Ecological Field Monitoring Protocols Manual

Using the Ecological Monitoring System Australia

Basal Area Module

tern Ecosystem Research Infrastructure

NCRIS National Research Infrastructure for Australia An Australian Government Initiative

Australian Government Department of Climate Change, Energy, the Environment and Water

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Version

Readers are advised that all modules of the Ecological Field Monitoring Protocols Manual regularly undergo revision. Readers should check the website tern.org.au/emsa-protocols-manual/ to ensure they are viewing the current version.

Version 2

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Acknowledgements and contributors

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Key components of this module were developed, written, and field tested by the TERN Ecosystem Surveillance team based at The University of Adelaide. Additional to the authors, the following team members made contributions to the project: Beth Cox, Kate Matthews, Tamara Potter, Rhys Morgan, David Peacock, and Carly Steen. Technical components, including the development of the accompanying app, were developed by the team led by Andrew Tokmakoff, including Luke Derby, Matthew Barty, Jin Zhou, Hoy Hai Huy Vo, Walid Al Naim, Muhummad Khan, and Michael Doroch. Aspects of the protocols that have been built on by this project are the result of the extensive and ongoing body of work conducted by the TERN Ecosystem Surveillance team, as part of TERN's field-based ecosystem monitoring program. A full list of team members who have contributed is available on the TERN eSupport Services website.

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Photographs presented in this report are provided by TERN unless otherwise indicated.

Main front cover photograph: Spring Gully Conservation Park, South Australia.

Version control

Readers are advised that all modules of the Ecological Field Monitoring Protocols Manual regularly undergo revision. Readers should check the website emsa.tern.org.au/documents to ensure they are viewing the current version.

The version history of this module is identified below. The Version history of the Ecological Field Monitoring Protocols Manual, the methods and data implications, both historical, current and future interpretations of data, are available from the TERN website. Enquiries should be directed to tern@adelaide.edu.au.

Version	Date	Version update overview
1	21 July 2023	First published version
2	28 November 2024	Updated details in the plot size and add tree steps in the DBH protocol; updated details in the record floristics voucher step in the basal wedge protocol.

About the Ecological Field Monitoring Protocols Manual

This module is one of many that form the *Ecological Field Monitoring Protocols Manual* using the *Ecological Monitoring System Australia* (EMSA), available at emsa.tern.org.au/documents. EMSA has been developed by the Terrestrial Ecosystem Research Network (TERN) in collaboration with the Australian Government Department of Climate Change, Energy, the Environment and Water (DCCEEW) to support the Natural Heritage Trust (NHT). The protocols included in the modules build on previous work by numerous ecologists throughout the country (acknowledged in the text) and have been refined with the help of Australia's natural resource management (NRM) community. They provide users with a clear set of protocols to measure and monitor most Australian ecosystems quantitatively and repeatably to enable the reliable quantification of environmental change.

The system addresses many limitations evident in previous NRM programs that have made this change quantification difficult. These included measuring or estimating environmental occurrences with disparate and often incompatible methods, particularly over a range of geographic scales, along with previous inefficiencies in data provision and analysis. The EMSA protocols presented in the modules provide clear and proven methods (built upon previous method/s where appropriate) to accurately measure environmental change for many variables of interest in Australian terrestrial environments. The modules are supported by a toolset to collect and deliver data to the Australian Government's Biodiversity Data Repository, which will see various management, policy and research outcomes informed by the data collected.

The current set of 24 modules is not an exhaustive list, and TERN and DCCCEEW may develop additional modules in the future as gaps are identified. We intend these modules and the supporting Monitor app to be widely accessible, with little assumed knowledge, using methods that NRM practitioners and ecologists can easily adopt. To support the uptake of the protocols, we are also developing a series of education and guidance materials and an in-person training course. We anticipate that users outside of the NHT funded projects may be interested in utilising these protocols. The team plans to make a version available in the near future that will be independent of the NRM project management system - the monitoring, evaluation, reporting and improvement tool (MERIT), to enable that widespread use.

We acknowledge, value and respect the experiences, perspectives and cultures of Indigenous Australians. We recognise the importance of combining Indigenous and western environmental knowledge systems to improve ecological monitoring in Australia. The EMSA protocols are designed to be implemented alongside First Nations protocols, procedures and policies, and we look forward to working in partnership with Indigenous land managers on future versions of these protocols.

The protocols detailed here are freely available for widespread use by acknowledging their source. The protocols will be refined over time, so we encourage you to download the latest version before using them. We look forward to continuously improving these protocols in the same way as we utilise an adaptive management framework on the environments we monitor. We know that the data collected and supported by this program will enable analyses in novel ways and at previously impossible scales. We thank you for joining us on that journey and look forward to working with you to implement the EMSA system to benefit all Australians.

We also welcome you to provide feedback to tern@adelaide.edu.au

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1 Module overview

1.1 Available protocols

This module includes three protocols for recording basal area within plots where there is a dominant growth form of trees, shrubs and/or mallee greater than 2 m in height:

1. Enhanced DBH protocol – Diameter at breast height (DBH) measures for all trees (trees, tall shrubs and/or mallee greater than 2 m in height with a DBH ≥10 cm or 5 cm for mallee and mulga) within the plot (100 x 100 m).
2. Standard DBH protocol – DBH measures for all trees (trees, tall shrubs and/or mallee greater than 2 m in height with a DBH ≥10 cm or 5 cm for mallee and mulga) within a 40 x 40 m central subplot. If the Condition Module is being undertaken, basal measures will be collected as part of the tree survey, and do not need to be repeated here.
3. Basal wedge protocol –TERN Basal Wedge measures of 'in' trees at nine point-sampling locations across the plot.

The Enhanced and Standard DBH protocols include the procedures and guidelines for the collection of DBH measures for all trees within the plot and subplot, respectively, including moving through the plots systematically, determining the Point of Measure (POM) using a measuring pole, measuring the DBH using a diameter tape or tree caliper, and recording the data into the app. The guidelines provide further information on addressing problem trees and dense plots.

The Basal wedge protocol includes the procedures and guidelines for the collection of TERN Basal Wedge measures, including the location of the nine sampling points (NW, N, NE, E, SE, S, SW and W points around the perimeter of the plot, as well as the centre of the plot; see Figure 1), determining if the use of the basal wedge is warranted, using the basal wedge, establishing which basal area factor (BAF) is appropriate for each species (0.1, 0.25, 0.5, 0.75, 1 and 2; see Figure 2), conducting a 360° basal sweep, and recording the data into the app. The guidelines provide further information on the rules to determine 'in', 'out' and 'borderline' trees and dealing with problem trees.

1.2 Relationship to other modules

1.2.1 Mandatory related modules

Complete before the Basal Area Module

- Plot Selection and Layout Module – will determine the boundaries of the survey plot, the location of the 40 x 40 m subplot for the Standard DBH protocol and basal wedge sample locations for the Basal wedge protocol.
- Floristics Module – basal area data per species are recorded using naming consistent with the flora species identifications/assigned field names recorded in the Floristics Module. Therefore, the Basal Area Module must be undertaken after the Floristics Module.

1.2.2 Optional complementary related modules

- Condition Module – basal area data can also be collected as part of the tree survey in the Condition Module. The Condition Module includes the Standard DBH protocol.
- Cover Module – transects laid out in the Cover Module can be used to delineate the 40 x 40 m subplot, as well as divide the plot and subplot into smaller units, which can simplify sampling. It is recommended that the Basal Area Module be completed at any time while the transects for the Cover Module are laid out.
- Photopoints Module – three sets of overlapping panorama photographs collected in the Photopoints Module can be processed using suitable algorithms to create a three-dimensional plot reconstruction. When software is readily available to run these algorithms, the Photopoints Module will offer an additional method to extract data from the panoramas, including basal area and biomass.

2 Introduction and background

Basal area is the average amount of area occupied by tree stems within a defined locale. It is quantified by measuring the cross-sectional area of all trees, over the bark, at breast height (1.3 m above ground level) and values are expressed per hectare (m^2/ha). Basal area provides information on stand density, is useful for monitoring tree growth, and can be used to calculating tree biomass and carbon sequestration using allometric equations (Eamus *et al.* 2000). The Basal Area Module is only required in plots where there is a dominant growth form of trees, shrubs and/or mallee greater than 2 m in height, but can also be undertaken as part of condition assessments.

Basal area can be measured using 'plot sampling' (i.e. the measurement of the basal area of all trees in a set area) or 'point sampling' (i.e. the estimation of basal area from a count of 'in' trees throughout a 360° sweep at a sampling point). For plot sampling, the basal area of a tree is calculated from its diameter at breast height (DBH), being the diameter of the trunk in metres as measured 1.3 m above the ground. DBH is converted to basal area based on the formula for the area of a circle:

$$Basal\ area = \pi \times (DBH \div 2)^2 \tag{1}$$

Basal area per hectare is calculated by adding the basal areas (as calculated above) of all the trees in a defined locale and dividing by the area of land in which the trees were measured. Basal area is generally measured for a plot and then scaled to m^2/ha to compare forest/woodland productivity and growth rate among multiple sites.

Basal area can be rapidly estimated at a sampling point using a hand-held angle gauge. A mathematical correlation exists between the distance from the observer's eye and the aperture of the device. This is referred to as the basal area factor (BAF). Basal area can be estimated in m^2/ha by multiplying the count of 'in' trees across a 360° sweep with the selected BAF. When using an angle gauge, a tree is 'in' if its trunk or stem at breast height is wider than the aperture of the selected BAF. Trees where the trunk or stem is the exact width of the aperture, are 'borderline' trees, for which a half count is tallied.

The Basal Area Module includes three protocols: (1) Enhanced DBH protocol that measures the DBH of all trees with a DBH ≥10 cm (or DBH ≥5 cm for mulga and mallee systems) within the core plot (100 x 100 m; Figure 1); (2) Standard DBH protocol that measures the DBH of all trees with a DBH ≥10 cm (or DBH ≥5 cm for mulga and mallee systems) in a 40 x 40 m sub-plot situated in the centre of the core plot (Figure 1); and (3) Basal wedge protocol where a 360° sweep is made at nine sampling points across the core plot (Figure 1) using a TERN basal wedge (Figure 2).

The Enhanced DBH protocol, although time-consuming, particularly in dense stands, is best practice and recommended for projects where accurate and repeatable measures of basal area are critical (e.g. forestry and forest ecology projects). The Standard DBH protocol offers a pragmatic approach to obtain accurate and repeatable measures of basal area based on DBH measures within a sub-sample of the plot. The Standard DBH protocol is recommended for time-limited projects where DBH measures are required and can be undertaken concurrently as part of other modules (e.g. Recruitment Module and Condition Module).

The Basal wedge protocol provides a simple and rapid method to estimate basal area across the plot. This approach extends the area sampled beyond the plot to provide a reliable estimate of basal area on a m2/ha basis for each species and the total basal area of the sampled vegetation association. The Basal wedge protocol is recommended for projects that require rapid but reliable measures of basal area. The TERN basal wedge comprises six Basal Area Factors (BAFs), ranging from 0.1 to 2 (Figure 2) that are suitable for use across Australia.

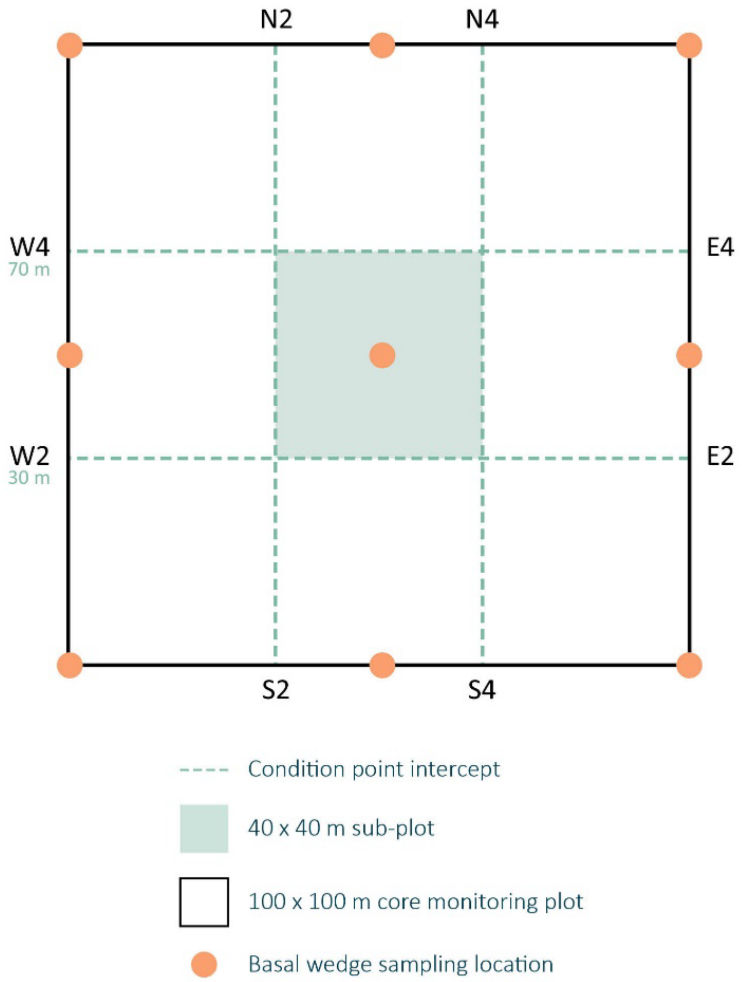

Figure 1. A 100 x 100 m core plot layout showing the 40 x 40 m central sub-plot and nine basal wedge sampling locations.

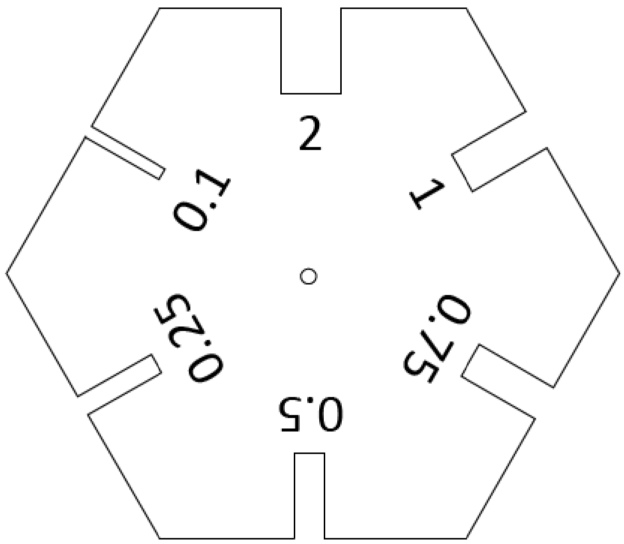

Figure 2. TERN Basal Wedge showing the six wedge apertures or basal area factors.

2.1 Key definitions and terminology

Table 1. Key definitions and terms used in the Basal Area Module.

Term	Definition
Allometric equations	Allometry studies the morphological, physiological and ecological characteristics of organisms' scale in relation to their size. In forestry, allometric equations are used to estimate tree biomass as a function of readily measurable characteristics, typically DBH and tree height. The equations follow a variety of mathematical specifications (e.g. log-linear, non-linear) and are derived based on measured values of tree weight related to its DBH and height from sample trees.
BAF	Basal Area Factor – the mathematical relationship between the angle formed by the aperture of the sights on the TERN Basal Wedge and the distance it is held from the observer's eye.
Basal area	The average amount of area occupied by tree stems within a defined locale. It is quantified by measuring the cross-sectional area of all trees (>2m tall), over the bark, at breast height (1.3 m above ground level) and values are expressed per hectare (m^2/ha). Convertible to standing biomass using allometric equations.
Biomass	The total quantity of matter (at any given time) of living organisms. Biomass can be expressed as all the species in a biotic community (community biomass) or by one or more species per unit of species (species biomass).
'Borderline' trees	Trees where the trunk or stem at breast height (1.3 m above ground level) is the exact width of the aperture of the BAF used on a TERN Basal Wedge.
Buttressed trees	Trees with buttressed roots – roots that grow laterally out from the trunk that help to support the tree (e.g. Moreton Bay Fig).
Circumference at breast height	The distance of the perimeter of a standing tree trunk or stem in centimetres when measured at 1.3 m above the ground.
DBH	Diameter at breast height - the straight-line distance in centimetres across the centre of a standing tree trunk or stem measured at 1.3 m above the ground.
Deformed trees	Trees with a distortion that prevents DBH from being measured at the standard 1.3 m breast height.
Ellipse trees	Trees with an elliptical rather than circular shaped trunk or stem.
GPS/GNSS enabled device	A device that is capable of logging the accurate coordinates of a location using the Global Positioning System (GPS) or the Global Navigation Satellite System (GNSS).
Hidden trees	Trees obscured by a tree or trees in the foreground when undertaking a 360° sweep during point sampling.
'In' trees	Trees where the trunk or stem at breast height (1.3 m above ground level) is wider than the aperture of the BAF used on a TERN Basal Wedge.
Monitor	Field data collection app for Ecological Monitoring System Australia. Collects data using the Australian Biodiversity Information Standard for delivery to the Australian Biodiversity Data Repository managed by the Department of Climate Change, Energy, the Environment and Water.
Multi-stemmed trees	Trees with two or more main stems that arise between near ground level and below breast height (1.3 m above ground level) but grow from one root system.
'Out' trees	Trees where the trunk or stem at breast height (1.3 m above ground level) is narrower than the aperture of the BAF used on a TERN Basal Wedge.
Plot sampling	The measurement of the basal area of all trees in a set area. Basal area is calculated from DBH measures and the formula for the area of a circle.
Point sampling	The estimation of basal area from a count of 'in' trees throughout a 360° sweep made at a sampling point. Basal area is calculated by multiplying the count of 'in' trees by the Basal Area Factor used on a TERN Basal Wedge.
POM	Point of measurement - the point at which the DBH of a tree is measured. As a standard, the POM is 1.3 m above ground level but may vary for problem trees. For repeatability, POM should be recorded every time DBH is measured.
Problem trees	Buttressed, multi-stemmed, leaning, deformed, dead and hidden trees, trees on a slope and tree ferns. Solutions to measuring DBH for problem trees are provided in the Additional guidelines.
TERN Basal Wedge	Angle gauge instrument used to provide a rapid and simple determination of basal area across Australia. Comprises six 'Basal Area Factors' (0.1, 0.25, 0.5, 0.75, 1 and 2; see Figure 2).
Tree	Woody plants greater than 2 m in height usually with a single stem, or branches well above the base. Includes trees, tall shrubs, or palms with DBH ≥10 cm (global forest ecology standard; Wood *et al.* 2015), and mallee and mulga with a DBH ≥5 cm (TERN 2015).

2.2 Rationale

All biological processes of plants and animals are dependent on the energy of primary production (i.e. the energy fixed and incorporated into biomass by plants), making it a fundamental component of an ecosystem. Measurements of biomass are important in ecosystem surveillance monitoring to help understand structural, functional and compositional ecosystem dynamics. For example, vegetation composition characterised by biomass is a prime indicator of species dominance within a vegetation association (Bonham 2013), and change in biomass over time is an important indicator of forest and woodland recovery during succession (Gilman *et al.* 2016).

Direct and accurate measurements of biomass can be obtained by felling, dissecting and weighing trees (West 2015). However, this method is destructive and unsuitable for ecological monitoring, which requires repeated measurements and in which the premise is to avoid environmental damage. Biomass is often therefore estimated from its allometric relationship with basal area, as both are related to stem diameter (Eamus *et al.* 2000; Sarmiento *et al.* 2005). Measurements of basal area can be easily obtained on ground and are good indicators for biomass as they integrate the effect of both the number and size of trees (Burrows *et al.* 2000).

Diameter at breast height (DBH) measured using a diameter tape or tree caliper is the standard for recording trunk or stem diameter (West 2015), and has thus been adopted for the Enhanced and Standard DBH protocols. Trees with a DBH ≥10 cm are measured as this is a global forest ecology standard for defining a tree (DECCW 2010; Wood *et al.* 2015). However, in sites dominated by mallee and mulga, all stems with a DBH ≥5 cm are measured (TERN 2015). The POM above ground level is recorded for every measurement as it may not be possible to measure DBH at 1.3 m in every circumstance (i.e. for problem trees). For mallee that often branch into multiple stems below 1.3 m and mulga that often branch close to the ground and then taper rapidly, it is recommended that diameter measurements are taken at 30 cm from the ground or if branching lower than 10 cm from the ground and the POM recorded as such (Williams *et al.* 2005; Paul *et al.* 2016). This ensures that the same position is measured on each occasion during repeat monitoring (West 2015).

The Basal wedge protocol uses point sampling to measure basal area in m^2/ha. This method has several advantages including its low cost, simplicity and rapidness, as individual tree measurements are not required (White *et al.* 2012; Balderas Torres and Lovett 2013). Since individual tree data are not collected, downstream analysis is limited to basal area data only. An explanation of point sampling is provided for reference in Appendix 1.

3 DBH protocol

3.1 Field collection

3.1.1 Pre-requisites

Pre-requisites for completing this protocol:

- The plot must be established using the Plot Layout and Selection Module prior to conducting the DBH protocol.
- Undertake the Floristics Module to ensure consistency with flora species identifications/assigned field names.

3.1.2 Time requirements

Survey activity time will vary depending on the options chosen, the density of vegetation to traverse, the number of trees to measure and the number and experience of personnel. As a general guide:

- Allow 1–2 hours for survey planning.
- Allow 20–40 minutes for plot set-up and laying tape measures (assuming the plot has been previously set-up using the Plot Selection and Layout Module).
- Allow 1–4 hours to complete the Enhanced protocol.
- Allow 0.5–2 hours to complete the Standard protocol.

3.1.3 Personnel requirements

Number of personnel and skills:

- Basal area DBH measurements are best conducted with two personnel, one taking measurements and one recording data directly into the Monitor app.
- The surveyor making observations should be familiar with, and experienced in, species identification and differentiating between species.
- Basal area DBH measurements do not involve interference with vegetation or wildlife. Therefore, scientific permits and wildlife ethics approvals are unlikely to be required but always check with the local authority. Access permissions are required.

3.1.4 Equipment

General:

- Mobile device (tablet/phone) with the Monitor app pre-loaded
- GNSS receiver capable of achieving <30 cm accuracy (e.g. Trimble® R1 or DA2), hand-held GPS, or device built-in GPS (least preferred)
- Diameter tape, measuring tape or tree calipers
- Measuring pole with 1.3 m clearly marked or 5−10 m tape measure
- Chalk
- Step ladder (for measuring buttressed trees).

Additional equipment required:

- 4 x 100 m tape measures or pegs/flagging tape to mark the sub-plot boundary (when completing the Standard protocol)
- 10 x 100 m tape measures (or ca. 40 coloured survey pins) to divide the plot into smaller units for ease of sampling (when completing the Enhanced protocol).

3.1.5 Instructions and procedures

1. Ensure the Plot Selection and Layout Module has been completed to mark out the plot boundary and define the current plot and visit in the Monitor App.
2. Survey area is determined by the protocol being undertaken:
    - If completing the Standard DBH protocol use the transects laid out for the Cover Module to delineate the 40 x 40 m sub-plot, between the N/S2 and N/S4, and E/W2 and E/W4 point-intercept transects (see Figure 1). This 40 x 40 m sub-plot will be the survey area.
    - If completing the Enhanced DBH protocol and the plot contains dense trees, tall shrubs and/or mallee, use the transects laid out for the Cover Module to partition the plot into smaller units. Alternatively, use coloured survey pins. The 100 x 100 m plot will be the survey area.
3. Open the Monitor app and navigate to the Basal Area Module and then the DBH protocol.
4. Select the relevant *plot size* for the project. Steps 5–13 are the same whether completing the Enhanced or Standard DBH protocol.
5. Select the *DBH instrument* you are using to measure DBH, either a diameter tape, tape measure or tree caliper.
6. Move through the plot section by section, systematically searching for trees, tall shrubs and mallee greater than 2 m in height and with a DBH ≥10 cm (or 5 cm for mallee and mulga dominated sites).
7. For each tree encountered, record:
    - The *floristics voucher* (i.e. the field name recorded for the species in the Floristics Module). If the tree is dead, leave the *floristics voucher* field blank and flag the tree as 'dead'.
    - If the tree is multi-stemmed, check the box:
        - The app will display stem labels (Stem 1, Stem 2, Stem 3, etc.).
        - Add additional stems by selecting the add button and complete step 8 for each individual stem.
    - If the tree is buttressed, check the box:
        - The app will require the input of the diameter and POM of the tree at its reach point (the highest point you can reach - approximately 2.2 m) and the diameter and POM of the tree at 50 cm above the buttress. If you cannot measure 50 cm above the buttress, leave the field blank, it will be recorded 'not collected'.
8. For each tree/stem, then locate the 1.3 m point of measurement (POM) (see note below) and:
    - Clear any moss, loose bark or other material that may distort the measurement and measure the diameter of the tree at the POM.
        - If using a diameter tape, measure the diameter of the tree (in centimetres) by pulling the diameter tape around the trunk or stem at the POM perpendicular to the main axis of the trunk or stem.
        - If using a 5–10 m measuring tape, record the circumference of the trunk or stem (in centimetres) at the POM. The app will automatically calculate and display the diameter measurement in the DBH field.
        - If using a tree caliper, close the caliper around the trunk or stem at the POM so that it is perpendicular to the main axis of the trunk or stem, rather than parallel to the ground (this provides an accurate measurement of leaning trees). Record the diameter in centimetres.
        - If when using the tree caliper to measure, the trunk or stem is an ellipse shape, check the *ellipse* checkbox and record a second diameter measurement at a 90° angle to the first diameter measurement to account for the ellipse. The app will automatically calculate the square root of the product of the two diameters to determine the measure of trunk or stem diameter and display the diameter measurement in the *calculated DBH* field.
    - Note: use the 1.3 m POM, or suitable POM for problem trees (see Figure 3).
9. Date and time will be automatically recorded. Update if required and save the observation.
10. Once measured, mark the tree or stem with chalk to avoid remeasuring.

11. Repeat steps 7–10 for every tree within the plot or sub-plot.
12. When all trees have been measured, queue the collection for submission.

3.1.6 Additional guidelines

Taking measurements

- It may be beneficial to undertake this module while the transects for the point-intercept measures in the Cover Module (5 N/S and 5 E/W; see Figure 1) are laid out. The transects can help to partition the plot into more manageable units that can be surveyed systematically. Alternatively, use coloured survey pins to divide the plot. This will be particularly helpful in dense plots.
- When recording a new tree using the *add tree* button, ensure that the app operator is standing as near to the tree as possible as the tree location is recorded with this action.
- Chalk that is light coloured such as pink and purple show up best when marking trees.
- Clearly mark the measuring pole at 1.3 m to easily locate the POM.
- If a measuring pole is not available, use the normal side of the diameter tape (i.e. the side of the tape with 1 cm increments) or a regular measuring tape to locate the POM. Mark the tape at 1.3 m to easily locate the POM.
- Loose litter and debris at the base of the tree should be brushed aside before determining the POM.
- The rule set to determine if a tree is in or out of the plot is illustrated in Figure 4. A tree is in the plot if more than 50% of the base of the trunk is within the plot.
- A rigid tape measure is accurate for measuring the circumference of smaller trees (~50 cm DBH) and where there is loose bark.
- For mallee or mulga trees that branch into multiple stems below 1.3 m it is recommended to take diameter measurements at 30 cm from the ground or if branching lower than this at 10 cm and record the POM as such.

Solutions to problem trees

The solutions to measuring DBH for problem trees are illustrated in Figure 3.

- Trees on a slope (Figure 3a), 1.3 m should be measured on the uphill side of the tree.
- Leaning trees (Figure 3c) should be measured on the inside of the lean, starting at the ground next to the base of the tree.
- Multi-stemmed trees (Figure 3d and e) are treated as single trees with multiple stems (Stem 1, 2, 3, etc.). A single DBH is recorded if the tree branches above 1.3 m (d), otherwise, each individual stem is measured (e).
- Mallee or mulga (Figure 3f) that branch very close to the ground should be measured at 30 cm or if branching lower than this, 10 cm and POM recorded accordingly.
- Deformed trees (Figure 3g and h) should be measured either above or below 1.3 m and the POM recorded.
- Buttressed trees (Figure 3i) are a significant source of error in repeat tree measurements and require careful attention in the field. Buttressed trees are measured at 1.3 m, at the highest point you can reach (e.g. approximately 2.2 m) and 50 cm above the top of the buttress. Every effort must be made for both the 1.3 m and the highest point you can reach during initial surveys.
- Dead trees in a baseline survey are flagged as *dead,* and all other attributes are measured as normal.

- The soft texture of tree fern trunks is not conducive to DBH measurements and therefore, tree ferns are not measured for diameter.

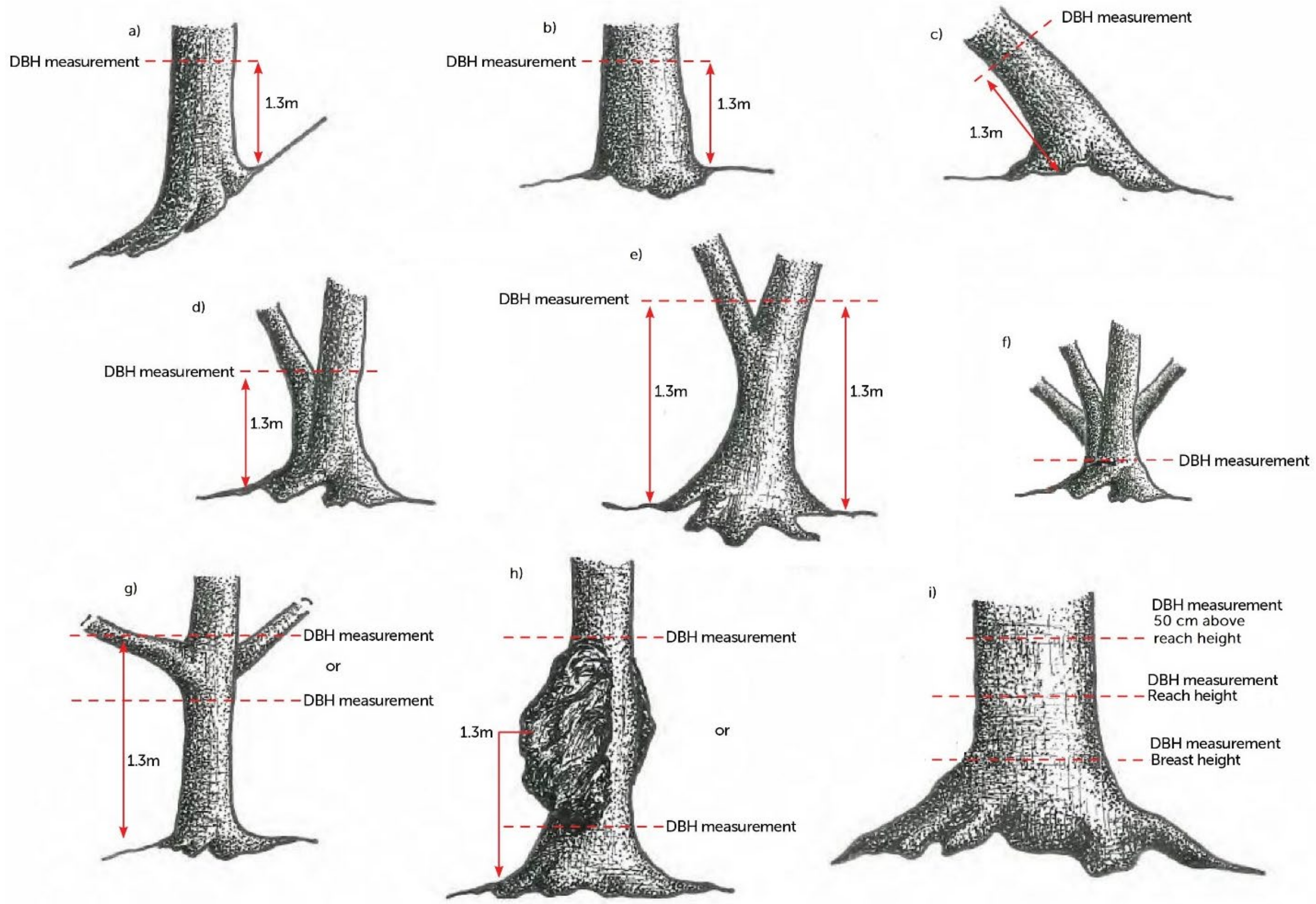

Figure 3. Solutions to measuring DBH for problem trees. Adapted from: Wood et al. (2015): a) trees on a slope, b) straightforward tree, c) leaning tree, d) and e) multi-stemmed trees, f) mallee/mulga, g) and h) deformed trees and i) buttressed trees.

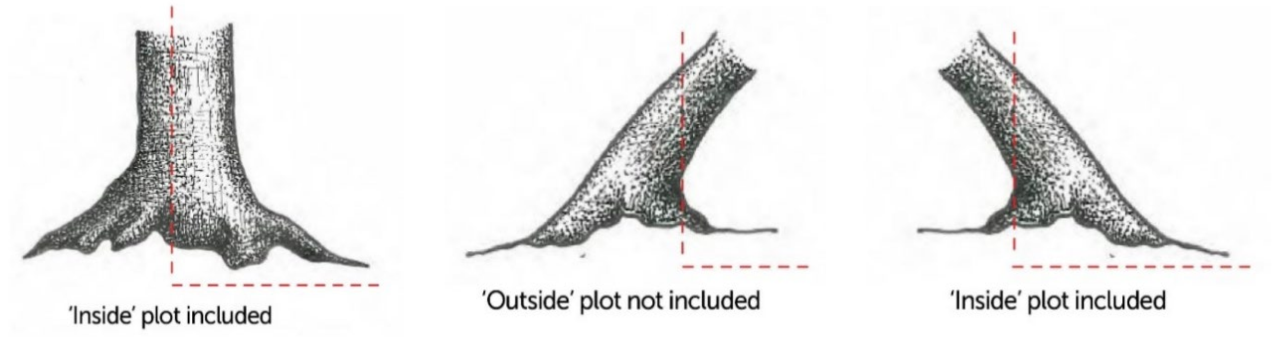

Figure 4. Rule set to determine if a tree is in or out of the plot (adapted from Wood *et al.* (2015).

3.2 Post-field survey tasks

3.2.1 Sample curation

The DBH protocol does not collect samples. There are no curation requirements.

4 Basal wedge protocol

4.1 Field collection

4.1.1 Pre-requisites

Pre-requisites for completing this protocol:

- The plot must be established using the Plot Layout and Selection Module prior to conducting the DBH protocol.
- Undertake the Floristics Module to ensure consistency with flora species identifications/assigned field names.

4.1.2 Time requirements

Survey activity time will vary depending on the options chosen, the density of vegetation to traverse, the number of trees to measure and the number and experience of personnel. As a general guide:

- Allow 30 minutes to complete the basal wedge survey per plot.

4.1.3 Personnel requirements

Number of personnel and skills:

- Basal wedge sweeps may be conducted by a single observer and the observations can be recorded directly into the Monitor app.
- The surveyor making observations should be familiar with, and experienced in, species identification and differentiating between species.
- Basal wedge sweeps do not involve interference with vegetation or wildlife. Therefore, scientific permits and wildlife ethics approvals are unlikely to be required but always check with the local authority. Access permissions are required.

4.1.4 Equipment

- Mobile device (tablet/phone) with the Monitor app pre-loaded
- TERN Basal Wedge (Figure 2) with attached string knotted at precisely 50 cm from the wedge.

4.1.5 Instructions and procedures

1. Ensure the Plot Selection and Layout Module has been completed to mark out the plot (including the centre point and north, south, east and west point sampling locations) and define the current plot and visit in the Monitor app.
2. Open the Monitor app and navigate to the Basal Area Module and then the Basal wedge protocol.
3. Stand at one of the nine basal wedge sampling locations (see Figure 1) and select the location from the drop-down list (Appendix 2). It does not matter which order the sampling locations are surveyed.
4. Hold the end knot of the 50 cm length of string attached to the wedge on your cheek below one eye – close the other eye. Hold the wedge so that the string is taut (see Figure 5).
5. Determine if the use of the basal wedge is warranted at the plot (i.e. are there sufficient trunks or stems of trees, tall shrubs or mallee that are large enough to obtain a score of seven or more from 'in' and 'borderline' trees for any species). If there are not sufficient trees to sample then the Enhanced or Standard DBH protocols are recommended to complete basal area measurements.
6. For each species, establish which Basal Area Factor (BAF; 0.1, 0.25, 0.5, 0.75, 1 and 2) to use. This is determined by selecting a BAF and undertaking a brief sweep around the point sampling location to determine if the selected BAF will sample seven or more 'in' trees (see Additional guidelines below for rules on counting 'in' and 'borderline' trees) for the sampling location. Ideally, aim to achieve the minimum seven 'in' trees with the largest aperture width.

7. Once you have selected the appropriate BAF for a species, rotate through a complete 360° sweep and, looking through the eye above the string, count the number of stems or trunks of each species at breast height, that are wider than the aperture of the chosen BAF as ‘in’, and the exact width of the aperture as ‘borderline’ (i.e. half count).
8. Record the *floristics voucher* (i.e. the field name recorded for the species in the Floristics Module). Species that cannot be easily distinguished from one another may be combined for the basal wedge count. In this case, check the *group species* box and select all relevant floristics vouchers. This is only applicable if they are of the same genus and growth form (e.g. mallee).
9. Record the BAF used (from the drop-down list; see Appendix 1), and the tally of ‘in’ and ‘borderline’ trees for that particular species/group.
10. Date and time will be automatically recorded. Update if required and then save the observation.
11. Repeat steps 6–10 for the remaining species at the sampling location using the blue *+* button.
12. Select the *finish sampling location* button to return to the sampling location selection screen.
13. Repeat steps 3–12 at each remaining sampling location.
14. When basal area has been recorded for each species at each sampling location, queue the collection for submission.

Figure 5. Surveyor correctly holding the end of the TERN Basal Wedge string on the cheekbone below the eye and holding the wedge at full length with the string taut.

‘in’ (+1) ‘borderline’ (+0.5) ‘out’ (0)

Figure 6. Examples of how to score trees using the TERN Basal Wedge.

4.1.6 Additional guidelines

Rules to determine 'in' trees

- Examples of how to score trees using the TERN Basal Wedge are illustrated in Figure 6.
- A tree is 'in' when its trunk or stem, at breast height (1.3 m, or the nearest point above if there is a deformity at 1.3 m), is wider than the chosen BAF (Figure 6).
- Species that cannot be easily distinguished from one another may be combined for the basal wedge count but this is only applicable if they are of the same genus and growth form (e.g. in mallee) as the basal area equation will be the same.
- Do not record the data if less than seven 'in' trees for a given BAF are achieved for each species. Data become meaningless with less than seven 'in' trees. Repeat the sweep using a smaller BAF, or if there are less than seven 'in' trees with the smallest BAF (0.1), no data is recorded.
- Where the trunk or stem is exactly the width of the BAF (i.e. 'borderline' tree), add a half count to your tally (Figure 6).
- Select the widest suitable BAF to sample seven 'in' trees for the species. This increases efficiency as it reduces the number of 'in' trees likely. For example, use the '1' BAF to record eight 'in' trees rather than the '0.5' BAF to record 15 'in' trees.
- It is more efficient to use the same BAF for every species at each sampling location. However, this is not always practicable. For example, the '0.5' BAF may be suitable to be used for *species x* at all sampling locations; while the '0.1' BAF may be required for *species y* at all sampling locations, etc.
- For each species, only use one BAF at each sampling location. Do not make separate counts of 'in' trees using different BAFs for the same species.

Solutions to problem trees

- For hidden trees (trees that are partially or fully hidden behind other trees or undergrowth), move sideways until the tree is fully in view, but be sure to maintain the same distance to the tree. Move back to the sampling point before assessing the next tree.
- Buttressed trees should be measured above the buttress.
- For multi-stemmed trees, measure each stem individually and add all 'in' stems to your tally.
- For trees on a slope, the 1.3 m POM should be measured on the uphill side of the tree.
- For leaning trees, hold the basal wedge at a tilt so that the view is at right angles to the trunk or stem.
- Deformed trees should be measured at the nearest point above 1.3 m that is not deformed.
- Dead trees are flagged as *dead* and all other attributes are measured as normal.
- The soft texture of tree fern trunks is not conducive to DBH measurements, and therefore, tree ferns are not measured for diameter.

4.2 Post-field survey tasks

4.2.1 Sample curation

The Basal wedge protocol does not collect samples. There are no curation requirements.

5 Data submission

Data from the Basal Area Module is collected in the field using the Monitor app. All data is checked for correctness and completeness in the app before it is submitted.

Once all data is finalised, and marked as completed, the data is submitted from the Monitor app to the staging server by an explicit user action. If the device is offline at the time, the data will be pushed as soon as it is reconnected to a network (i.e. either back in mobile phone range or a wi-fi network). Once data reaches the staging server it is prepared in an export interface for delivery to the Biodiversity Data Repository. DCCEEW is then responsible for managing the data. In the future, it is anticipated that data curation tools will be made available to project personnel.

6 Data use and reason for collection

6.1 Data use to date

TERN's Ecosystem Surveillance platform collects standardised basal area data from point sampling using a TERN Basal Wedge (Figure 2), as per the method outlined in White *et al.* (2012). The data has been used to validate a general ecosystem model to guide the recovery planning process for the diverse woodlands of southern Australia (Good *et al.* 2021).

6.2 Future use of the data

Collection of standardised basal area data provides the opportunity to undertake several investigations, including: developing and refining allometric relationships for Australian trees (Eamus *et al.* 2000); identifying locations and regions with decreasing, stable and increasing tree growth to implement adaptive management (Voelker *et al.* 2008); monitoring ecosystem succession and restoration trajectory (Clewell 1999; Parrotta and Knowles 1999; Van Breugel *et al.* 2006); identifying habitat selection drivers for threatened wildlife and vertebrate pests (Irwin *et al.* 2018; Valenzuela-Sánchez *et al.* 2019); identifying changes in basal area increments to map relative risk from invasive sap-feeding insects (Livingston *et al.* 2017); identifying locations with high basal area where thinning can prevent wide-scale tree mortality due to warmer and drier conditions (Giuggiola *et al.* 2013; Bradford and Bell 2017); and developing growth models to understand climatic influence and predict future stand dynamics (Saud *et al.* 2019).

Basal area from DBH and point sampling measurements can also be used to validate and compare stem counts and DBH and basal area measures derived from photogrammetry (i.e. obtaining reliable information about physical objects and the environment through the process of recording, measuring and interpreting photos) and terrestrial Lidar systems (Muir *et al.* 2015). The three sets of overlapping panorama photos collected in the Photopoints Module can be processed to create a three-dimensional plot reconstruction, from which trunk or stem diameters can be deduced to calculate basal area. Actual basal area measurements collected in the Basal Area Module can then be used to corroborate these plot reconstructions and generated basal area outputs. Thus, over time, these algorithms can be refined so that the panorama photos can be used to produce a seamless 360° plot photo with computed basal area data, providing a quicker and more efficient alternative to completing the Basal Area Module.

The Enhanced and Standard DBH protocols also have other applications; mean DBH generally increases with stand age and can be used to discriminate between successional stages in forests (Chazdon *et al.* 2005), standard deviation of tree DBH is a measure of tree size variability and can indicate the diversity of micro-habitats within a stand (Acker *et al.* 1998), the number of large trees (i.e. trees exceeding a threshold DBH) can be indicative of the potential number of occupied hollow bearing trees, dead standing trees, and logs (McGee *et al.* 1999; Gibbons *et al.* 2000) and a frequency distribution across a range of diameter classes can be used to indicate stand structure (Tyrrell and Crow 1994).

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8 Appendices

Appendix 1. Basal wedge – point sampling explanation

In point sampling, basal area is estimated based on the concept of circles (trunks or stems) within circles (variable circular plots; see Figure. a.). The area of one circle varies proportionally to a change in the area of the other circle (i.e. the area sampled is greater for larger than smaller trees) and trees are sampled with a probability proportional to their basal area. Therefore, large trees, which contribute more to the basal area of a stand, are sampled in greater proportions than small trees (Hovind and Rieck 1970).

An observer rotates 360° at a sampling point and counts all the trunks or stems that form an angle greater than the chosen BAF. In effect, every tree counted is sampled in a variable circular plot with a radius that is a function of the tree's DBH (Figure. a). Because a tree's DBH determines its basal area, and the plot radius determines the sampling area for that tree, the contribution of each counted tree to total stand basal area can be determined. For such a sample of trees, there is a constant relationship between tree DBH and effective sampling area, and therefore each tree counted represents the same contribution to the basal area of the stand. To estimate the total stand basal area, the only calculation required is to multiply the count of 'in' trees by the BAF used, which is determined from the aperture width used with an angle gauge and the fixed distance that the angle gauge is held from the eye (Fastie 2010). Measurements of variable circular plot radii and DBHs are not required as these values are proportional to the aperture width used with an angle gauge and the fixed distance that the angle gauge is held from the eye (Figure. b.).

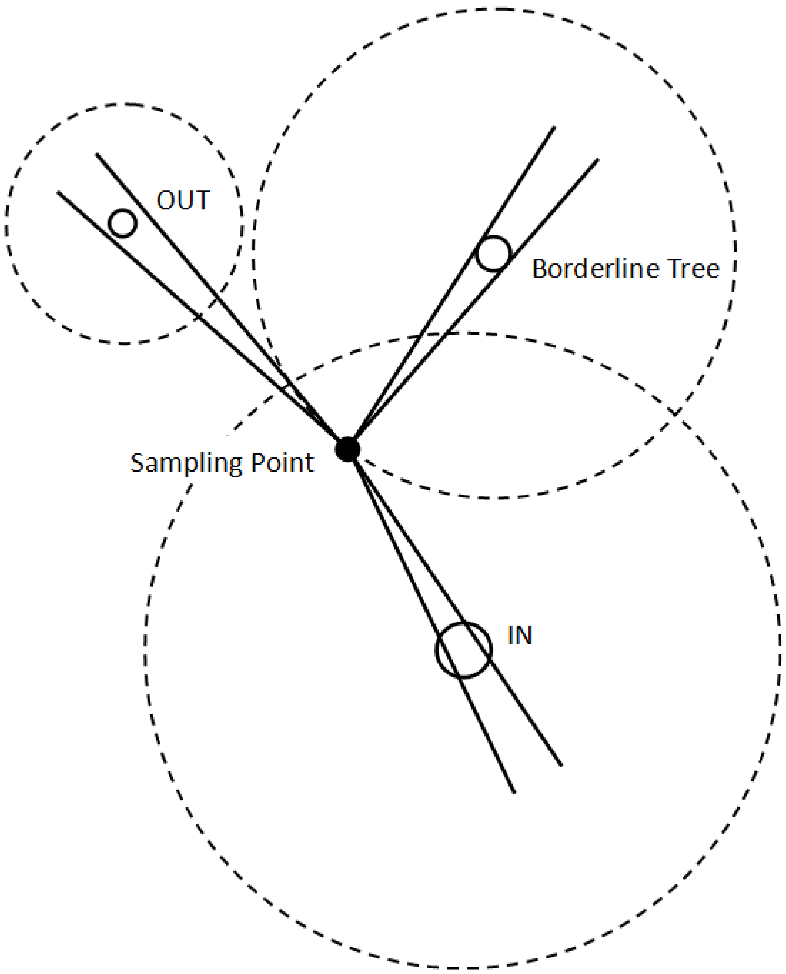

Figure. a. 360° point sampling sweep showing an 'in' (counted), 'out' (not counted) and 'borderline' tree (half counted). The dashed circles represent the variable circular plot for each tree that is proportional to its diameter at breast height (not to scale).

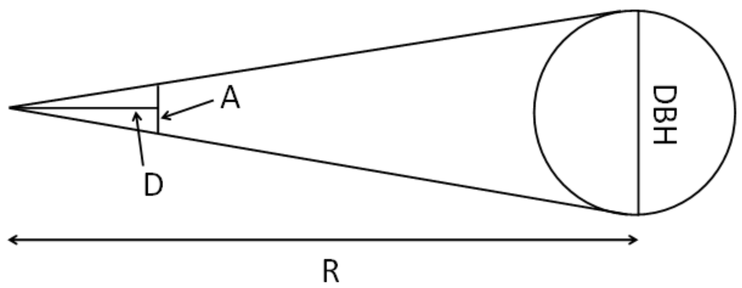

Figure. b. Principle of point sampling. The diameter at breast height (DBH) and variable circular plot radius (R) of a 'borderline' tree are proportional to the aperture (a) width of an angle gauge and the fixed distance (d) that the angle gauge is held from the eye.

The Basal wedge protocol measures basal area at nine sampling points (Figure 1) using a TERN Basal Wedge (Figure 2). The TERN Basal Wedge is an angle gauge designed by TERN Ecosystem Surveillance for monitoring basal areas across Australia. The hexagonal basal wedge has six fixed angle gauges that represent six different BAFs. The wedge is held at the fixed distance of 50 cm from the observer's eye using a taut string, as this produces a sighting ratio of 1:50. At this ratio, a 1 cm aperture corresponds to a BAF of 1 or a basal area of 1 m^2/ha. To determine the aperture for the specific BAFs of the basal wedge, the following equation was used:

$$A = \sqrt{}(BAF \times D^2 \div 0.25) \quad (2)$$

Where A is the aperture in centimetres and D is the fixed distance that the wedge is held from the eye in metres (i.e. 0.5 m; Muir *et al.* 2011)

TERN Basal Wedge basal area factors and corresponding wedge apertures and angles formed.

BAF (Basal area [m^2/ha])	Aperture (cm)	Angle formed
0.1	0.32	0.37°
0.25	0.50	0.57°
0.5	0.71	0.81°
0.75	0.87	1.00°
1	1.00	2.29°
2	1.41	3.23°

Appendix 2. Data collection fields from the Basal Area Module

Complete lists are provided in the Monitor app, as well as the TERN Linked Data Services page.

DBH instrument

Code	DBH instrument
DIA	Diameter tape measure
TAP	Tape measure
CAL	Tree calliper

Basal sweep sampling point

Code	Basal sweep sampling point
NW	Northwest
N	North
NE	Northeast
E	East
SE	Southeast
S	South
SW	Southwest
W	West
C	Centre

Basal area factor

Code	Basal Area Factor
0.1	0.1
0.25	0.25
0.5	0.5
0.75	0.75
1	1
2	2

As part of its Ecological Monitoring System Australia (EMSA), the Australian Government has partnered with Australia's Terrestrial Ecosystem Research Network (TERN) in the co-design of a suite of ecological monitoring protocols and a data exchange system. The protocols build on TERN's long-established data aggregation systems and well-tested survey protocols.

The primary purpose of the standardised monitoring protocols is to support natural resource management (NRM) programs that benefit the environment, agriculture and communities, as well as making the protocols freely available for use by other environmental land managers and environmental consultants.

The Australian Government and TERN protocols ensure NRM service providers and ecologists collecting field data:

- have ready access to comprehensive instructions for each of the standardised collecting protocol modules
- are able to use mobile-based applications in the field to enter data and images
- and can easily submit and share data.

Data collected from the application of the standardised collecting protocol modules will help evaluate the current NRM program and support research on changes to Australia's ecosystems and biodiversity.

TERN acknowledges the traditional owners and their custodianship of the lands on which TERN operates. We pay our respects to their ancestors and their descendants, who continue cultural and spiritual connections to country.