



Research article

Efficient protocol of complete inventory for tree regeneration and recruitment studies over one hectare in selected tropical natural forests, Kenya

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Abstract: This study sought to establish an efficient inventory protocol to estimate regeneration stock and dynamics in natural forests. Field and computer outputs were integrated to develop complete inventory protocol for selected natural forest types in Kenya. Inventory cost and precision for four plot sizes (5 m × 5 m, 10 m × 5 m, 10 m × 10 m and 20 m × 20 m) were determined and compared. Specific objectives were to determine (i) precision levels of estimating tree seedling density using different plot sizes across forest types; and (ii) optimum plot size which minimise both sampling error and inventory effort for use in each forest type. Seedling counts and time taken per plot were recorded systematically over 400, 200, 100 and 25 plots ha⁻¹ for the respective plot sizes. Larger plots and their data were created by merging smaller ones through programming with R Software. Smallest population mean-variance, $\sigma^2 N^{-1}$ was obtained using data from 5 m x 5 m plots. Both precision and inventory effort varied with plot size used, but in reverse directions. Seedlings population mean errors were 15.4% of the mean for rain forest, 14.7% for moist montane forest and 9.9 % for dry forest type. Inventory cost decreased with increasing data compilation unit size, e.g., 50.42 hrs ha⁻¹ for 25 m² unit to 3.21 hrs ha⁻¹ for 400 m² unit in rainforest. Similar trend was observed in other forest types. Recommended plot sizes for tree seedlings are 75 m²; 62.4 m² and 88.4 m² for Kakamega rain forest, Mt Elgon montane forest and Loruk dry woodland forest, respectively. These plot sizes gave acceptable uncertainty levels between ±11% and ±17% of mean estimate ha⁻¹. Tree diameter distributions from 5 m x 5 m plots revealed that tree component recruitment was irregular over time across forest types.

Keywords: Climatic factors - Deciduous - Homegarden - Meitei - Phenology.

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INTRODUCTION

According to Weiskittel *et al.* (2011), regeneration is the renewal of a forest by natural self-sown seed, coppice, suckers, lignotubers, or by artificial means. Recruitment refers to individuals that reach a prescribed size or established seedlings that have survived its first year, following germination. Both regeneration and recruitment processes significantly influence the outcome of forest growth-model projections; particularly in areas dominated by naturally regenerated forests (Weiskittel *et al.* 2011). The number of tree seedlings is used as a measure of regeneration potential of a forest; and may be assessed in sample plots, subplots or microplots (McWilliams *et al.* 2015). Rates of recruitment are often gaged from analyses of tree diameter size distribution curves which reflect tree regeneration, growth and mortality in the forest over time (Churski 2006, Wang *et al.* 2009). For example, the logarithm of the number of trees over diameter class becomes a straight line for regular recruitment and sufficient regeneration (Devis & Johnson 1987). Fluctuating trend line indicates good but discontinuous regeneration over time which results in a wave-like recruitment of small individuals into the larger size classes (Harper 1977, Devis & Johnson 1987, Poorter *et al.* 1996, Hitimana *et al.* 2004).

Forest regeneration and recruitment are attributes of high ecological, silvicultural and conservation

significance in forest conservation and management (Serna 1986, Grainger 1993, Schreuder *et al.* 1993, Wong *et al.* 2001, Bellefontaine *et al.* 2002, Sarkar & Devi 2014, Pandey *et al.* 2016, Raj 2018). Information on regeneration in forests is needed for making policy decisions and for strategic planning of rehabilitation and/or restoration of degraded ecosystems (Evans & Turnbull 2004); or to conserve threatened species and other components of biodiversity that are valuable to mankind (Groombridge & Jenkins 2000, Njunge & Mugo 2011, Oldfield & Newton 2012, Hanief *et al.* 2016). Tropical natural forests and woodlands are of diverse entities with lesser-known and understood species mix and stand structure (Girma 2012, Mulatu *et al.* 2017). These ecosystems are difficult to analyse and understand in their pristine state (Grainger 1993, Singh 1993, Lanly 1997) due to lack of established; reliable and widely acceptable inventory protocols (Arellano *et al.* 2016). Inventory protocol components consist of plot size, plot shape, number of plots and spatial or temporal pattern of the same units (Wong *et al.* 2001).

An efficient inventory protocol must be accurate, precise and cost-effective (Husch *et al.* 2003). According to Wong *et al.* (2001), deciding on how many plots to be used in an inventory is critically required for the management of sampling errors. The greater the number of plots, the smaller the sampling error; and the more precise and potentially accurate the results will be. However, the relationship between the number of plots and sampling error is non-linear, with diminishing returns as numbers increase (Shiver & Borders 1996, Nassiuma 2000). There is need to determine an optimal sample size below or above which the precision or accuracy levels may fall to undesirable level. The choice between “few but large” and “many but small” plot sizes has implications on both the cost and precision in opposite directions. The acceptable target sampling error in documented forest inventories is between 10 and 20 % of the mean (Wong *et al.* 2001) but not known for tropical natural forests in Kenya.

The cost of enumerating items in a plot is also critical but not well documented. The relationship between plot size and cost or effort of inventory would enable to identify and use cost-effective inventory protocols. In this study, a sampling scheme for tree seedling inventory refers to a combination of sampling design, plot size and sampling intensity used to assess seedlings (individuals <1 cm DBH and not taller than 150 cm) over one hectare. There is little information on the relative efficiency of different schemes to floristic assessment in tropical natural forests (Herold & Skutsch 2011, Shijo *et al.* 2013, Nduati *et al.* 2016). There is need for research on accurate and efficient forest inventory schemes to be used in resource assessment for the support of sustainable forest management and conservation of the diverse tropical forests and woodland formations, which are highly variable in composition, diversity, physical and dynamic structures (Hemp 2006, Talbot *et al.* 2014).

There is a gap for research towards standardisation of inventory designs to enhance monitoring of forest resource conditions within and across habitats (Feld *et al.* 2009, Hicks *et al.* 2014). We note, however, that field methods are situation-specific (Schreuder *et al.* 1993, Burkhart & Tome 2012, Arellano *et al.* 2016); and that they target specific population characteristics (Gillison & Brower 1985, Philip 1994, Myers & Patil 1995, Greenwood 1996, Wong *et al.* 2001). Therefore, field protocols should be calibrated and validated for suitability before they are adopted (Pretzsch 2009, Weiskittel *et al.* 2011). In validating inventory methods, target species and ecosystem components should be identified and evaluated using cost-effective studies.

Forest resource managers, including silviculturists, lack accurate and timely quantitative resource information on regeneration and other parameters to make good decisions (Schreuder *et al.* 1993, Wong *et al.* 2001). It is worth noting that tropical flora remains chronically understudied and that the lack of floristic understanding hampers ecological research and large-scale conservation plans (Phillips *et al.* 2003). Precision level, accuracy and cost are major concepts in selecting efficient sampling schemes (Jayaraman 1999, Wong *et al.* 2001). The precision is high when errors are small; and accuracy is high when the estimated value is close to the population true value (Nassiuma 2000, Wong *et al.* 2001). The lack of knowledge of the true value of a variable is also known as uncertainty which is measured by the sampling error of an inventory (Lackmann 2011). According to Morais & Schreuber (1997), sampling inventories should provide the statistical precision of estimated quantities within accepted limit, that is, uncertainty levels of estimates must be disclosed. In many cases, inventories are designed to achieve a specific precision level expressed by a fixed sampling error.

This study sought to develop field sampling protocol suitable for use to count and quantify regeneration in selected tropical natural forests, using a “1 ha-method” (Alder & Synnott 1992, Wong *et al.* 2001, Phillips *et al.* 2003) by determining optimum data compilation unit size within the one-hectare standard area. The main objective was to provide efficient protocol to use in forest tree seedling stock inventories across the ‘tropical rain forest- moist montane forest dryland forests /woodlands gradient. Specific objectives were: (i) to quantify population mean-variance of the seedling stocks across selected tropical rainforest- moist montane forest - dry

woodland forest spectrum in Kenya; (ii) to determine efficient and cost-effective data compilation unit size to estimate the number of seedlings over one hectare and a high precision level for each natural forest type; and (iii) determine recruitment trends of the tree component in the studied forest types. It was hypothesized that: (i) Precision levels of forest regeneration estimates from complete inventory per hectare vary with used plot size in mixed natural forests; (ii) there exist optimum plot size [*i.e.* data compilation unit size] in a complete inventory of tree seedlings in the selected forest types; (iii) regeneration dynamics is regular over time leading to stable recruitment process of the tree component in the selected forest types.

MATERIALS AND METHODS

Study area and sites

Data used to test the performance of different plot sizes were collected from three distinct forest sites that mimic a climate gradient from low rainfall dry zone (Loruk woodland; <700 mm year⁻¹) to high rainfall humid zone (Kakamega rainforest; 1900–2000 mm year⁻¹) through the intermediate moist zone (Mt Elgon forest; 1400–1700 mm year⁻¹) (Kokwaro 1988, Fashing *et al.* 2003, Hitimana *et al.* 2004, Mutiso *et al.* 2013). These sites also differed in altitude from <1000 m a.s.l. at Loruk (low altitude dry woodland) to >2000 m at Mt. Elgon (montane forest) through <1600 m a.s.l. at Kakamega (mid-elevation tropical rain forest). In terms of ownership and governance; Loruk woodland is community-owned and under silvopastoral land use system. Kakamega and Mt Elgon are protected state-owned forests; surrounded by highly populated settlements involved in mixed farming. Therefore; selected forest types and sites represent ecological; climatic and socio-economic complexities of natural forest resources in Kenya and the tropics. Kakamega mixed tropical rainforest (TRF); Mt Elgon moist lower montane forest (MMF) and Loruk dry woodland forest (DWF) locations in Kenya are shown in figure 1.

The Kakamega forest vegetation is influenced by high rainfall and average annual temperature of 20°C with February as the hottest month (21°C) and July as the coldest month (19°C). Despite past disturbances, the forest is on the recovery path and near climax development stage (Mutiso *et al.* 2013). Mt. Elgon forest ecosystem (located on the steep slopes of the extinct volcano and occurring at a height of 4321 m a.s.l. on the Kenya - Uganda boarder) is also influenced by high rainfall and mean annual temperature of 15–18°C (Jaetzold & Schmidt 1983, Hitimana 2000, Hitimana *et al.* 2004). It is in a building phase of succession, following intensive historic selective logging activities (Hitimana *et al.* 2004) which affected the population structure and regeneration of some target species (Hitimana *et al.* 2010). Finally, Loruk woodland forest is a typical dryland ecosystem with short trees (<6 m on average; Hitimana *et al.* 2019) and poorly developed undergrowth, in the wider Baringo landscape of Kenya (Kiyiapi 1994, Omondi 2016). The climate is characterized by erratic rainfall and high temperatures (22–25 °C).

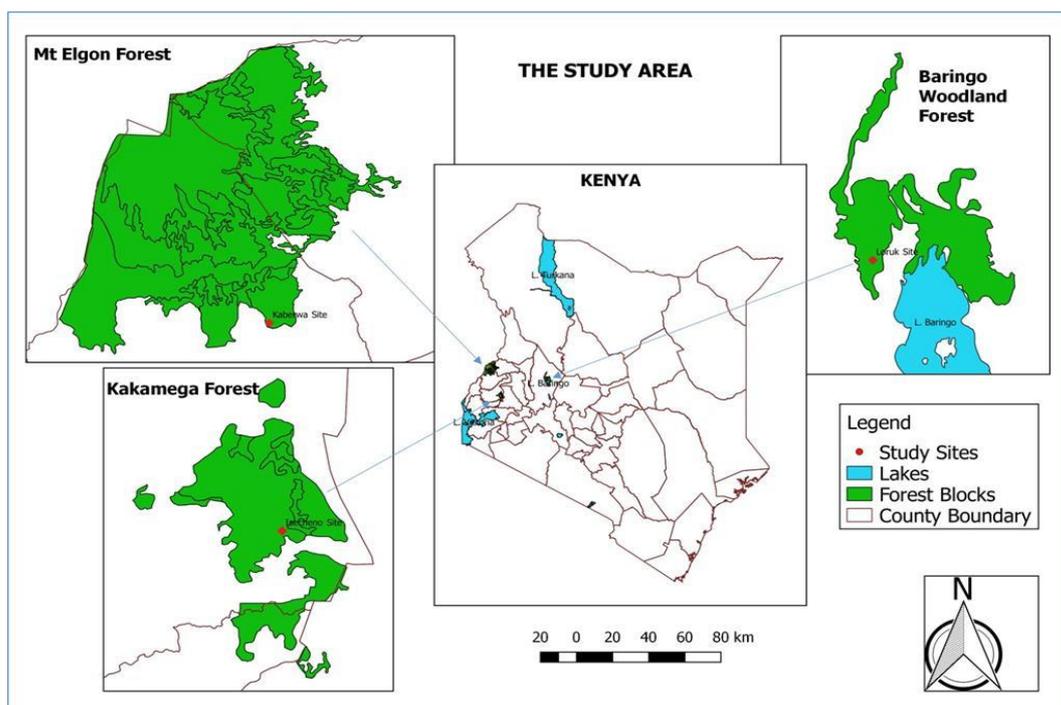


Figure 1. Location of study sites in Kenya.

Field methods and simulations

Fieldwork and data organization: Data collection over 1 ha-forest unit of reference was done in the field to determine “true” values of forest attributes for each forest type. It was achieved by establishing four hundred 5 m × 5 m plots (Fig. 2) to ensure accurate field observations of forest attributes including seedlings. A complete enumeration of seedlings was systematically done within 1 m² (i.e. 1 m × 1 m) subplots, one after the other, within the 5 m × 5 m plots in order to enhance accuracy of observations on seedlings. Records on seedlings from were put together for each 5 m × 5 m smallest data compilation unit. Data were recorded on field sheets and were later transferred into the computer MS Excel spreadsheet. Each 5 m × 5 m unit was assigned a unique code (Fig. 2 for illustration) for easy identification, retrieval and manipulation during data analysis. Data were organized per forest type and plot size.

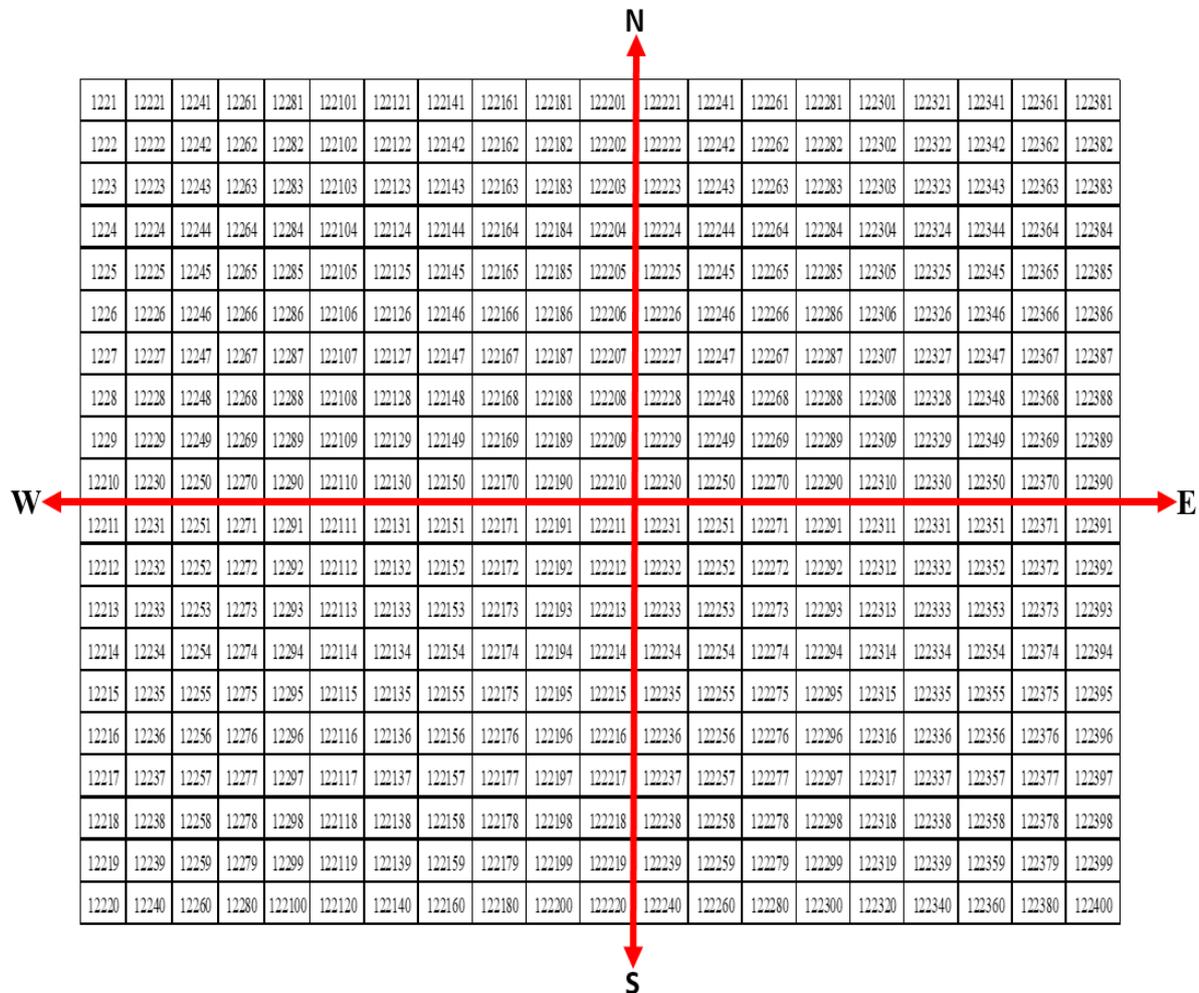


Figure 2. Example of field arrangement for four hundred 5 m by 5 m plots in the forest. [Each cell with a number represent a coded 5 m x 5 m plot for easy data set identification; entry; storage; retrieval and use in sampling simulation activity. First three digits denote the forest site (122-Kakamega site; 111- Mt Elgon site; 131- Loruk site). The subsequent digits represent serial plot number within the 100 m x 100 m frame (Hitimana *et al.* 2019)]

Study variables: Study variables include plot size, sampling intensity, inventory cost per hectare, percentage sampling error and number of trees in different diameter size classes.

Plot size: Four plot sizes were tested for efficiency and cost-effectiveness as data compilation units (Table 1) for seedling stocks over one hectare (100 m × 100 m). Plot sizes larger than 5 m × 5 m were formed by merging contiguous smaller units through the confounding technique in R software: 5 m × 5 m → 10 m × 5 m → 10 m × 10 m → 20 m × 20 m (see R codes in Appendix I). Display of plots of different sizes over 1 ha area is in Appendix II.A–D. The merging of smaller units was automatically associated with collating records they contained. Totals, averages and other data computations in each unit were performed in R Software.

Sampling intensity: Complete inventory (100% intensity) of seedlings over 1 ha (100 m × 100 m forest unit) was carried out using the four different plot sizes in each selected forest type. The number of compilation units for each plot size used varied from 25 to 400 (Table 1).

Table 1. Number of plots (N) in a hectare for different plot sizes.

Sampling Intensity (%) ¹	Plot Sizes			
	5 m × 5 m (25 m ²)	10 m × 5 m (50 m ²)	10 m × 10 m (100 m ²)	20 m × 20 m (400 m ²)
100	400	200	100	25

Note: ¹n= Sample size (no. of sample plots selected from one- hectare forest unit); N= population size (total number of plots in a one- hectare forest)

Inventory cost over one hectare: The inventory cost or effort per hectare was determined for each plot size 25 m², 50 m², 100 m² and 400 m². Sampling effort was measured by the time taken to complete work within the 1 ha plot area. Time taken to collect data in each 5 m × 5 m plot was recorded in the field using a watch chronometer. The forest inventory protocol developed for one hectare is a standard to be used in any inventory where a network of several 1 ha plots may be established as permanent sample plots or independent temporal sampling plots (Picard *et al.* 2010, Brown & Williams 2016).

Percentage sampling error: Conventionally, the precision of an estimate is measured by the sampling error % (uncertainty level %) (Lackmann 2011, Klauberg *et al.* 2016) (Equation 1). Sampling error was computed for each plot size for different sampling intensities, up to the complete inventory, and based on standard error of the mean (Equation 2).

$$\text{Sampling Error \%} = \frac{1/2 (95\% \text{Confidence interval width})}{\mu} \times 100 = \frac{SE \times t}{\mu} \times 100 \dots \dots \dots \text{(Equation 1)}$$

where, μ is the mean of the distribution; and sampling error (error %) is the 95 percent confidence interval expressed as a percentage of the mean.

Standard error of the mean (SE) for each plot size was computed as follows (Equation 2):

$$SE = S / \sqrt{n} \dots \dots \dots \text{(Equation 2)}$$

where, S = Standard deviation given per hectare for each plot size; n = sample size (*i.e.* no. of plots for 100% intensity and plot size used).

Number of tree seedlings, saplings and large trees: Individuals in each tree development stage (seedling, sapling and large trees) were counted from each 5 m × 5 m plot. Diameter at breast height (DBH), measured at 1.3 m from ground level, was used to distinguish saplings from individuals in other development stages. Veneer caliper was used to measure small size trees *e.g.* saplings; and large calipers were used on larger diameter trees (Avery & Burkhart 2015). In this study, seedlings were individuals <1 cm DBH and < 1.50 m tall; saplings were small trees with 1–5 cm DBH; and large trees were individuals ≥ 5 cm DBH (adopted from Stride *et al.* 2018). Tree diameter size distributions are often used to indicate rates of recruitment, growth and mortality in a forest over time, and they are used to analyse forest stability, regeneration history and impact of past disturbances (Poore & Sayer 1991). The numbers of individuals were converted per hectare for each DBH size class.

Data analysis

Efficient plot sizes for natural tree seedlings stock inventories in “1 ha-method”: Population mean-variance for seedling stocks in each selected forest type was determined based on 5 m × 5 m plot size and 100% intensity (complete inventory) using (Equation 3) and interpreted (Hitimana *et al.* 2019).

$$\text{Population mean variance} = \frac{\sigma^2}{N} \dots \dots \dots \text{(Equation 3)}$$

where, σ² = population variance; N = Total number of plots per ha which varied with plot size.

This mean variance was used as a measure of standard [inherent] variability for the density of seedlings in the forest. It was also used to compute standard [inherent] sampling error percent. Percentage sampling error was computed for each plot size (compilation unit type) for seedling counts.

Both sampling error % and inventory effort (cost) were plotted on the same graph as dependent variables over plot size (independent variable). The lower the sampling error % produced by a plot size, the more precise, reliable and suitable is that size as a compilation unit. The optimum plot size was identified at the intersection of the two-line graphs (*i.e.* inventory cost and sampling error % line graphs). Regression analysis (IBM SPSS) was applied to obtain regression equations and ascertain the probability level of significance of the observed regression relationships. Solving both equations simultaneously enabled the identification of optimum plot size for each forest type.

Regeneration variability and recruitment characteristics in studied forests: Recruitment of tree individuals from one development stage to the other was evaluated based on the ratios of number of seedlings - to - number of saplings; and the ratios of individuals in different successive diameter size classes (the “q” ratio; Equation 4) as dependent variables and diameter classes as independent variable. The graph of q over DBH classes is a measure of how regular regeneration and recruitment have been in the forest (Hitimana *et al.* 2004, Marimon *et al.* 2012).

$$q = \frac{D_{(i-1)}}{D_i} \dots\dots\dots \text{(Equation 4)}$$

where, $D_{(i-1)}$ is density in a lower DBH class; and D_i is density in the immediate upper DBH class.

RESULTS AND DISCUSSION

Efficient plot sizes for natural tree seedling stock inventories in “1 ha-method”

Inherent true variability of seedling stocking in the selected forests determined based on 5 m × 5 m plot size and complete inventory is as shown in table 2.

Table 2. Inherent true variability of tree seedlings stocking per hectare compiled using 5 m × 5 m plot size for three natural forest types in Kenya.

Forest attribute	Forest	Smallest σ^2/N	Inventory cost (ha h ⁻¹)	Plot size (m × m)
Seedlings ha ⁻¹	TRF	1,726,559.16	0.02	5 × 5
	MMF	223,003.91	0.02	5 × 5
	DWF	3,033.49	0.04	5 × 5

Observed true variability in the distribution of number of seedlings in the forest varied from one plot size to the other; and was inversely proportional to the sample size. Inherent variability in tree seedling stocks was by far highest in tropical rain forest; intermediate in tropical moist montane forest and lowest in dry woodland forest. This variability in tropical rainforest (TRF) was 7.74 and 569 times that of Mt Elgon tropical moist montane forest (MMF) and Loruk dry woodland forest (DWF); respectively. If the extent of variability indicates the level of complexity of the variable under consideration, then the complexity continuum in tree regeneration from the highest across forest types to the lowest levels was found to be TRF – MMF – DWF.

For 100 % inventory over 1 ha, the choice of plot size influences the cost of operations, level of uncertainty and level of precision (Table 3). The smaller the sampling unit, the higher the cost of sampling was experienced. The choice between many small plots and a few larger plots for a constant sampling intensity makes a difference.

Table 3. Precision level and costs of complete tree seedlings inventory using different plot sizes per ha, for selected natural forests in Kenya.

Plot size (m ²)	Tropical rain forest				Moist montane forest				Dry woodland forest			
	Pop. Mean	Pop. Error (%)	Pop. CV (%)	Inventory Cost (hr ha ⁻¹)	Pop. Mean	Pop. Error (%)	Pop. CV (%)	Inventory Cost (hr ha ⁻¹)	Pop. Mean	Pop. Error (%)	Pop. CV (%)	Inventory Cost (hr ha ⁻¹)
25	16,764	15.4	157	50.42	6,279	14.7	150	40.68	1,094	9.9	101	22.38
50	16,764	16.2	117	25.28	6,279	15.6	113	20.10	1,094	10.7	77	11.35
100	16,764	18.2	92	12.70	6,279	18.0	91	9.98	1,094	11.9	61	5.65
400	16,764	29.0	70	3.21	6,279	24.1	58	2.43	1,094	18.7	45	1.45

Note: Plot size (m²)= 25 → 5 m × 5 m; 50 → 10 m × 5 m; 100 → 10 m × 10 m; 400 → 20 m × 20 m; Pop. Mean= Population Mean; Pop. Error (%)= Sampling error (%) = Uncertainty (%) = (Standard Error* student’s t/mean)*100 as a measure of precision level; Pop. CV (%)= It measure levels of true inherent variability of seedlings stocking per hectare being reflected by a specific plot size.

The other aspect of efficient plot size is the desired precision level of the estimates. Sampling error is a measure of uncertainty level or bias which is inversely proportional to the precision level in a complete inventory context. The smaller the error, the higher is the precision level. In this study, the bias (error) decreased with decreasing plot size (Fig. 3). It means that, all factors held constant, smaller plot sizes were accurate and more precise. Smallest plot size (25 m²) produced highest internal variability (CV% >100%) for all forest types (Table 3) and 400 m² plots produced the lowest CV%. Variability is an inherent property of the system of nature, and not of the analyst; thus, it can only be reduced by sampling entire populations or stratification of the area. Variability refers to the observed true heterogeneity or diversity of elements in a population and is an inherent property of the system of nature (Lackmann 2011). A trade-off between cost and precision levels determined the efficient plot sizes in different forests (Fig. 3). The precision of an inventory depends on the

trade-off between using larger plots which have a lower inter-plot variance or using a larger number of smaller plots which tend to reduce the standard error of the mean (Evans & Viengkham 2001). Plot sizes that balanced desired precision level (uncertainty %) and cost were 75 m² (CV between 92 and 117%; Table 3) for TRF; 62.4 m² (CV between 91 and 113%) for MMF and 88.4 m² (CV between 61 and 77%) for DWF. These optimum compilation units (*i.e.* plots) result in 95% Confidence Interval of the total number of seedlings $\pm 17.0\%$ of the total number of seedlings over one hectare within TRF; $\pm 16.3\%$ of the total number of seedlings over one hectare within MMF and $\pm 11.3\%$ of the total number of seedlings over one hectare within DWF.

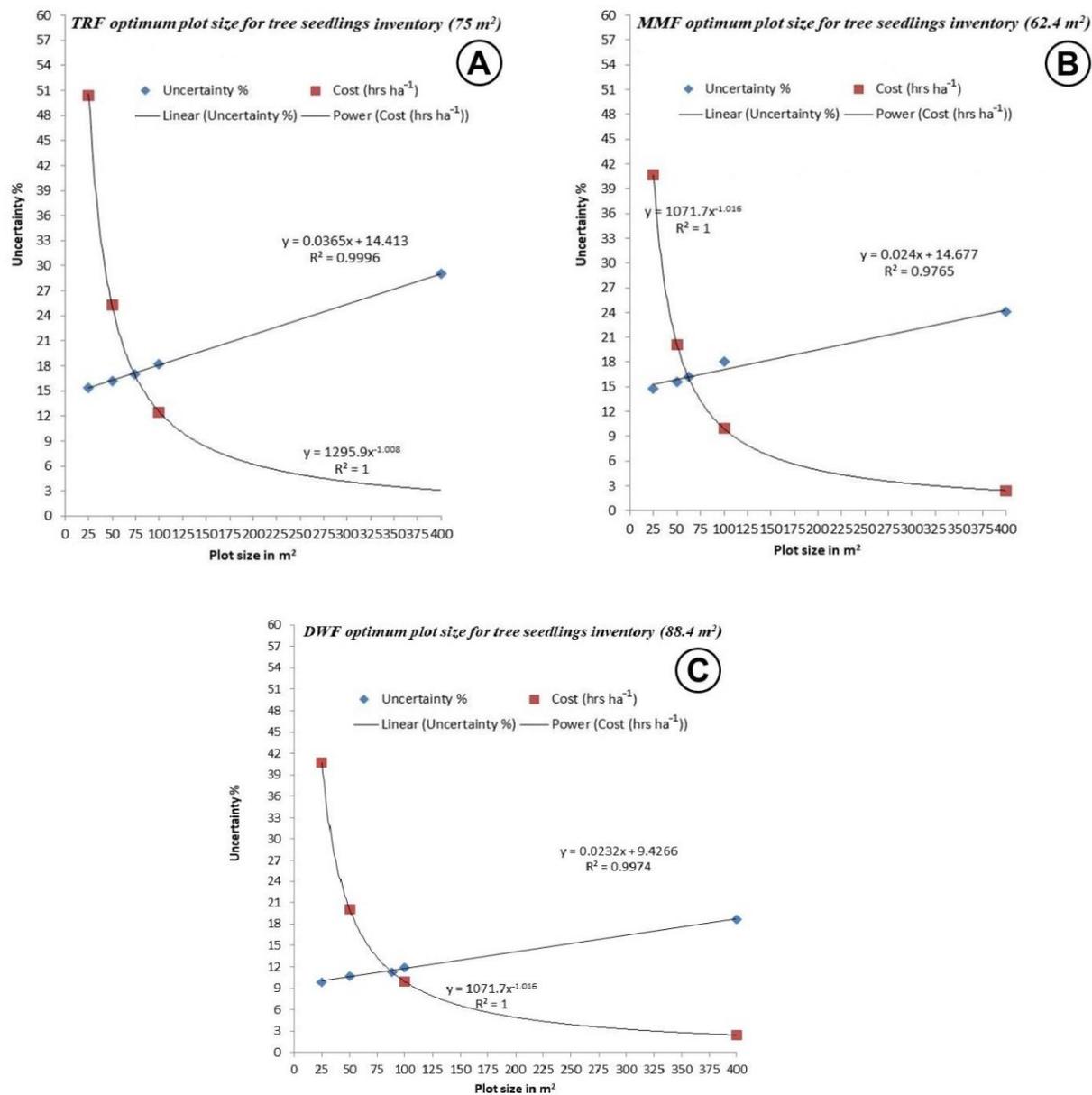


Figure 3. Efficient plot size for 100% inventory of 1 hectare for the number of tree seedlings in Kenya: **A**, Kakamega tropical rain forest (TRF); **B**, Mt Elgon moist montane forest (MMF); **C**, Dry woodland forest (DWF).

The reliability levels of estimates in the three tropical natural forests in Kenya compare well with findings by Lackmann (2011) for estimation of carbon stock changes in complex forests [mean carbon stock $\pm 10\%$ of the mean at 95% confidence and at a modest cost]; and with desired precision level by Cavalcanti *et al.* (2011) for plantation forests ($\pm 10\%$). The sampling errors associated with optimum plot sizes found in this study are also within the range of recommended precision levels for diagnostic inventories in Amazon forest (Klauber *et al.* 2016), that is, 20% for two forest species assessment and 15% for one species assessment. Cielo-Filho *et al.* (2009) recommend $\pm 20\%$ sampling error at 95% confidence level for tree species abundance and importance value estimates in a tropical forest stand in Brazil.

Data compilation units larger than 100 m² (*e.g.* 10 m \times 10 m) have low precision level (Table 3) in the 1 ha-method.

Regeneration variability and recruitment characteristics in studied forests

The proportion of tree seedlings (<1 cm DBH individuals) dominated with 86% in the Kakamega tropical rainforest (TRF) (all sizes tree density = 19, 448 individuals ha⁻¹) and 81% in Mt Elgon moist montane forest (MMF) (total density = 7,711 individuals ha⁻¹). In Loruk dry woodland forest (DWF) (total density = 2,369 individuals ha⁻¹); seedlings and saplings dominated almost equally with 46% and 41% relative abundances; respectively (Fig. 4). Saplings contributed only 8% in both TRF and MMF; being under-represented if the reverse-J curve describing a stable natural forest is referred to (Devis & Johnson 1987). These results indicate a deficient seedling stage in dry woodland forest and a deficient sapling stage in moist montane forest; where large trees were exceptionally more abundant than saplings. This shows a degenerating population if such trend in recruitment continues. In absolute terms, TRF had the highest stocking ha⁻¹ (2.5 times than MMF and 8 times the stocking in DWF) in Kenya. Abiotic factors such as soil, topography, precipitation, temperature and drought are known to influence regeneration success including seeding; seed germination; tree seedling establishment and early sapling survival and growth (Schwartz & Caro 2003, Principe *et al.* 2014).

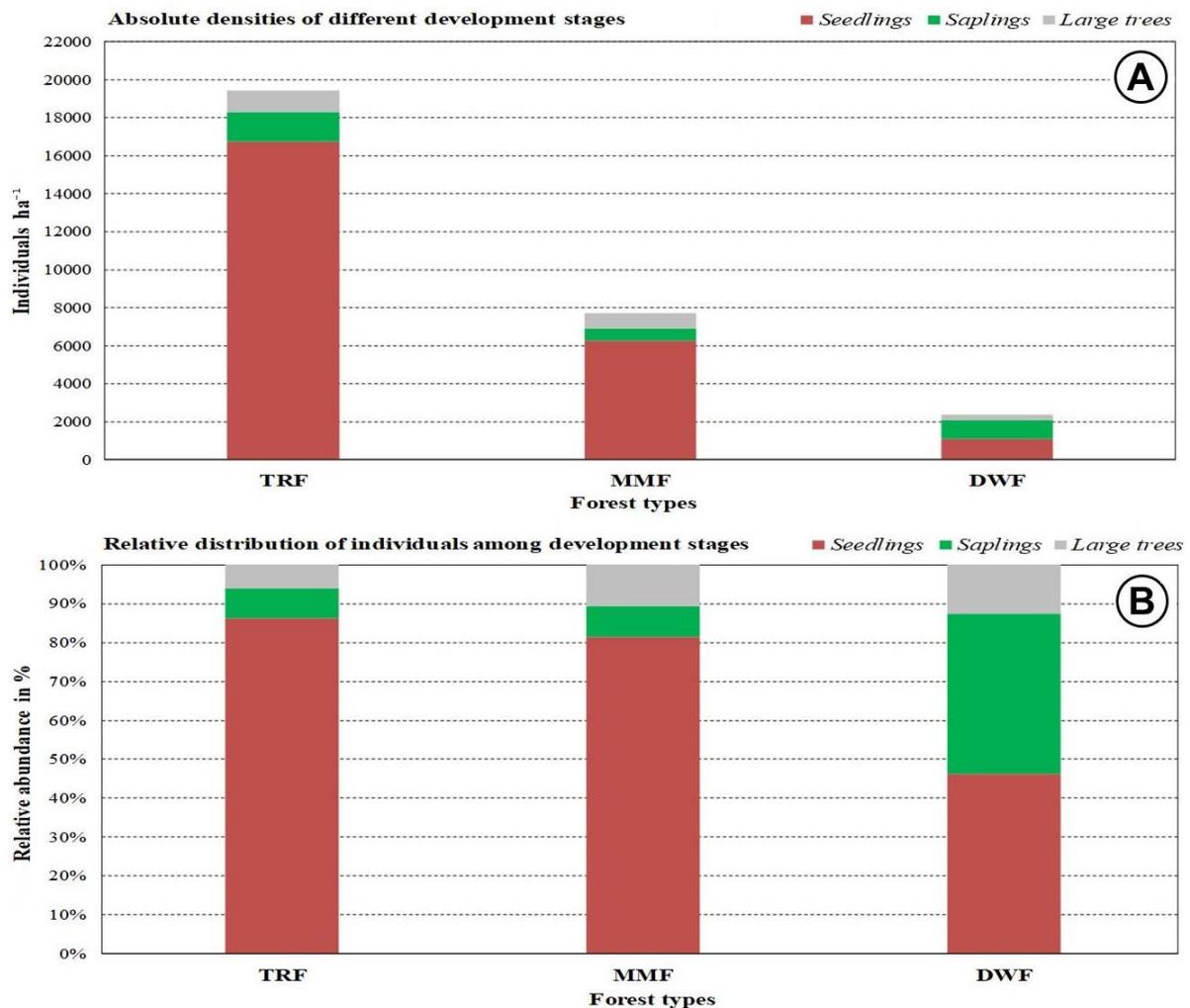


Figure 4. Recruitment patterns of trees for different tropical natural forest types in Kenya: **A**, Absolute density (Individuals ha⁻¹); **B**, Relative distribution (Relative abundance in %). [TRF= Tropical rainforest; MMF= Moist montane forest; DWF= Dry Woodland Forest; Seedlings= Individuals <1 cm dbh and <1.50 m tall; Saplings= Small trees with 1–5 cm dbh; Large trees= Individuals >5 cm dbh]

Based on the *q* quotient (Fig. 5); regular recruitment was only observed in the tropical rainforest in tree sizes (post sapling size) up to about 110 cm DBH class. Recruitment of trees in MMF Site followed same trend as in TRF Site up to 80 cm DBH class. However, at Mt Elgon Site; some exceptional events or processes occurred and distorted diameter size distribution for trees with DBH >50 cm; causing drastic departure from the balanced trend observed in Kakamega tropical rain forest site. The narrower range of DBH classes in the DWF Site would suggest; notwithstanding environmental and ecological constraints to tree growth; that this ecosystem is the simplest and perhaps the youngest in succession. To this extent; tropical rain forest was judged more stable than the other forest types; and the woodland ecosystem was the least stable. Rising “*q*” quotient at the tail-end of

diameter size distribution in TRF is characteristic of mature; self-regulating tropical forests. Protection and rehabilitation measures are needed in management and conservation of the structurally unstable ecosystems: MMF and DWF. Periodic monitoring programmes; say every 10 years; are encouraged to follow up the recovery and development processes over time.

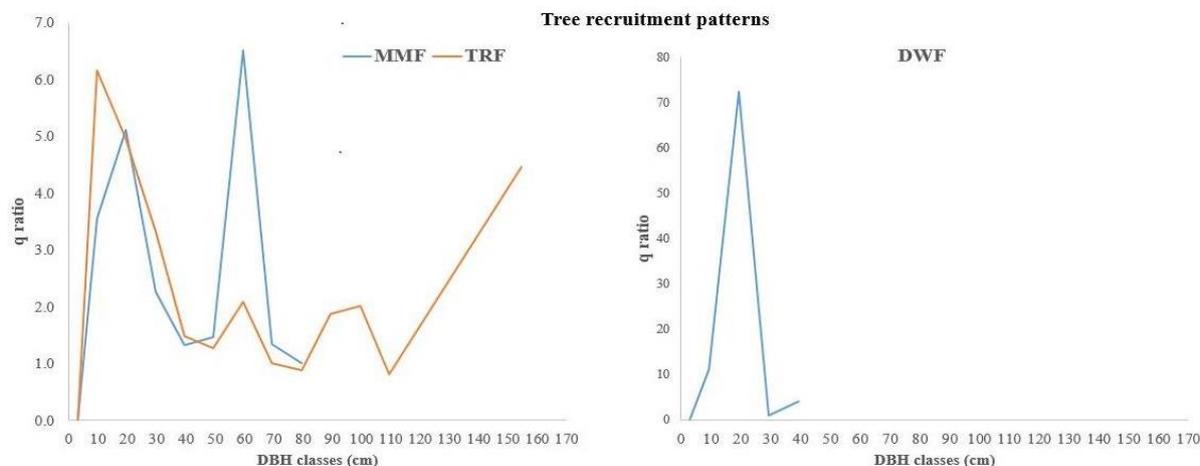


Figure 5. Trend in regeneration and recruitment process in three natural forest types in Kenya. [TRF= Tropical rain forest; MMF= Tropical moist montane forest; DWF= Tropical dry woodland forest]

The recruitment process of individuals into the different development stages was not regular (Fig. 5). There has been reported heavy logging activities in Kakamega (Fashing *et al.* 2003, Momanyi 2007, Mutiso *et al.* 2013) and at Mt Elgon forests over past decades (Hitimana *et al.* 2004, Hitimana *et al.* 2010) which may have distorted recruitment patterns. The number of seedlings is higher than the number of saplings. There was an observed irregular trend in the moist montane forest where the stocking of trees larger than 5 cm DBH was lower than saplings (1–5 cm); with large trees: saplings ratio of 100:80. Ordinarily; there should be more saplings than large trees in forests that experience regular recruitment patterns such as in TRF (100:130) and in DWF (100:330). Seedling establishment and sapling development may have been tempered with by logging and charcoal production (Hitimana *et al.* 2010). However, the monitoring of regeneration establishment and resilience are required for MMF and DWF. Seed germination and seedling establishment are known to be vulnerable stages; very much sensitive to variations in microsite conditions such as edaphic, droughts, fires, trampling and grazing (Hitimana *et al.* 2004, Pretzsch 2009, Eshete *et al.* 2011, Kiruki *et al.* 2017). Grazing may prevent young seedlings from reaching mature stages through trampling, uprooting and accelerated site degradation (Zida *et al.* 2007, Eshete *et al.* 2009). Uniquely low recruitment trends in dry woodland forests could be as a result of environmental hardships working against seed germination and or seedling establishment. A similar trend of low seedling and sapling counts in the wider Baringo woodland was observed for *Acacia tortilis* as a result of high mortality rate occasioned by competition for moisture, drought, shading effects of mature trees and intense browsing (Kiyiapi 1994). Overall; the TRF was found to be more complex and diverse than the moist montane and dry woodland forest types; with DWF being the simplest and perhaps most vulnerable ecosystem among them. Rehabilitation work is required to improve stocking levels in MMF and DWF.

CONCLUSIONS

This study on regeneration and recruitment assessment in tropical forests of Kenya revealed that closed-canopy forests (TRF and MMF) had higher stocking levels and higher stocking variability for seedlings per hectare than dry woodland forest (DWF). Complete inventory effort per hectare varied with plot sizes in a reverse order across all studied forest types. The inventory cost was highest in TRF (most complex in structure and diversity) and lowest in DWF (least complex). Efficiency of complete inventory in tropical natural forests to estimate the number of seedlings per hectare depends on the size of the plot used as the data compilation unit. The required optimum data compilation units for tree seedlings were found to be below 100 m² for all forest types. Data obtained from the 5 m x 5 m compilation units enabled to gather quality data on all diameter size classes and allowed analysis of diameter size distributions across the studied natural forest types in order to model recruitment of the tree component and trace regeneration dynamics over time. Recruitment was found to be irregular over time in all the selected forests, perhaps due to socio-ecological factors associated with each forest type.

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Appendix I: R codes for creating various plot sizes.**1. Introduction**

This process is the same in R studio for all the three forests. We use Mt. Elgon site to illustrate it. We just update the name of the forest in the function and run to get output.

2. Merging 5 m × 5 m plots to create 10 m × 5 m plots

Field data collection from the forest was done and organized in 400 plots of equal size of 5 m × 5 m (Smallest plot size tested in the study).

Display of grid for four hundred 5 m × 5 m plots is available (Appendix II. A.)

Reorganising field data from same forest in 10 m × 5 m plot size was done in R as described below. It required having 1 ha forest divided it into 200 plots of 10 m × 5 m each. Each plot here is going to be twice as large as the the plots in the previous part.

We create the 200 plots here by merging every two consecutive plots (vertically) from the initial grid of 400 plots.

First, let us identify the unique plots in order

```
plots =unique(mt_elgon$plot.no.)
plots =as.character(plots)
```

We take the *odd* plot number eg *1111* to represent the new plot that is created by merging the two plots *1111* and *1112*. The unique plots are arranged in ascending order from 1 through 400. The position of the plot in this arrangement (between 1 and 400) can be separated as either *even* eg *2* or *odd* eg *1*. The first and second lines of the code below checks if the position is even or odd and creates a list with the values *TRUE* if the position is even and *FALSE* if the position is odd.

```
is.even =function(x) x%%2 ==0
even =is.even(1:length(plots))
```

Finally, the two lists *plots* and *even* are merged together to create a table with two rows, one for plot number and another indicating whether the position is odd or even, and 400 rows, one for each unique plot number.

```
mytable=cbind(plots,even)
mytable=as.data.frame(mytable)
```

Our new table is named *mytable*

Unique number for the new created plot of 10 m × 5 m is the *odd* plot number from each pair of small plots that were merged. In R, we create another column in *mytable*. This column will contain the uniqueplot number. The first line of code below creates another column and calls it *newplots*. The second part of the code adds the values of plot number that we want.

```
mytable=mutate(mytable, newplots = plots )
mytable[mytable$even ==T,][3] =mytable[mytable$even ==F,][3]
```

We use this table to check for all values of *plot number* in our *mt_elgon* data set that match the values of *plots* in *mytable* and we replace them with the values of *newplots* in *mytable*. We also ensure the values in these three columns are of the same “data type”.

```
mytable$plots =as.character(mytable$plots)
mytable$newplots =as.character(mytable$newplots)
mt_elgon$plot.no. =as.character(mt_elgon$plot.no.)
for (i in 1:nrow(mt_elgon)) {
  for (j in 1:nrow(mytable)) {
    if (mt_elgon$plot.no.[i] ==mytable$plots[j]) {
      mt_elgon$plot.no.[i] =mytable$newplots [j]
    }
  }
}
length(unique(mt_elgon$plot.no.))
## [1] 200
```

We now have 200 unique plots from initial 400. We can now go ahead with our analysis just in the same way as it is done in the 400 plots.

```
uniq_plots =as.character(unique(mt_elgon$PLOT.NO.))
length(uniq_plots)
## [1] 200
```

Arranging the plots appropriately;

```
uniq_plots =cbind(uniq_plots[1:20], uniq_plots[21:40], uniq_plots[41:60], uniq_plots[61:80],
uniq_plots[81:100], uniq_plots[101:120], uniq_plots[121:140], uniq_plots[141:160], uniq_plots[161:180],
uniq_plots[181:200])
uniq_plots =as.data.frame(uniq_plots)
```

Display of grid for two hundred 10 m × 5 m plots is available (Appendix II.B)

3. Merging 10 m × 5 m plots to create 10 m × 10 m plots

The 200 plots grid is made of 20 columns and 10 rows. We need to merge two consecutive plots (horizontally) to create 10 columns, and obtain a grid of 10 columns by 10 rows as follows.

```
x =unique(mt_elgon$plot.no.)
x =as.data.frame(x)
y =x
y[11:20,] =y[1:10,]
y[31:40,] =y[21:30,]
y[51:60,] =y[41:50,]
y[71:80,] =y[61:70,]
y[91:100,] =y[81:90,]
y[111:120,] =y[101:110,]
y[131:140,] =y[121:130,]
y[151:160,] =y[141:150,]
y[171:180,] =y[161:170,]
y[191:200,] =y[181:190,]
mytable=cbind(x,y)
names(mytable) =c("plots", "newplots")
mytable$plots =as.character(mytable$plots)
mytable$newplots =as.character(mytable$newplots)
mt_elgon$plot.no. =as.character(mt_elgon$plot.no.)
for (i in 1:nrow(mt_elgon)) {
  for (j in 1:nrow(mytable)) {
    if (mt_elgon$plot.no.[i] ==mytable$plots[j]) {
      mt_elgon$plot.no.[i] =mytable$newplots [j]
    }
  }
}
length(unique(mt_elgon$plot.no.))
## [1] 100
```

We now have 100 unique plots from initial 200 plots. We can now go ahead with our analysis just like in the 400 plots.

```
uniq_plots =as.character(unique(mt_elgon$PLOT.NO.))
length(uniq_plots)
## [1] 100
```

Then we arrange the plots appropriately.

```
uniq_plots =cbind(uniq_plots[1:10], uniq_plots[11:20], uniq_plots[21:30], uniq_plots[31:40],
uniq_plots[41:50], uniq_plots[51:60], uniq_plots[61:70], uniq_plots[71:80], uniq_plots[81:90],
uniq_plots[91:100])
uniq_plots =as.data.frame(uniq_plots)
```

Display of grid for one hundred 10 m × 10 m plots is available (Appendix II.C)

4. Merging 10 m × 10 m plots to create 20 m × 20 m plots

4.1. Merging pairs of consecutive plots vertically to create 20 m × 10 m plots

First, let us identify the unique plots from the list of 10 m × 10 m - plots

```
plots =unique(mt_elgon$plot.no.)
plots =as.character(plots)
```

The unique plots are arranged in order from 1 through 100. The position of the plot in this arrangement (between 1 and 100) can be separated as either *even eg 2* or *odd eg 1*. The first and second lines of the code

below check if the position is even or odd and create a list with the values *TRUE* if the position is even and *FALSE* if the position is odd.

Finally, the two lists *plots* and *even* are merged together to create a table with two rows: one for plot number and another indicating whether the position is odd or even and 100 rows, one for each unique plot number.

```
is.even =function(x) x%%2 ==0
even =is.even(1:length(plots))
mytable=cbind(plots,even)
mytable=as.data.frame(mytable)
```

Our new table is named *mytable*

Unique number for the new created plot of 20 m × 10 m is the *odd* plot number from each pair of 10m×10m-plots that were merged. In R, we create another column in *mytable*. This column will contain the uniqueplot number for 20 m × 10 m plot. The first line of code below creates another column and calls it *newplots*. The second part of the code adds the values of plot number that we want.

```
mytable=mutate(mytable, newplots = plots )
mytable[mytable$even ==T,][3] =mytable[mytable$even ==F,][3]

mytable$plots =as.character(mytable$plots)
mytable$newplots =as.character(mytable$newplots)
mt_elgon$plot.no. =as.character(mt_elgon$plot.no.)
for (i in 1:nrow(mt_elgon)) {
  for (j in 1:nrow(mytable)) {
    if (mt_elgon$plot.no.[i] ==mytable$plots[j]) {
      mt_elgon$plot.no.[i] =mytable$newplots [j]
    }
  }
}
length(unique(mt_elgon$plot.no.))
## [1] 50
```

We now have 50 unique plots from initial 100 plots

4.2. Merging consecutive 20 m × 10 m plots horizontally to form 20 m × 20 m plots

The fifty 20 m x 10 m plots are arranged in 5 rows and 10 columns. In R, we need to reduce the 10 columns with 10 m length each to 5 columns with 20 m length each.

```
x =unique(mt_elgon$plot.no.)
x =as.data.frame(x)
y =x
y[6:10,] =y[1:5,]
y[16:20,] =y[11:15,]
y[26:30,] =y[21:25,]
y[36:40,] =y[31:35,]
y[46:50,] =y[41:45,]

mytable=cbind(x,y)
names(mytable) =c("plots", "newplots")

mytable$plots =as.character(mytable$plots)
mytable$newplots =as.character(mytable$newplots)
mt_elgon$plot.no. =as.character(mt_elgon$plot.no.)

for (i in 1:nrow(mt_elgon)) {
  for (j in 1:nrow(mytable)) {
    if (mt_elgon$plot.no.[i] ==mytable$plots[j]) {
      mt_elgon$plot.no.[i] =mytable$newplots [j]
    }
  }
}
length(unique(mt_elgon$plot.no.))

## [1] 25
```

We now have 25 unique plots from initial 50 and can go ahead with our data analysis from them.

```
uniq_plots =as.character(unique(mt_elgon$PLOT.NO.))
length(uniq_plots)
## [1] 25
```

Appropriate arrangement of the plots through are codes:

```
uniq_plots =cbind(uniq_plots[1:5], uniq_plots[6:10], uniq_plots[11:15], uniq_plots[16:20], uniq_plots[21:25])
uniq_plots =as.data.frame(uniq_plots)
```

Display of grid for twenty-five 20 m × 20 m plots is available (Appendix II.D)

Appendix II: Sampling frames for different plot sizes.

II.A: Grid of the 400 5 m × 5 m-plots: case in Mt Elgon 100 m × 100 m - Forest Unit.

1111	11121	11141	11161	11181	111101	111121	111141	111161	111181	111201	111221	111241	111261	111281	111301	111321	111341	111361	111381
1112	11122	11142	11162	11182	111102	111122	111142	111162	111182	111202	111222	111242	111262	111282	111302	111322	111342	111362	111382
1113	11123	11143	11163	11183	111103	111123	111143	111163	111183	111203	111223	111243	111263	111283	111303	111323	111343	111363	111383
1114	11124	11144	11164	11184	111104	111124	111144	111164	111184	111204	111224	111244	111264	111284	111304	111324	111344	111364	111384
1115	11125	11145	11165	11185	111105	111125	111145	111165	111185	111205	111225	111245	111265	111285	111305	111325	111345	111365	111385
1116	11126	11146	11166	11186	111106	111126	111146	111166	111186	111206	111226	111246	111266	111286	111306	111326	111346	111366	111386
1117	11127	11147	11167	11187	111107	111127	111147	111167	111187	111207	111227	111247	111267	111287	111307	111327	111347	111367	111387
1118	11128	11148	11168	11188	111108	111128	111148	111168	111188	111208	111228	111248	111268	111288	111308	111328	111348	111368	111388
1119	11129	11149	11169	11189	111109	111129	111149	111169	111189	111209	111229	111249	111269	111289	111309	111329	111349	111369	111389
11110	11130	11150	11170	11190	111110	111130	111150	111170	111190	111210	111230	111250	111270	111290	111310	111330	111350	111370	111390
11111	11131	11151	11171	11191	111111	111131	111151	111171	111191	111211	111231	111251	111271	111291	111311	111331	111351	111371	111391
11112	11132	11152	11172	11192	111112	111132	111152	111172	111192	111212	111232	111252	111272	111292	111312	111332	111352	111372	111392
11113	11133	11153	11173	11193	111113	111133	111153	111173	111193	111213	111233	111253	111273	111293	111313	111333	111353	111373	111393
11114	11134	11154	11174	11194	111114	111134	111154	111174	111194	111214	111234	111254	111274	111294	111314	111334	111354	111374	111394
11115	11135	11155	11175	11195	111115	111135	111155	111175	111195	111215	111235	111255	111275	111295	111315	111335	111355	111375	111395
11116	11136	11156	11176	11196	111116	111136	111156	111176	111196	111216	111236	111256	111276	111296	111316	111336	111356	111376	111396
11117	11137	11157	11177	11197	111117	111137	111157	111177	111197	111217	111237	111257	111277	111297	111317	111337	111357	111377	111397
11118	11138	11158	11178	11198	111118	111138	111158	111178	111198	111218	111238	111258	111278	111298	111318	111338	111358	111378	111398
11119	11139	11159	11179	11199	111119	111139	111159	111179	111199	111219	111239	111259	111279	111299	111319	111339	111359	111379	111399
11120	11140	11160	11180	111100	111120	111140	111160	111180	111200	111220	111240	111260	111280	111300	111320	111340	111360	111380	111400

II.B: Grid of the 200 10 m × 5 m-plots: case in Mt Elgon 100 m × 100 m - Forest Unit.

1111	11122	11141	11161	11181	111100	111120	111140	111160	111180	111201	111221	111241	111261	111281	111300	111320	111340	111360	111380
1113	11124	11143	11163	11183	111102	111122	111142	111162	111182	111203	111223	111243	111263	111283	111302	111322	111342	111362	111382
1116	11126	11145	11165	11185	111104	111124	111144	111164	111184	111205	111225	111245	111265	111285	111304	111324	111344	111364	111384
1118	11128	11147	11167	11187	111106	111126	111146	111166	111186	111207	111227	111247	111267	111287	111306	111326	111346	111366	111386
11111	11131	11149	11169	11189	111108	111128	111148	111168	111188	111209	111229	111249	111269	111289	111308	111328	111348	111368	111388
11113	11133	11150	11170	11190	111111	111131	111151	111171	111191	111210	111230	111250	111270	111290	111311	111331	111351	111371	111391
11115	11135	11152	11172	11192	111113	111133	111153	111173	111193	111212	111232	111252	111272	111292	111313	111333	111353	111373	111393
11117	11137	11154	11174	11194	111115	111135	111155	111175	111195	111214	111234	111254	111274	111294	111315	111335	111355	111375	111395
11119	11139	11156	11176	11196	111117	111137	111157	111177	111197	111216	111236	111256	111276	111296	111317	111337	111357	111377	111397
11120	11140	11158	11178	11198	111119	111139	111159	111179	111199	111218	111238	111258	111278	111298	111319	111339	111359	111379	111399

II.C: Grid of the 100 10 m × 10 m-plots: case in Mt Elgon 100 m × 100 m - Forest Unit.

1111	11141	11181	111120	111160	111201	111241	111281	111320	111360
1113	11143	11183	111122	111162	111203	111243	111283	111322	111362
1116	11145	11185	111124	111164	111205	111245	111285	111324	111364
1118	11147	11187	111126	111166	111207	111247	111287	111326	111366
11111	11149	11189	111128	111168	111209	111249	111289	111328	111368
11113	11150	11190	111131	111171	111210	111250	111290	111331	111371
11115	11152	11192	111133	111173	111212	111252	111292	111333	111373
11117	11154	11194	111135	111175	111214	111254	111294	111335	111375
11119	11156	11196	111137	111177	111216	111256	111296	111337	111377
11120	11158	11198	111139	111179	111218	111258	111298	111339	111379

II.D: Grid of the 25 20 m × 20 m-plots: case in Mt Elgon 100 m × 100 m - Forest Unit.

1111	11181	111160	111241	111320
1116	11185	111164	111245	111324
11111	11189	111168	111249	111328
11115	11192	111173	111252	111333
11119	11196	111177	111256	111337