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THE ORIGIN, DEVELOPMENT AND STRUCTURE OF DEMAND FOR PLANT GENETIC RESOURCES. THE IMPACT OF THE IN TRUST AGREEMENTS TO THE CGIAR COLLECTIONS AVAILABILITY

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ABSTRACT

The objective of this paper is to explore how the demand of germplasm held by CGIAR genebanks changed over time in order to assess the possible influence of the 1994 In Trust Agreements on germplasm demand. The proposed theoretic model motivates the realistic hypothesis that the consequences of the In-Trust Agreements lead to an enhancement of CGIAR germplasm utilization. Therefore the paper firstly examines the classical literature on biodiversity's valuation and its recent developments and subsequently it investigates the origin of the agricultural biodiversity's economic value, providing a basic conceptual framework to infer on factors determining the demand for germplasm. Two Bayesian estimation frameworks are applied to the IRRI accessions distribution's time-series to provide formal evidence to the hypothesis, exploiting Markov Chain Monte Carlo methods, Gibbs sampling in particular. Evidence suggests that the demand variation implies a change in the genetic collections economic value, impacting therefore on their direct use search value.

Keywords: Crop genetic resources, germplasm collection, search theoretic framework, count data, changepoints.

[JEL codes: O19, Q18, Q57, C11]

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1. INTRODUCTION

This paper has three purposes. The first is to develop a theoretical framework through which it is possible to derive the demand of genetic resources and explain how it is affected by the demand's factors. The second is to examine the hypothesis that the In Trust Agreements had an impact on the availability and therefore on the economic value of the CGIAR germplasm held In Trust as a result of the signed agreements. The third purpose is to conduct formal investigations on factors affecting germplasm demand, testing the assumed hypothesis on the agreement's effects throughout the utilization of econometric frameworks.

The study's background is the conservation, use and exploitation of plant genetic resources (PGRs). Nowadays crop genetic resources are considered as an indispensable humanity's agricultural heritage. In the recent past, genetic erosion and cultures homogeneity's issues rose. The destructions of natural ecosystems and the incessant spread of high yielding cultivars began to deteriorate agricultural diversity. Agricultural biodiversity is defined by FAO (1998) as the key element of food and livelihood security improvement, assuring rural development and environmental sustainability as well as establishing the basis for future technological innovations in agriculture. Crops' genetic improvement in fact has assured considerable productivity gains in agriculture: nearly the 50% of the U.S increased yields during 1930-1980 has been attributed to genetic resources by recent studies (Johnson *et al.*, 2003). Since the 1960s the increase utilization of genetic resources has promoted a multilateral international collaboration between countries and International Agricultural Research Centres (IARC) to exchange genetic resources and breeding new varieties: 50 members countries and donor agencies established in 1972 the Consultative Group on International Agricultural Research (CGIAR), worried by the common apprehension that many developing countries would lose soon their agricultural resources and plant diversity.

PGRs for food and agriculture are today mainly stored in ex-situ collection (genebanks) through several laboratory methods. Genebanks constitute the more accessible and inexpensive source of PGRs, gaining plant breeders' preferences especially thanks to the evaluative information attached to each germplasm sample (Fowler *et al.*, 2000). Latest discoveries in plant breeding methods and especially in

genetic engineering have further increased the value of ex-situ genetic collections. IARC carries out frequently research on new ways of utilization and screening of the valuable traits, commercializing cultivars and recombinant breeding lines, assigning directly great economic value to the resources. To illustrate the importance, FAO (1998) statistics refer to almost 6 million of crop accessions collected by nearly 1400 genebanks worldwide located.

The recent intellectual property rights' international debate involved also the germplasm held by CGIAR centres. The political debate on the ownership of the PGR held in the CGIAR genebanks resulted in the establishment of In Trust Agreements between FAO and the CGIAR Centres in 1994 that formalized the legal status of "public goods" of the ex-situ germplasm held by CGIAR genebanks. Since 1994 more than 600.000 accessions stored in the 11 CGIAR genebanks, are held "In Trust", "for the benefit of the international community", practically freely available, according to the agreements. Furthermore the "In Trust" collections are highly diversified, well organized and documented, and for these reasons they are largely used worldwide, especially by developing countries (Fowler, 2000). An impressive economic value, but presently unknown, is probably associated to a resource so much used and with so large potential use: thus several motivations occur to investigate genetic stocks demand and to infer on the economic value associated to their utilization.

A search theoretic framework is chosen to model the genebanks samples demand with the scope to assess the infer of the In Trust agreements on it and their economic consequences on the genetic resources' value. Some econometric models will be proposed to face the statistical change-point's problem, with the prospect to individuate the effects of the In Trust protocols on the samples demand. The data utilized have been provided by IRRI. Firstly, a generalized linear Poisson model specific in the change-point investigation is applied. Secondly a Gaussian linear model is adopted, extending the model to handle count data, and exploiting dataset characteristics with a single-layer hierarchical setup. The proposed procedures for conceptual and empirical evaluations can be applied to prove other hypothesizes, assessing any factors determining germplasm demand, investigating therefore their contributions to the economic value of plant genetic resources.

2. THE ECONOMIC VALUE OF PLANT GENETIC RESOURCES

The economic value of the In-Trust Agreements lies in the value of the collections that are kept in trust in CGIAR genebanks. According to Ehrlich and Wilson (1991), a biodiversity resource should be valued by considering its ethical and aesthetical aspects, the direct economic benefit, and recognizing its role as the natural provider of several ecosystem services. The human race being the undiscussed ruler of the earth has a moral absolute responsibility in the preservation of all species living. Furthermore there is an effective consumers' demand for the biodiversity preservation for its aesthetic characteristic as estimated by numerous studies using revealed preferences techniques on the willingness to pay for wild-life regions' preservation (see for example the studies of Kramer and Mercer, 1997, Jakobsson and Dragun, 2001 and Barnes *et al.*, 1999) or to avoid animal extinction (Cicia *et al.*, 2003). The direct economic benefit derives from the biodiversity's characteristic to be a "genetic library", thus helping new crops breeding and being the source of new industrial or pharmaceutical products. The reason, enunciated lastly by Ehrlich and Wilson (1991), is nowadays being more considered by public opinion: different living organisms form the natural ecosystem and an alteration of its constitution because extinctions or indiscriminate humanization or taming of wild area, may cause atmosphere's alteration, impacting on climate changes, aggravating undefined social costs.

Economic theory helps us fixing the criterions to assign an absolute worth to a complex good such as the biodiversity. The Total Economic Value (TEV) framework has been used largely in natural resources economic literature and applied to biodiversity valuation for the first time by Pearce and Moran (1994). Even if the exact terminology may change among the studies, TEV scheme identifies three primary valuations of natural resources, which jointly constitute the total value measure one may attribute to the genetic resource stock. As notes by Smale and Koo (2003), the main values consist of so-called 'use value' (UV); 'non-use value'; (NUV) and 'option value' (OV).

Use Value may be sub-divided into categories describing direct (DUV) and indirect use value (IUV), whether conferred benefits are clearly observed when the resource is consumed. Direct use includes the value of the consumptive uses, deriving directly from the material consumption of the good and the value of non-

consumptive's uses that refers to the benefits of activities such as recreational that do not require a persistent alteration of the products. Indirect use value covers all benefits originated from the resources' services and their secondary functions. Use value embraces present use value and expected future use value, as well as the value of maintaining the possibility to meet some unknown, future event or potential use — called option value (OV).

Non-use value, also measured in both present and future terms, refers to the consumers' benefit gained as a result of the simple existence of the resource, its so-called existence value (XV). This value is otherwise called Bequest value (BV) if the worth is derived from the knowledge that others can instead use the good.

Other economists cite the 'quasi-option value' also. They refer to the value to conserve a known low option value, waiting for new information that can change irreversibly the scenario. On the subject, Swanson (1998) includes the quasi-option value to the total economic value of plant genetic resources, mentioning the value to preserve a known poor value variety with the scope to use it in the rare event that the particular disease occurs.

In these contexts, estimation of the value of PGRs is a difficult task. This assignment is further exacerbated given the multidimensional and inter-temporal natures of germplasm stocks. A direct evidence of the value for each element in the PGRs total economic value is absolutely more difficult to account than the value of other goods that benefit an efficient market. The peculiarity of natural reproducibility of the good, the impossibility to clearly establish the property rights and to identify distinctly the beneficiaries intensify the public good characteristics of PGRs, making the economist task worse.

As Pardey *et al*. (2001) stress, to attribute the right agronomic gains to the conserved germplasm used in a crop production system seems empirically highly problematic. If during experimental yield trials the agronomic gains associated with the introduction of a variety causing higher crop production or less tilling costs may be quite easily observables, in the open field several components can interact with each other, enhancing or thwarting the effects, making hard to separate the productive gain deriving the breeding activity from new agricultural adoptions and climate and soil particular characteristics. In the absence of any market for unimproved genetic

resources, value cannot be measured directly. This is why, according to Pardey *et al*., methodologies developed so far are mainly unreliable. Furthermore to separate the human capital's effort from unimproved genetic resources' contribution in the breeding and genetic selection activity is seldom possible. For the above reason, many authors prefer simply to focus the study on the "genetic enhancement" valuation (Rubenstein *et al*., 2005). Lastly the individual production's gains have to be aggregated successively to the industry level, considering the global impact on the producers and consumers of other crops and other countries too, accounting for all possible externalities, in order to evaluate fully the social surplus deriving by the introduction of a genetic improvement.

When the market price is unavailable, intellectual fashion suggests applying direct methods to elicit consumer preferences. Direct methods are so used largely in the economic valuation of environmental resources. In the PGRs' case, a survey's efficacy, based, for example, on willingness to pay (perhaps elicited through contingent valuation or a choice experiment), is reduced by the subject matter's scientific complexity (Smale and Koo, 2003). As Evenson and Santaniello (1998) state, contingent valuation methods seem more applicable to value consumers' goods rather than production inputs because respondents have difficulty comprehending PGRs production functions and attendant difficulties assigning subjective value to their inputs.

According to Smale and Koo (2003), PGRs 'non-use value' estimation appears trifling: the conservation activity of a genebank implies an effective present or future use. At the same time, PGR 'option value' refers to the expected future value of a completely unknown benefit. Because of this strong uncertainty characteristic, estimation of non use value is beset with difficulties and it is highly challenging. Furthermore, because option value is likely positive, the total PGR value is usually underestimated by analysis employing market prices and quantities. Furthermore, analytical approaches employing these market derived variables are intrinsically ineffective in capturing a non-marketable economic value. Similarly, evaluation of a marginal accession requires 'significant expense in time, talent and money' (Pardey *et al*., 1999). Also, such estimation, when enacted, generally underestimates the total value of the resources' stock because the material is often used more than once, in

subsequent breeding efforts, at different times and in different places (Rubenstein *et al*., 2006).

An antithetical approach with merit performs cost evaluation of collecting and conserving accessions. Studies by Pardey *et al*. (1999, 2001) and Koo *et al*. (2003) cover this estimation option. The objective is to elaborate a conservative evaluation of marginal accession costs, in order to justify germplasm conservation, if the costs result generally less than the potential benefits conferred. Studies by Pardey *et al*. (1999, 2001), exploit microeconomics concepts in order to extract marginal accession costs, and calculate the amount of the endowment necessary to ensure endurable future conservation for the genetic materials held by the CIMMYT genebank. The same methodology is applied later by Koo *et al*. (2003), to value the resources held by CGIAR genebanks. The investigations highlight the insignificance of the costs of holding resources compared to the present and future potential benefits available.

Several recent empirical studies focus estimation on the use value of PGR stocks through the benefits of breeding acquired by improvement of crop varieties on agricultural productivity, or on cost reduction. Hedonic pricing approaches, and production functions analysis methodology share this common principle (Milne *et al*., 2002).

A hedonic approach exploits a resource's marginal value through regression estimation of the explicit price of the tradable product on the implicit prices of a non-marketable good's attributes. The same principle has been applied by Evenson and Gollin (1998) to link the Indian rice productivity of several regions with the peculiar characteristics of the genetic material adopted in each location. According to the results, the varietal improvements account for more than one third of the total rice productivity gains achieved during the period 1972-1984. Furthermore the contribution of certain PGRs' stocks in the rice productivity in India result quite high, nearly $74 millions per year overriding largely maintenance and operative costs of the germplasm collection, 10$ millions per year.

Production function analysis has been used by Evenson and Gollin (1997). They evaluate the economic role of the International Rice Research Institute (IRRI) in improving rice cultivars. IRRI's activities include germplasm's collection and exchange, and direct supply of bred varieties to farmers. A genealogical analysis has

been conducted to highlight progenitor traits in 20 improved modern varieties. IRRI's global economic impact is estimated through an econometric analysis directed to determining the contribution of accessions to the average value of modern rice varieties. With conservative assumption on the discount rate, the provided estimations are impressive: over a period of 20 years the whole IRRI impact is around $1.9 billion. Moreover the present value of a single accession implemented succesfully into a modern variety is also estimated to be nearly $50 millions, meanwhile 1,000 catalogued accessions are accounted for $325 millions. Other examples of this approach are available from the literature. One noteworthy is Smale *et al.* (1998) who analyze the impact of the PGRs in enhancing agricultural productivity, reducing production fluctuations and affecting cropped variety diversity in wheat production in the Punjab, Pakistan. Genetic resources and diversity data are assembled and their marginal contribution to production is estimated through use of the Just and Pope stochastic production functions. Thirtle (1985) valuates the share of the 'biological change' including the genetic enhancements, in the production of five major U.S food crops during the period 1939-1978. The author, nesting CES and Cobb-Douglas production functions, infers that the biological component has assured a yield improvement in average of 1% per year, nearly the 50% of the total yield growth observed.

3. THE DEVELOPMENT OF THEORETICAL MODELS: INVESTIGATING GERMPLASM DEMAND FACTORS

This paragraph has the objective to present some of the most renowned conceptual models published in the literature on genetic resource stocks' valuation. The scope is to review the theoretical foundations of bioprospecting and genetic resources economics, attempting to assign mathematical rigour to the follower empirical application. Furthermore, any judgement and valuation, also economic, on preservation of biodiversity, genebanks management, and bioprospecting, need an analytical simplification and efficacious model helping to infer on. The complexity of the subject infact leads sometimes to a generalized confusion. The several conflicting motivations and the different values involved during the decision-process exacerbate further the situation. Although strong assumptions may sometimes imply diverse consequences among different theoretical framework. Three conceptual models will be

so briefly discussed and lastly a simple theoretical framework will be developed. It is based on the *search models*, which appear most efficacious and suitable given available data and paper's aims.

Valuing option value, Polasky's theoretical model

The *Polasky's theoretical model* (Polasky *et al*., 1993, Polasky and Solow, 1995) is based basically on two assumptions. Firstly, the motivations to conserve species are essentially related to its uncertain potential value to provide in future some benefit (a medicinal cure for example). Secondly the phylogenetic closeness makes the species substitute for each other, because the relative similarity of their genes. For the above reasons decisions on species conservation have to be assumed valuing their potential value first, and so precisely focusing the attention on the option value and then preferring more heterogeneous set of species to less. According to the author, considering other sources of value in the decision process is quite useless: species with a recognized direct use value benefit already survival's possibility thanks to the market. However the author highlights that direct valuable species can influence, because of their gene pools, the option value of the other species too.

$T = (s_1, \ldots, s_n)$ is the set of species under investigation, while S is the set under conservation. C is the potential benefit, P(S) denotes the probability that the S set has C. The option value to conserve the set S is simply:

(1) $\quad B(S) = CP(S) = CP(S, T) \, P(T)$

where P(S,T) is the conditional probability that S contains the potential benefit given that T contains it: P(S, T) can be interpreted as a diversity measure, introducing in the calculation of the conditional probability, a coefficient that considers the relative diversity genetic of S in T through specific spatial measures.

The Polasky framework is innovative mainly for introducing in the genetic stocks economic value directly a measure of genetic diversity. The measure is then linked to the probability to gain a benefit, the basis of bioprospecting problem, retrieved also by the *search* model. The result is a model that even though seems appropriate to valuing collection of species like a genebank, it results lacking in the cost of searching valuable traits.

Modelling extinction risk, Weitzman's Ark

Noah's Ark problem is the fascinate metaphor name used by Weitzman to call his simple analytical framework in biodiversity economic issue. The author in several works (Weitzman, 1993 and 1998, and Metrick and Weitzman, 1998) investigates the problem of biodiversity's preservation, with the aim to derive criteria or priorities to follow in the decision process for the choice of the conservation strategy. The model has its roots in a simple constrained optimization problem wherein the biodiversity appears in the objective function: for *n* available species, indexed $i = 1,2,...,n$

$$(2) \qquad\qquad \text{maximize}_{\{Pi\}} \ [W(\{P_i\}) + U(\{P_i\})] \ ;$$

while the constraint is represented by a budget function including the costs to increase for each species *i* the probability of surviving; practically the cost to involve it in a conservation, preservation program. Under the budget constraint, the problem is solved selecting values of $\{Pi\}$, the probability that the *i* species survives, maximizing the sum of the '*expected direct utility function*' $U(\{P_i\})$, approximately the total economic value of the *i* species preserved, (the author refers to a "combination of commercial, recreational and, emotional benefits") and $W(\{P_i\})$, called by Weitzman the '*expected diversity function*', representing the genetic diversity of the species *i*, related to the information content in the hold genes. The '*boarding Ark*' allegory becomes so easily comprehensible: investing in a conservation project improves the probability of survival of the selected species, but since the *Ark* has a limited capacity, the optimization routine set the priority species. From the maximization problem, the author derives also an easy formulation in order to give an effective ranking criterion.

$$(3) \qquad\qquad R_i = [D_i + U_i]\left(\frac{\Delta P_i}{C_i}\right);$$

where for each species *i*, U_i is the direct utility, D_i the distinctiveness, C_i the cost to improve the survivability of ΔP_i, while R_i is the monetary-diversity measure.

Noah's Ark theoretical framework points out several useful remarks in the economics of genetic stocks' discussions. These features make the model especially suitable to minimization of biodiversity loss problems as some practical applications prove. Specifically, Simianer *et al.*, (2003) and Reist-Marti *et al.*, (2003), exploiting the *Ark*, provide successfully indication on preservation of cattle breeds programs.

Practically the authors verify some difficulties assigning arbitrarily probabilities value reporting furthermore that the observed ranking criterion is more affected by diversity genetic than extinction's risk. Infact as reported by the same Weitzman, the maximization routine may suggest 'counterintuitive' actions: 'sacrificing' one high risks extinction species, deciding to increase the protection of the safer one. Even if the Weitzman's framework performs well for decision-making process, the provided formulation does not allow to investigate either an economic value of biodiversity, (the objective function is expressed in a diversity-monetary term) or to explain correctly genetic stock users demand and crops' genebanks management. The two above frameworks share this problematic. It is known infact that the principal aim of ex-situ conservation of the plant genetic resources is prevalently addressed, satisfying plant-breeders needs, to sustain agricultural productivity growth, to reduce biotic and abiotic crops' vulnerability. The diversity genetic is a value that in the PGRs case is quite misleading: world's largest genebank is generally specialized in a small number of species, preferring to maximize intra-species and not inter-species diversity. They infact constitute huge collections of the same species, facilitating in term of reproductive reasons the breeders' activities. Hence the effort to build the phylogenetic structure of the species hold in the genebank does not seem to reward a theoretical improvement of the conceptual model, at least for this work's purposes.

Searching for a direct use value, the literature

Search-theoretic frameworks attempt to simulate the stochastic nature of breeding research and the successes and failures that they experience. When the probability of failure is non-zero, search must be conducted in order to determine whether particular genetic traits may be useful. Thus the search process may be time-consuming and costly because all the activities required for the trait evaluation such as molecular screening or agronomic tests (set by Zohrabian *et al*., 2003, at about 7$ per accession, per a single trait), in addition to the acquisition-transaction costs. This aspect of the research enterprise is worth emphasizing because often the germplasm stored in public genebanks lack detailed information concerning genetic characterization and the likelihood that a single accession will be useful. In addition, breeding outcomes can be quite unpredictable because of the unpredictable nature of genotype environment interactions. The *search* methodology assigns a present value to the expected future benefits of the research activity wherein benefits are compared to

costs in order to optimize the search activity. In the PGRs specific case, the probability of discovering a valuable trait during the search process is combined with its expected yield enhancement effects in order to evaluate the worth of a single germplasm accession. Seminal work of Evenson and Kislev (1976) gave impetus to several studies in valuing genetic stocks through this approach. That methodology, which is the first apply search theory to genetic resource evaluation, has roots grounded in a classic paper by Stigler (1961) who models consumer demand when a consumer, facing a price proposition, has uncertainty as to whether it is a minimum among possible alternatives. It is worth mentioning that this basic idea of Stigler (1961) spawned a vast growing literature related to job search, unemployment and related macroeconomic phenomena. An introduction to *search* formal analysis is contained in Sargent (1987), meanwhile Rogerson *et al*., (2005), present a recent literature survey on the subject. In the genetic resource Evenson and Kislev (1976), consider sugar-cane varieties' discovery and model search within a distribution of the genetic trait – the random variable of interest – and assume that research effort can shift the mean of the distribution, change the variance or generate new distributions when new technologies are discovered. In their context it is possible to determine an optimal search strategy, and evaluate the impact that a gene stock might have, at least conceptually.

A subsequent application by Gollin *et al*. (2000) extends the basic idea that search, which is costly, generates potential benefits and that these benefits have probability distributions attached to them. By exploiting the basic principle that marginal cost of an accession search should never exceed the marginal expected benefit that it generates, the authors simulate a search process and conduct Monte Carlo experiments, drawing probability distributions for the 'useful' trait from the Monte Carlo simulations. Gollin *et al*. (2000) evaluate the optimal size of a 'search' for a genetic trait, judging the usefulness of large collections characterized by low utilization, modelling the search for a resistance trait in wheat germplasm. Significantly, they note that a genebank's existence value is justified, despite possible infrequent utilization whenever maintained traits are rare and economically relevant. Of course, determining the latter is sometimes very difficult, given the data constraints that typically occur. Notwithstanding this feature of the data-generating environment, *search* theory has inspired several noteworthy recent contributions. For example with reference to crop breeding, Zohrabian *et al*. (2003) estimate the marginal value of the

genetic material held in the U.S. National Plant Germplasm System. The genesis of their work is the common denominator in the contributions exploring search, namely the notion that search, which is costly generates potential benefits. Exploiting this notion, they employ maximum entropy methods to estimate research success probabilities of discovering the trait for resistance to soybean cyst nematode. Data on soybean prices and area planted are used in order to evaluate present value of the benefits deriving from search. The paper is highly appreciated reporting in details main average costs concerning the acquisition (340$ per accession), conservation (185$ per accession, per year) and evaluation (7$ per accession, per trait) of the genetic stocks. The authors lastly determine that even so the accessions marginal values are low, largely outweighs their costs of maintenance.

Along similar lines, Simpson *et al*. (1999) assess the probability for a marginal species to be used in a commercial product for pharmaceutical purposes. They consider the search process as a sequence of Bernoulli trials in which the outcome is a discretized random variable assuming one of the two results, namely 'success' or 'failure'. The Bernoulli distributions well adapt to simulate the search for both qualitative (discrete) and quantitative genetic traits. Even if the characteristic of the quantitative traits is a continuous outcome, to impose a threshold value adapts them easily to a Bernoulli trials, 'success' if the value exceed the threshold, 'failure' otherwise. They use their model to assess the marginal economic value of a single 'species' hold in-situ. The authors conclude that, in general, genetic resources stocks are characterized by low value and diminished attractiveness for pharmaceutical purposes.

4. SEARCHING FOR A DIRECT USE VALUE, THE MODEL

The model here proposed (Gotor *et al.*, 2007) aims to describe the principal characteristic of the search process: choosing the best outcome from a set of random trials. The model attempts to simulate the researcher action of locating the genetic material stored in a gene bank that offers the maximum return for the desired trait, such as disease resistance or yield productivity enhancement. Each trial is an agronomic test or a genetic screening of a single accession requested from a genebank. In other related *search* works, for example in Zohrabian *et al*. (2003), the most desired

return is associated with the minimum. Simpson *et al*. (1996) instead set the necessary condition that the desired value is simply over a prearranged threshold. Let $x_1, x_2, x_3,$ … x_n denote the quantities obtained from N successive accessions or searches for the trait, and assuming that the quantities are random variables, distributed according to a given probability function with density *f(x)*. Furthermore the trials are supposed to be independent of each other. If N denotes the number of the accessions, N^* is the optimal number of accessions that maximizes the research process's objective function. The form of the objective function assumes so a primary interests, driving researcher behaviour, to imply subsequent empirical developments and theoretical considerations. For the above reasons, attempting to impose assumption less restrictive as possible, the objective function is arranged to be simply constituted by an expected benefit from the outcome of the search process, and by the costs occurred during the search process. Imposing $y_N \equiv \max\{x_1, x_2, .., x_N\}$, with y_N clearly function of N, the selection of the optimal level of $N = N^*$ is determined by the solution to the following maximization problem:

$$(4) \qquad \max_N \Phi(N; \cdot) \equiv E\{U[Benefits(y_N) - Costs(y_N)]\},$$

where U[·] denotes utility derived from search process, Benefits (y_N) is the benefit function that describes completely the gains obtained from locating y_N, the maximum among the N accessions, and Cost (y_N) is the costs function that include the costs incurred in seeking the trait. For simplicity it is assumed that both benefits and costs are linear in y_N. The benefits function can assume so the form Benefit (y_N) $\equiv \alpha \, y_N$, with $\alpha > 0$ and equal to the benefits that the researcher receives for each successful realization of the N trials. In the same way the costs function is supposed to have the form Cost (y_N) $\equiv k\,N$ with $k > 0$, and representing the unit constant cost to perform each search and screening exercise, with k N evidently equal to the total cost of screening of N trials. The utility derived from transacting N accessions is therefore:

$$(5) \qquad U[\cdot] \equiv \alpha \, y_N - k\,N.$$

To investigate the actual form of the objective function and proceed to model the demand for accessions, namely the optimal value N^* chosen by the researcher, it is necessary to know the form of the distribution *f(x)* and so how the outcomes of the research $x_1, x_2, .., x_N$ are distributed. In this regard, Gollin *et al*. (2000) stated that the

traits are distributed in the set in several ways. Although normal distribution roughly fits quantitative genetic traits such as crop's yield or height, generally traits for biotic resistance or abiotic tolerance follow uncertain patterns. This work follows the Stigler basic model, (1961). To simplify essentially the computations the unknown outcome of the trials is assumed to be a continuous random variable, on the standardized interval [0,1]: the function assumes 1 if $X \in [0,1]$ and assumes the value zero, otherwise.

As explained before this assumption is not fully realistic, but considering the purpose of this work, it allows to make some further deductions facilitating the computation task. Maintaining the assumption, it is possible to derive from the probability distribution function $f(x)$ the cumulative distribution $F(h) = \int_{-\infty}^{h} f(x)\,dx \equiv \wp(x \leq h)$, that in the case of the unit uniform distribution become $F(h) = \int_{0}^{h} 1\,dx = h$.

To locate the maximum among N possible trials is necessary to look up the problem of defining a distribution function for the maximum. This problem is highly simplified principally thanks to the assumption that the originating distribution $f(x)$ is standard uniform. Following the *order statistics* theory, the first step to locate the maximum is to derive the *cdf* corresponding to the maximum within the sample: $F_{yn}(y) = \wp[\,y_N \leq y\,] = \wp[\,x_1 \leq y;\, x_2 \leq y; \ldots; x_N \leq y\,]$. Considering the trials independent from each other, then $F_{yn}(y) = \Pi_i\, \wp[\,x_i \leq y\,] = \Pi_i F_{xi}(y)$. If the draws are made from the same distribution, as it happens, $F_{yn}(y) = F_x(y)^N$. By differentiating is possible to obtain the *pdf* associated with y_N, $f_{yN}(\,y\,) = N[\,F_X(y)]^{N-1} f_x(\,y\,)$. Lastly benefiting that the originating distribution $f_x(\cdot)$ is standard uniform, $f_{yN}(\,y\,) = Ny^{N-1}$, naturally function of N and y. At this point is possible to obtain an explicit solution to the optimization problem (4):

$$(6) \qquad \max_{N} \Phi(N;\, \alpha,\, k) \equiv \int_{y\,\max}^{y\,\min} \alpha\, N\, y^N\, dy - k\, N,$$

where $y_{min} = 0$ and $y_{max} = 1$, because they are respectively the minima and maxima available across the support of the standard uniform distribution. Resolving the integral, the first order condition necessary that is necessary and sufficient to find the maximum is therefore:

$$(7) \qquad \phi(N;\alpha,\kappa) \equiv \frac{\alpha(N+1)-\alpha N}{(N+1)^2} - k = 0.$$

The above formula implies easily a realistic search situation: the solution of the equation, N^*, infact, increases with the increasing of α, (the benefit coefficient) and decreases with the increasing of the screening costs, k. Graphically, the first-order condition generates a solution of the form:
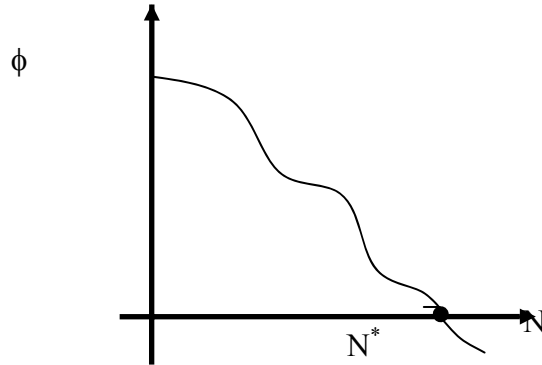
These basic concepts lay the basis for the successive considerations on the changes of the demand for the genebanks' accessions, that is equivalent in changes in the optimal value N*, because a variation of the perceived costs or benefits of accessions. For example, in the case of increased benefits, or reduction of screening costs, the demand should be boosted, and N* should perform a change of the possible pattern depicted by the following graphic:
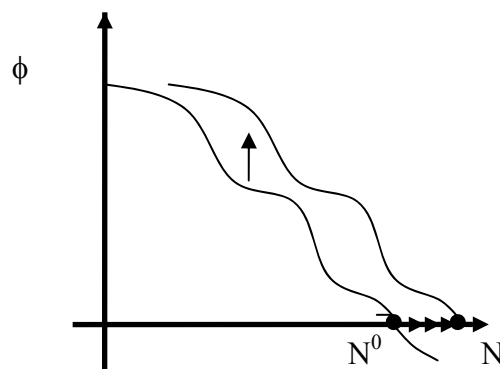
And instead, with the increase of the costs, or reduction of the outcome's benefits, a change of the form below should be observed.
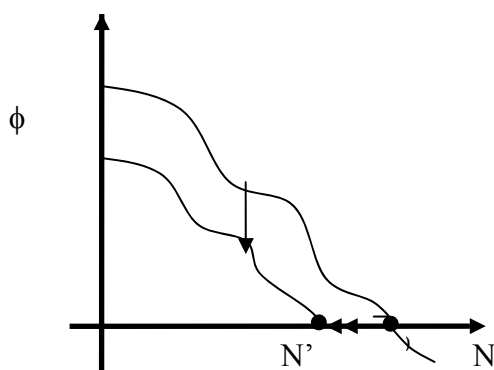
In this way, it is possible to explain changes in the demand for germplasm, considering the fluctuating pattern of the *counts data* of germplasm's accessions recorded in the CGIAR genebanks databases. Furthermore, because the CGIAR collections have a direct use value strictly related to the search process modelled here, a variation of the demand imply automatically a change in the whole resources' stock economic value. The incremented value so is caused for example by a diminution of the transactions costs associated with the reduction in effort required to screen samples, or for an introduction of an international agreement that makes the resources freely accessible. In the framework presented here, this situation is modelled credibly as a reduction in the value of the parameter k that reflects, as said before, the per-unit cost of each single accession. Consequently, the relative contribution of establishment and the enforcement of the *In-Trust* Agreements, among the other factors' demand, is expected be positive, reducing the k term, causing an increase in the search activity, implying so a higher number of accession or N* in the terminology adopted here.

5. ASSESSING THE IMPACT OF THE *IN TRUST AGREEMENTS* ON GERMPLASM DEMAND

In this paragraph empirical applications will be provided, in order to give statistical evidence of the *In-Trust* influence on the genetic stocks' demand. As described above, the favourable impact of the agreements on the availability and utilization of *In-Trust* material is the main hypothesis to prove statistically. The immediate impact of the In-Trust Agreements is on lowering transaction costs of germplasm's accessions exchange, because the agreements assured a clear legal status (freely available) to the genetic resources, removing the uncertainty regarding property

rights of the resources that characterized the period immediately after the Convention of Biological Diversity's enactment (1993). Therefore thanks to the agreements, the demand for "*In Trust*" PGR should be relatively enhanced, increasing the genetic stocks direct-use value (*search value*), and consequently providing an economic improvement of the CGIAR collections' value.

Two are the empirical models selected to investigate the hypothesis. The Chib's changepoints framework (1998) with latent state variable is chosen because it is explicitly formulated to assess count data changepoints, and so particularly qualified in estimation process without the inclusion of other covariates. Secondly, the Gaussian hierarchical count regression model, although its simplicity, is used to exploit the information provided by the hierarchical characteristics of the dataset. The estimations are conducted including data on genebanks utilizations and acquisitions provided by IRRI database.

Data Description

Prior to consider the empirical frameworks we present a broad overview of some of the data made available to us from IRRI genebank. The International Rice GenBank Collection (IRGC) at IRRI comprises the largest collection of rice germplasm held In-Trust for the world community. In fact, out of 111,631 accessions collected since 1961, 97,651 (87.5%) are In-Trust whereas 13,980 (12.5%) are not In-Trust. More than 102,861 accessions belong to Asian cultivated rice (Oryza sativa), of which 92,040 (89%) are In-Trust and 2,809 accessions are from African cultivated rice (Oryza glaberrima), 1,201 (43%) of which are kept not In-Trust. IRRI maintains records of breeding pedigrees of all modern rice varieties derived from mating traditional varieties.

Until the 2007 IRRI genebank distributed approximately 340,000 accessions. The overall distribution trend change significantly over time as shown in figure 5.1. The 1991 peak is followed by a constant diminishing of distribution numbers that ebbs and flows, but generally follows an upward-increasing trend after 1997.

Figure 5.1: IRRI overall germplasm distribution, 1983-2006
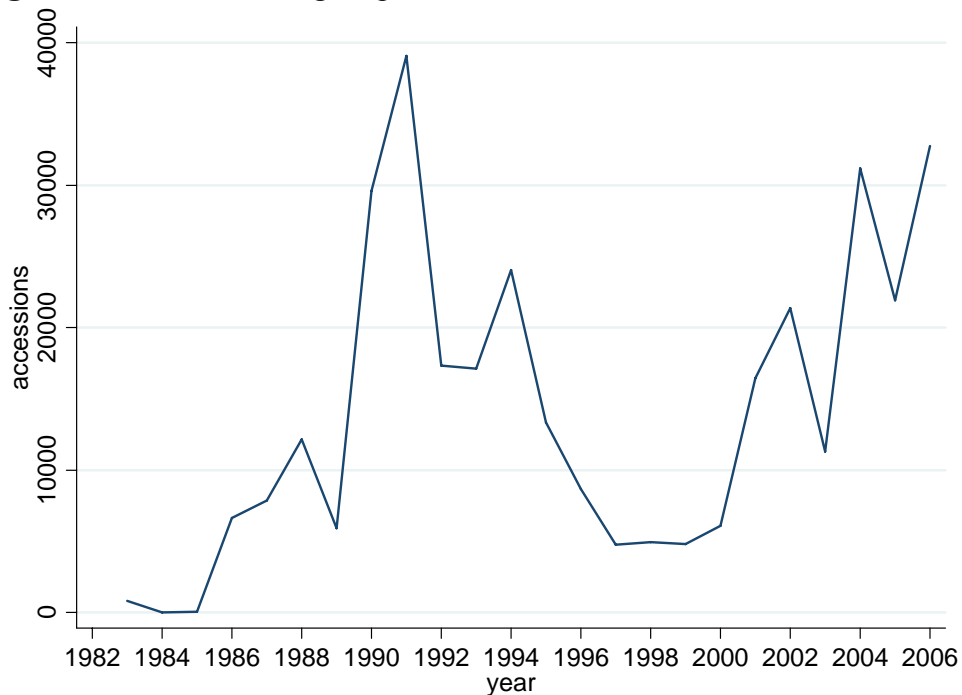
Dividing the overall flow, according to the different types of germplasm requests (within IRRI or outside IRRI), purposes (for research or other purposes as characterization and restoration), users' organization (Universities, genebanks, privates or other CGIAR centres), and legal status of the requested germplasm (In Trust, or Not), (figure 5.2) it is possible to highlight a possible effect of the agreements adoption, providing a benchmark for further enhanced empirical enquiry.

Fundamental in this regard is the movements around the time that the *In-Trust Agreements* were enacted. There are some indications of a "switch" around the time that the agreements were signed for the "In-Trust" accessions especially for "research" purposes. Of course, attributing such a switch to a single event – admittedly the focus of this review – would be nonsensical. However, the flow lines serve to motivate a juncture for considering additional detail, and accompanying them, the types of problems that one encounters in considering the possibilities of using accessions like those availed by the IRRI database to shed more light on the issue concerning trends and their relationship to various agreements alleged to have impact.

Figure 5.2: IRRI germplasm distribution for selected sub-categories. 1983-2006, (*standardized*)
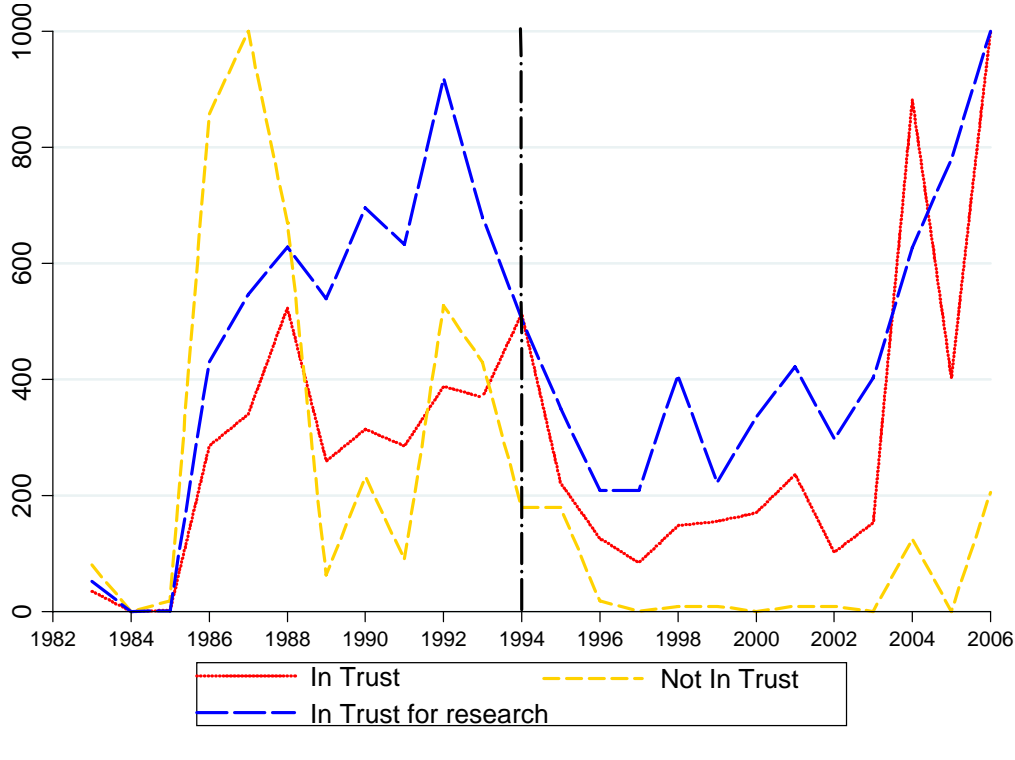
The broader empirical and methodological issues concerning formal statistical analysis of accessions counts are analysed in the next session.

Multiple changepoints with latent state variable

The Chib's approach (1998) to model multiple cases of change-points is proposed in this paragraph. The main innovation introduced in the framework, is the analysis of the change-point's problem through the use of an unobserved discrete state variable that marks the possible phases into which the sample is split: furthermore this formulation makes the model not restricted to the existence of only one change-point. The counts data are modelled through a hierarchical Poisson relation:

$$(8) \qquad f^P(y_t|\xi_t) \equiv \xi_t^{y_t} \exp\{-\xi_t\}/y_t!$$

wherein y_t denotes the count in the year t; the density of y_t is function of the parameter ξ_t. The value of ξ_t changes at unknown time points, $\Gamma_m = \{\tau_1, \ldots, \tau_m\}$, (Chib, 1998). In a two times changepoints model, for example, $\Gamma_m = \{\tau_1, \tau_2\}$, ξ_t is assumed to be subjected to two breaks, one at time τ_1 and another at time τ_2 such that $\xi_t = \lambda_1$ for $t \leq \tau_1$, $\xi_t = \lambda_2$ for $\tau_1 < t \leq \tau_2$ and $\xi_t = \lambda_3$ for $\tau_2 < t \leq n$, where $\tau_1 > 1$ and $\tau_2 < n$. The estimation effort is focused on the vector of the parameters λ, and on the unknown change points Γ_m. In order to reach the objective, Chib introduces in each period latent class data, s_t,

referred to as the 'state' of system at time t, corresponding to the m+1 phases in which the samples can be split. In details, $s_t = k$, means that the observation y_t is drawn from the distributions $f(y_t|Y_{t-1}, \theta_k)$, where Y_{t-1} represents the observations up to time t-1, and θ_k the parameters marking the state k of the system. This latent state variable is formulated in the way to evolve according to a discrete-time, discrete-state Markov process with the transition probability matrix, $\wp$, forced so that s_t either remains at the current value or jumps to the next highest value (Chib, 1998). Each elements of the jump probability matrix ($\wp$) denote the probability of moving to regime j at time t, given that the state at time t-1 resides in regime i: $p_{ij} = \text{Prob}(s_t = j|s_{t-1} = i)$. The objective of the estimation is the posterior density $p(S_N, \boldsymbol{\theta}, \wp|Y_N)$ defined over the quantities $\boldsymbol{\theta} \equiv \{ \theta_1, \theta_2, \ldots, \theta_{m+1} \}$, the jump matrix $\wp$, and S, the unknown class of states, $S \equiv (s_1, s_2, \ldots, s_N)'$. The derivation of the general forms of conditional distributions, the application of the Gibbs sampler algorithm with the right sequence of drawn are well explained in Chib, 1998 and Chib, 1996. Furthermore this model can be extended, to include additional data, replacing the determining parameters λ with sample information through the multiple $\mathbf{x_i'}\boldsymbol{\beta}$, attending carefully to the precise locations and scales of the elements of $\boldsymbol{\beta}$.

The above algorithm is used on the IRRI dataset previously described and used for the Gaussian count hierarchical model. The estimation is executed imposing only one change-point in the time-series of the IRRI distribution of samples, focusing on the samples demanded outside IRRI genebank, for *research purpose*, benefiting the *In-Trust* status: we focus on this sub-category because according to the figure 5.2, it seems to be affected by the In Trust Agreements effects more than other categories. The MCMC algorithm is implemented with 10,000 iterations, (with commands executed in MATLAB 7). The posterior means for λ_1 and λ_2 as showed in figure 5.3, are respectively 3275 and 2828. The model performs efficiently, identifying as change-point the period t = 13, occurring at the point of intersection of the two probabilities of *st* corresponding to the year 1995 (figure 5.4). The change-point marks the beginning of a new rising trend of the distributed germplasm (figure 5.2).

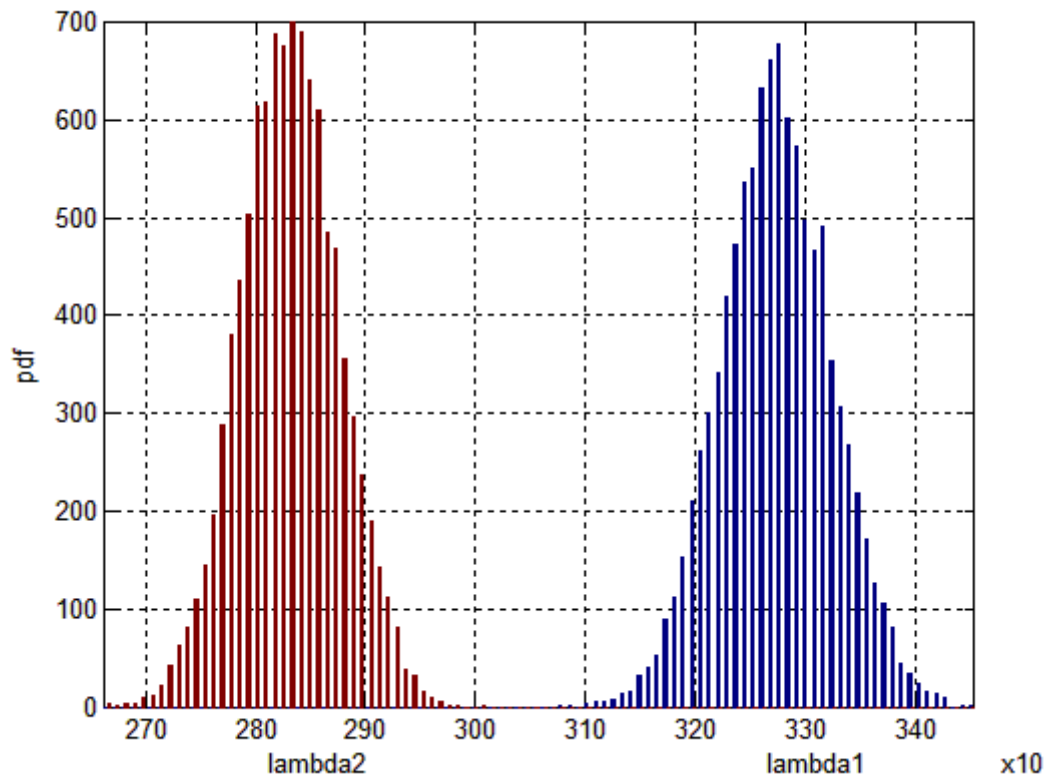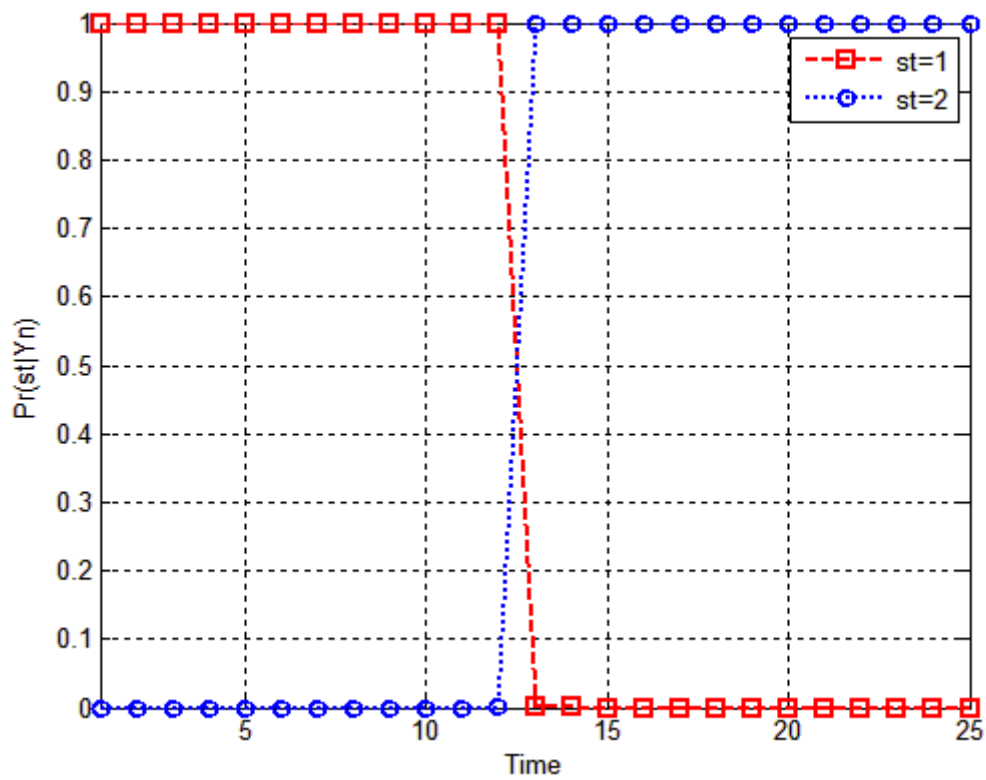**Figure 5.3:** Posterior marginal densities of λ_1 and λ_2

Figure 5.4: Pr(st = k | Yn), Germplasm demand dataset.

As said before it is not possible to attribute such changepoint to a single event, the In-Trust Agreements. This estimation outcome represents only the formal answer that is possible to give now with the current available data, without including in the model any possible covariates. But the model presented here can be extended to include further information. It is possible to account other factors affecting the germplasm demand, making the estimation effort more accurate. The following empirical framework will include other sources of information, attempting to highlight properly the "*In-Trust*" effect.

A Gaussian Hierarchical Count Regression model

The first empirical framework under investigation is simply an adaptation of the normal linear regression model, characterized by both a latent variable and hierarchical regression setup. Main reference's source of this model's structure is represented by Holloway, Barret and Ehui (2001) that applied it previously to model count data of stocks resources adoption among Ethiopian farmers. In detail, the model is described by the equation (9):

$$(9) \qquad z_{ih} = \alpha + \alpha_h D_{hi}^{\ t} + \mathbf{x}_{ih}' \boldsymbol{\beta} + u_{ih}, \qquad i = 1, 2, .. N$$

where $\mathbf{x}_{ih} \equiv (x_{ih1}, x_{ih2}, .., x_{ihK})'$ is the vector of covariates affecting z_{ih}, $\boldsymbol{\beta} \equiv (\beta_1, \beta_2, .., \beta_K)'$ is the relative coefficients' vector of the covariates, and u_{ih} reflects the error term, generated from the distribution $f^N(u_i|0,\sigma)$. To include count data characteristic of the dependent variable, z_i is constrained to assumed values in the interval $[j, j+1)$ if $y_i = j$; α_h represents the coefficient of the constant term, that for this work's purpose is modelled hierarchically, corresponding to each sub-component of the data. It is also convenient to account through the hierarchical components the policy the supposed changepoint effect. A fixed effect dummy in fact is added splitting practically the time-series sample in pre and after introduction of the agreements that coincides with the year 1994. $D_{hi}^{\ t} = 1$ for $t > 1994$; $D_{hi}^{\ t} = 0$ for $t \leq 1994$, with t =1983, 1984, …,2006. $\boldsymbol{\alpha} \equiv (\alpha_1, \alpha_2, …, \alpha_H)$. h = 1,2, …,12, equals to the number of the sub-components of the IRRI germplasm demand included in the estimation. The only covariate used in the previously described hierarchical setup is a simple additive trend variable which parameter β accounts the effect. In the Gibbs sampler routine each α_h is assumed to be drawn from a common distribution with mean μ and variance ω^2. For the complete

analytical discussion of the model, and for the succesfully Gibbs sampling algorithm application, see Holloway, Barret and Ehui (2001).

6. RESULTS DISCUSSION AND CONCLUSION

Table 5.1 presents the results of the estimations; the numerical values in the central column are the means of the posterior densities. Ninety-five percent highest posterior density (hpd) intervals are also given. The estimates are obtained from a Gibbs sample running for 20,000 iterations (with commands executed in MATLAB 7, adapting a previous code elaborated by Holloway *et al.*, 2001).

Table 5.1: Estimates of the hierarchical count model

Coefficient	Means and 95% intervals		
α	-60.9	12.6	192.6
β (trend coefficient)	15.0	20.8	27.6
μ (mean of α_h)	-387.1	-269.1	-197.2
ω (st. dev. of α_h)	0.5	36.1	153.3
α_1 (Not *In-Trust*)	-513.1	-306.3	-227.7
α_2(to CGIAR centres/*In-Trust*)	-528.5	-306.9	-227.4
α_3(to Genebank/*In-Trust*)	-417.8	-276.3	-186.8
α_4(to National Program/*In-Trust*)	-428.7	-279.3	-197.1
α_5 (to University/*In-Trust*)	-297.8	-225.6	-34.1
α_6 (to Other Organization/*In-Trust*)	-450.3	-284.7	-217.2
α_7 (to Private/*In-Trust*)	-371.0	-257.4	-135.4
α_8(for Research/*In-Trust*)	-296.1	-223.7	-31.85
α_9 (for Other purposes/*In-Trust*)	-445.4	-286.2	-212.1
α_{10} (*In-Trust*)	-350.5	-249.5	-114.7
α_{11} (Within IRRI/*Not In-Trust*)	-386.2	-264.7	-160.6
α_{12} (Within IRRI/*In-Trust*)	396.1	-266.0	-163.4
σ	244.6	267.6	292.3
R^2	0.55		

Overall the trend of germplasm demand is positive (β coefficient, table 5.1). The positive trend of germplasm is however affected by the constant term that is subdivided into different categories (α coefficients) relative to the utilization of germplasm in correspondence of the 1994 agreements' enactment. The mean of the all α coefficients reported (μ) is negative, demonstrating that despite the positive trend of germplasm demand over the years, in correspondence of the 1994 agreements there is a minor level of germplasm utilization. In fact from table 5.1 we can observe how certain coefficients might be less affected compare to others. So material held not *In-*

Trust (α_1) is reporting more negative results compared with those of the material held *In Trust* (α_{10}). The reason of this might be manifold and cannot be empirically demonstrated. However this result is supporting the hypothesis, strengthened by interviews conducted with key informant, that the *In-Trust* Agreements actually maintained the germplasm flow that given the CBD threats, could have gone lost. Material *In Trust* requested for conducing research (α_8) and the material requested by university (α_5) are the one that reported a less negative decrease of utilization because of the agreements. This is an important results because it is the material utilized for research purposes that have a direct use economic value more important that the one that might occur because of other utilizations. Furthermore the efficacy of the model is also proved analyzing the parameters α_{11} and α_{12}. We can not reject the null hypothesis H_0: $\alpha_{11} = \alpha_{12}$. In fact the In-Trust Agreements do not affect IRRI accession distributed within the research centre since scientists could freely use the material hosted by the centre even before the negotiations of the agreements.

In conclusion, the In-Trust Agreements, signed in 1994 between FAO and 12 CGIAR Centres, were the result of a lengthy process of protracted negotiations that had the single objective of regulating CGIAR germplasm, its acquisition and its distribution. A considerable challenge existed. This challenge was to find an agreement that could accommodate the needs of a heterogeneous set of key stakeholders. These stakeholders involved as many as twelve heterogeneous research centres, with distinct boards of trustees, distinct directorships and distinct internal infrastructures; and twelve distinct states, each with their own idiosyncratic regulations and legal infrastructures. The Agreements had also to meet the requirements of FAO Member States. The feasible solution that emerged was to apply to CGIAR collections the concept of 'trusteeship.' The key contribution of the In-Trust Agreements is that there is now an internationally recognized accord for the multilateral exchange of PGR, which in turn has prepared the ground for further multilateral agreements on PGR.

Scope exists for nuanced empirical assessments of the fundamental values we should place on collections of genetic resources stocks, such as those 'In-Trust' in the CGIAR collections. We have proposed a link between a conceptual model of search and an empirical framework from which improved understanding of the fundamental

value of genetic resources may emerge and we have itemized an agenda of data needs for this purpose.

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