analyse** search outputs		20 mins	Formative feedback/ Q&A session	Discuss the shared document, comment on the results described by the pairs
Drawing & contextualising conclusions	*With guidance, can draw conclusions... coherent with the research hypothesis... **Learning to critically contextualise results**; draws the most obvious conclusions, but struggles to see patterns... **Learning to recognise how independence of multiple methods applied to similar data/problems supports reproducible conclusions.***	To show the importance of running *independent* searches, & how **combining** multiple, independent search results leads to more reliable functional conclusions	**B5: synthesise** LO7: **Combine** results of multiple search outputs to draw functional conclusions about novel protein sequences	45 mins	Work in pairs	Ask learners to discuss the results obtained in the previous activity for the *uncharacterised* sequences. Specifically, ask them i) to combine results of their multiple searches, noting the independence (or otherwise) of the underlying search methods & ii) to assess their biological significance & hence draw functional conclusions, writing their conclusions to a shared document
		To give specific feedback on the outcome of each pair's work, to ensure learners can **synthesise** multiple search outputs. To stimulate critical thinking		45 mins	Formative feedback/ Q&A session	Discuss the shared document, ask learners to explain how they arrived at their conclusions, provide feedback

The table above illustrates how to amalgamate key components of the MR-Bi with Bloom's levels of cognitive complexity and some of the principal components of Nicholls' five phases of course design. Following this approach helps you to build individual modules – and ultimately entire courses – in a structured way.

Looking at the table more closely, you can see that judicious choice of KSAs allows you to define the full scope of your module or course, helping you to keep your instruction 'on topic'. Drilling down to specific aspects of the cognate PLDs of those KSAs further helps to constrain what you teach (your TGs), what you want learners to be able to do (your intended LOs) following your course of instruction, and – crucially – at what Blooms' level; this helps to ensure that you pitch your instruction at the relevant Bloom's level and don't expect LOs to be achieved at a higher level.

This structured approach also gives you the opportunity to consider both the LEs that you believe are the most appropriate for delivering your intended LOs, and the assessments that will allow you to determine whether they've actually been achieved. In addition, the time available for instruction and/or the time needed to accomplish the LOs is included in the table; importantly, this allows you to determine whether what you've set out to achieve is realistic within the time-frame you've chosen or that you've been given – if not, the approach gives you scope either to reduce the number of LOs to be delivered within that time-frame, if you can't change the time available, or, if you can, simply to allocate more time in which to be able to achieve them.

Bringing all these components – these best practices – together is an efficient and powerful way to ensure that your TGs and LEs are fully aligned with your LOs, that the time set aside for instruction is appropriate, and that your selected LEs (and assessments) will help to deliver the LOs effectively. This is the first, and currently the only, tool that succinctly synthesises key components of the MR-Bi and Bloom's levels of cognitive complexity with elements of Nicholl's five phases of course design.

Note that a further column could be added to the table above, outlining the requisite teaching materials for each LO (as shown in **SM2**); moreover, additional rows could be added to allow inclusion of course evaluation; however, the table is already large, and space doesn't permit us to include further columns and rows here. Nevertheless, adopting the structured approach distilled into the table shown here in **SM3** should help you plan your instruction more effectively in future – as such, we strongly recommend that you try to incorporate it into your routine teaching practice.

References & further reading

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GOBLET Professional Guides build on GOBLET's Critical Guide concept, using layout ideas from the Higher Apprenticeship specification for college-level students in England. The contents herein build on *The Mastery Rubric for Bioinformatics: a tool to support design and evaluation of career-spanning education and training* by Tractenberg *et al.*, 2019[4].

Licensing & availability

Disclaimer

About the organisations

GOBLET

GOBLET (Global Organisation for Bioinformatics Learning, Education & Training; **www.mygoblet.org**) was established in 2012 as a not-for-profit foundation to unite, inspire and equip bioinformatics trainers worldwide; its mission, to cultivate the global bioinformatics trainer community, set standards and provide high-quality resources to support learning, education and training.

GOBLET's ethos embraces:

- ***inclusivity****: welcoming all relevant organisations & people*
- ***sharing****: expertise, best practices, materials, resources*
- ***openness****: using Creative Commons Licences*
- ***innovation****: welcoming imaginative ideas & approaches*
- ***tolerance****: transcending national, political, cultural, social & disciplinary boundaries*

For general enquiries, contact **info@mygoblet.org**.

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ELIXIR

ELIXIR is an intergovernmental organisation that brings together life-science resources (databases, software tools, training courses, cloud storage, *etc.*) from across Europe. The aim is to create a single infrastructure, making it easier for scientists to find and share data, exchange expertise, and agree on best practices: **elixir-europe.org**.

Through its Training Platform, ELIXIR is:

- providing services and tools for bioinformatics training, such as the Training e-Support System, TeSS (**tess.elixir-uk.org**), the ELIXIR Training Metrics Database (**training-metrics-dev.elixir-europe.org**) and the training Toolkit;
- supporting training providers across Europe by creating and delivering training for developers, researchers and trainers;
- building a sustainable training infrastructure.

Since 2015, the ELIXIR Training Platform and GOBLET have worked closely to promote and develop standards and best practices in bioinformatics training; the outcomes of this enterprise (peer-reviewed articles, training documents (Guides), posters, slides) are available from the F1000Research Bioinformatics Education & Training collection (**f1000research.com/collections/bioinformaticsedu**). Together, they have built a Train-the-Trainer (TtT) programme, which comprises a standard curriculum, associated training materials and well-trained instructors. To date, thousands of scientists have benefitted from this programme.

For general enquiries, contact **info@elixir-europe.org.**

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